

STIC-Biotech/ChemLib

140467

my

From: Myers, Carla
Sent: Wednesday, December 15, 2004 11:31 AM
To: STIC-Biotech/ChemLib
Subject: sequence search in 08/974584

Please search SEQ ID NO: 118 and provide a printout of the first 40 results

The CRF has been entered: http://expoweb1:8001/cgi-bin/expo/BioInfo/bioquery.pl?APPL_ID=08974584

Thank you

Carla Myers
AU 1634
Remsen Bldg / Rm 2E79
Mailbox: REM 2C70
571-272-0747

RECEIVED
DEC 15 2005
STIC/CHEN Division
(STIC)

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence :# _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

mis Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 20, 2004, 15:41:19 ; Search time 90 Seconds

(without alignments)
4512.017 Million cell updates/sec

Title: US-08-974-584C-118
Perfect score: 5963
Sequence: 1 MPAPRCRAVRSILRSYRE.....TALEAANPALPSDFKTLID 1132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 120 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5963	100.0	1132	2	AAW56113 Human tel
2	5952	99.8	1132	2	AAW46957 Human tel
3	5952	99.8	1132	2	AAW90251 Human cat
4	5952	99.8	1132	2	AAV28881 Human tel
5	5952	99.8	1132	2	AAV28090 Human tel
6	5952	99.8	1132	2	AAV43621 A human t
7	5952	99.8	1132	2	AAV26580 Human tel
8	5952	99.8	1132	4	AAAG64859 Heart mus
9	5952	99.8	1132	4	AAAG64329 Human pro
10	5952	99.8	1132	4	AAAB99930 Human tel
11	5952	99.8	1132	4	AAAB82765 Human tel
12	5952	99.8	1132	5	AAAE29226 Human tel
13	5952	99.8	1132	5	AAU72735 Human tel
14	5952	99.8	1132	6	ABR42384 Human tel
15	5952	99.8	1132	6	ABR42063 Human tel
16	5952	99.8	1132	6	ABP56676 Human tel
17	5952	99.8	1132	6	ABP56676 Human tel
18	5952	99.8	1132	7	ADDD21420 Human TER
19	5952	99.8	1132	7	ADH72743 Human pro
20	5952	99.8	1132	8	ADG70114 hTERT pro
21	5952	99.8	1132	8	ADG90599 Human TER
22	5952	99.8	1132	8	AD182172 Human tel
23	5952	99.8	1154	2	AAW61350 Human tel
24	5952	99.8	1189	2	AAW47008 Glutathio
25	5946	99.7	1285	2	AAW47000 HTS tagge

26	5945	99.7	1132	2	AAW71376 Human tel
27	5945	99.7	1132	2	AAV00627 Human tel
28	5945	99.7	1132	2	AAV00638 Human tel
29	5945	99.7	1132	2	AAV28401 Human EST
30	5945	99.7	1132	3	AAV96566 hEST2, a
31	5945	99.7	1132	7	ADG47061 Human TER
32	5945	99.7	1132	7	ADG40482 Human tel
33	5929	99.4	1405	2	AAW56101 Enhanced
34	5918	99.2	1166	2	AAV00647 Telomeras
35	5902.5	99.0	1199	2	AAW47007 Glutathio
36	5873	98.5	1120	2	AAV00641 Telomeras
37	5864	98.3	1120	2	AAV00650 Telomeras
38	5712	95.8	1150	2	AAW47006 Glutathio
39	5546	93.0	1053	2	AAV00640 Altered C
40	5507	92.4	1093	2	AAV00649 Altered C
41	5458	91.5	1041	2	AAV00652 Altered C
42	5458	91.5	1041	2	AAV00643 Altered C
43	5002	83.9	948	2	AAV00639 N-termina
44	4998	83.8	948	2	AAV00648 Truncated
45	4936	82.6	936	2	AAV00642 Truncated
46	4917	82.5	936	2	AAV00651 Truncated
47	4894	82.1	949	2	AAW61349 Human tel
48	4505	75.5	1152	8	ADG90609 TERT cons
49	4046	67.9	807	2	AAW46997 Human tel
50	4046	67.9	807	2	AAV00637 Human tel
51	4046	67.9	807	2	AAV00646 Truncated
52	3619	60.7	1128	7	ADD21416 Golden ha
53	3619	60.7	1128	8	ADG90603 Hamster T
54	3496	58.6	1122	8	AAV26579 Murine te
55	3466	58.6	1122	8	ADG90601 Murine TE
56	3466	58.1	1122	5	ABD06711 Mouse tel
57	3288	54.3	617	2	AAV00636 N-termina
58	3154	52.9	588	2	AAV00635 N-termina
59	3138	52.6	588	2	AAV00644 N-termina
60	3125	52.4	622	2	AAV25463 Human CRT
61	3038	50.9	591	2	AAW97384 A catalyt
62	2851	44.3	500	6	AAO29840 Human tel
63	2573	44.1	499	6	ABD99678 Amino aci
64	2253	37.8	1131	7	ADD21415 Frog TERT
65	2178	36.5	436	6	ABD99680 Splice va
66	2178	36.5	436	2	AAV25462 Human CRT
67	2167.5	36.3	743	8	ADG90607 Dog TERT
68	2167	36.3	463	6	ABD99679 Splice va
69	2163.5	36.3	437	2	AAV25461 Human CRT
70	2079	33.9	564	2	AAW56109 Human tel
71	2007	33.7	575	8	ADG90605 Rat TERT
72	1863	31.2	348	2	AAV00645 Truncated
73	1541	25.8	538	2	AAW47001 Glutathio
74	1506	25.3	514	2	AAW47004 Glutathio
75	1484	24.9	291	6	AAO29774 hTERT MHC
76	1447	24.3	531	2	AAW47002 Glutathio
77	1438	24.1	283	3	AAV43128 Human tel
78	1417.5	23.8	516	2	AAW47005 Glutathio
79	1338.5	22.4	514	2	AAW47003 Glutathio
80	1293	21.7	520	8	ADG858224 Human tel
81	1090	18.3	259	2	AAW46998 Human tel
82	902	15.1	174	6	AAO29775 hTERT MHC
83	708	11.9	379	4	AAE00431 Consensus
84	667	11.2	174	6	ABD99681 Splice va
85	645	10.8	131	2	AAW97385 Amino aci
86	588	9.9	988	2	AAW56107 S. pombe
87	565	9.5	816	8	ADG70135 HIV RT/HT
88	555	9.3	806	8	ADG70131 HIV RT/HT
89	555	9.3	806	8	ADG70134 HIV RT/HT
90	535	9.3	816	8	ADG70133 HIV RT/HT
91	535	9.3	816	8	ADG70133 HIV RT/HT
92	534	9.0	100	6	ABD99682 Splice va
93	503	8.4	100	5	ABG71627 hTERT fta
94	478	8.0	576	8	ADG70112 HIV RT/HT
95	478	8.0	592	8	ADG70120 HIV RT/HT
96	478	8.0	605	8	ADG70121 HIV RT/HT
97	461	7.7	816	8	ADG70132 HIV RT/HT
98	459	7.7	456	8	ADG70126 HIV RT/HT

99 459 7.7 462 8 ADG70124 ADG70124 HIV RT/HT
 100 459 7.7 552 8 ADG70123 ADG70123 HIV RT/HT
 101 459 7.7 605 8 ADG70122 ADG70122 HIV RT/HT
 102 452 7.6 586 8 ADG70125 ADG70125 HIV RT/HT
 103 443 7.4 244 4 AAM8748 Human hnm
 104 440.5 7.4 1031 2 AAM8748 Euploies
 105 401 6.7 75 8 ADG70117 hTERT ant
 106 362 6.1 867 7 ADG70117 hTERT ant
 107 360 6.0 867 4 AAE00423 Candida a
 108 356 6.0 867 4 AAE00424 Candida a
 109 355.5 6.0 864 2 AAM71375 Yeast tel
 110 355.5 6.0 884 2 AAM59778 Amino aci
 111 332.5 5.6 364 2 AAE00430 Schizosac
 112 308 5.2 61 2 AAY00633 Human tel
 113 244 4.1 48 6 AAY86593 Telomeras
 114 239 4.0 48 6 ABB99684 Amino aci
 115 223 3.7 48 2 AAY26581 Peptide s
 116 186 3.1 35 3 AAY86597 Telomeras
 117 184.5 3.1 960 7 ADD21422 G Intesti
 118 179.5 3.0 3530 8 ADQ18982 Human sof
 119 179 3.0 2675 3 AAB07564 Protein e
 120 176 3.0 34 3 AAY86596 Telomeras

ALIGNMENTS

RESULT 1
 ID AAM56113 standard; protein; 1132 AA.
 AC AAM56113;
 DT 13-AUG-1998 (first entry)
 XX
 DE Human telomerase reverse transcriptase protein refined sequence.
 XX
 KM Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
 KM cell proliferation; cancer; ageing; ribonucleoprotein.
 OS Homo sapiens.
 OS
 PN GB2317891-A.
 PD 08-APR-1998.
 XX
 PF 01-OCT-1997; 97GB-00020890.
 XX
 PR 01-OCT-1996; 96US-00724643.
 PR 18-APR-1997; 97US-00844419.
 PR 25-APR-1997; 97US-00846017.
 PR 06-MAY-1997; 97US-00851843.
 PR 09-MAY-1997; 97US-00854050.
 PR 14-AUG-1997; 97US-00911312.
 PR 14-AUG-1997; 97US-00912951.
 PR 14-AUG-1997; 97US-00915503.
 XX
 PA (GERO-) GERON CORP.
 PA (UYTE-) UNIV TECHNOLOGY CORP.
 PI Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB,
 PI Andrews WH;
 XX WPI; 1998-171633/16.
 DR N-PSDB; AAV22428.
 XX
 PT Pure and recombinant human Telomerase Reverse Transcriptase and its
 PT variants - are useful in the diagnosis, prognosis and treatment of cell
 PT proliferation conditions especially cancer and ageing.
 XX
 PS Example 1; Fig 74; 387pp; English.
 CC The present sequence represents human telomerase reverse transcriptase

(hTERT), which is a ribonucleoprotein. The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTERT, by detecting the change in hTERT recombinant protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein preparation of hTERT with a telomerase RNA component; (C) detection of the hTERT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or amplification product with presence of hTERT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTERT expression; and (E) the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTERT and the polynucleotide encoding hTERT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions that are associated with high telomerase activity. A protein preparation of hTERT can also be used in the new methods

Sequence 1132 AA;

Query Match 100.0%; Score 5963; DB 2; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0; Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPCRAVRSLSRSHYREVLPATFVRRLGPGQMRVLVORGDPAPAFALVACLYCPW 60
 DB 1 MPRAPCRAVRSLSRSHYREVLPATFVRRLGPGQMRVLVORGDPAPAFALVACLYCPW 60
 QY 61 DARPPAPSPFROVSCLEKELVAVLORLCERGAKNVLAFFALDDGARGPPPAFTTSVR 120
 DB 61 DARPPAPSPFROVSCLEKELVAVLORLCERGAKNVLAFFALDDGARGPPPAFTTSVR 120
 QY 121 SYLENTVTDALRSGANGLLLRVGDVVLVHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180
 DB 121 SYLENTVTDALRSGANGLLLRVGDVVLVHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180
 QY 181 ATQARPPHAGSPRRRLCERAMNHSVREAGVGLGAPARARRGSSASLSLPRPRR 240
 DB 181 ATQARPPHAGSPRRRLCERAMNHSVREAGVGLGAPARARRGSSASLSLPRPRR 240
 QY 241 GAAPERTPTVGQSWAPGRTGSPSDGFCVSPAPAEATSLGALSGTRHSPSVG 300
 DB 241 GAAPERTPTVGQSWAPGRTGSPSDGFCVSPAPAEATSLGALSGTRHSPSVG 300
 QY 301 ROHHAGPSTSRPPRPMDTFCPPVYATKHFLLSSGDKELRSFLLSIRBSLTGARRL 360
 DB 301 ROHHAGPSTSRPPRPMDTFCPPVYATKHFLLSSGDKELRSFLLSIRBSLTGARRL 360
 QY 361 VETIFLGSRRPMMCTPRRLPRLPQRYQWRPLLELGNHAQCPYGVILKTHCPLRAAYT 420
 DB 361 VETIFLGSRRPMMCTPRRLPRLPQRYQWRPLLELGNHAQCPYGVILKTHCPLRAAYT 420
 QY 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVOLLFOHSSPMQVYGFVACLRRLVPGLMGS 480
 DB 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVOLLFOHSSPMQVYGFVACLRRLVPGLMGS 480
 QY 481 RHNERRRLNTKKFISLKGAKLSLOELTWKMSVRCAMLRSPGVCPPAARHRLREEL 540
 DB 481 RHNERRRLNTKKFISLKGAKLSLOELTWKMSVRCAMLRSPGVCPPAARHRLREEL 540
 QY 541 LAKFLHMLSVVYVELLSFFVYTETTFQKNRLFFRPSWSKLQSIGIRQLIKRVOLRE 600
 DB 541 LAKFLHMLSVVYVELLSFFVYTETTFQKNRLFFRPSWSKLQSIGIRQLIKRVOLRE 600
 QY 601 LSEAVRQHEARPPALITSLRFLPKPDGRLPYMNDYVVGATFRREARELTSRVYA 660
 DB 601 LSEAVRQHEARPPALITSLRFLPKPDGRLPYMNDYVVGATFRREARELTSRVYA 660
 QY 661 LFSVLANERARRPGLGASVTLGLDILHRAARTFVLVRADQDPPELHYFVKVDVTGAYDTI 720
 DB 661 LFSVLANERARRPGLGASVTLGLDILHRAARTFVLVRADQDPPELHYFVKVDVTGAYDTI 720

QY 721 PODRLTEVIAIITKPTQYCVRRYAVVQKAAHGVKAKFSKSHVSTLTDLPYWRQCFVHL 780
 CC (hTERT) which is a ribonucleoprotein. The present invention also
 CC describes the following methods: (A) determining whether a test compound
 CC is a modulator of hTERT, by detecting the change in hTERT recombinant
 CC protein or polynucleotide, on administration of the compound; (B)
 CC preparation of recombinant telomerase by contacting a protein preparation
 CC of hTERT with a telomerase RNA component; (C) detection of the hTERT RNA or
 CC protein in a sample by binding a relevant probe to the sample and
 CC detecting the complex formed or in the case of RNA detection, amplifying
 CC the product and correlating the presence of complex or amplification
 CC product with presence of hTERT in the sample; and (D) increasing the
 CC proliferation of a vertebrate cell by increasing hTERT expression; and (E)
 CC the use of an agent that causes an increase in cell vertebrate cell
 CC proliferation to create a medicament that inhibits ageing. A protein
 CC preparation of hTERT and the polynucleotide encoding hTERT can be used in
 CC the manufacture of medicaments for inhibiting the effect of ageing or
 CC cancer. Inhibitors of telomerase activity can be used to treat conditions
 CC that are associated with high telomerase activity. A protein preparation
 CC of hTERT can also be used in the new methods

QY 721 PODRLTEVIAIITKPTQYCVRRYAVVQKAAHGVKAKFSKSHVSTLTDLPYWRQCFVHL 780
 Db 721 PODRLTEVIAIITKPTQYCVRRYAVVQKAAHGVKAKFSKSHVSTLTDLPYWRQCFVHL 780
 QY 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHAVIRKSKSYVQCQGIPOGSILSTL 840
 Db 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHAVIRKSKSYVQCQGIPOGSILSTL 840
 QY 841 LCSIACVDMENKIFAGIRRDGILLRLVDDPLVTPHITAKTETRLTGVGPEVGVNL 900
 Db 841 LCSIACVDMENKIFAGIRRDGILLRLVDDPLVTPHITAKTETRLTGVGPEVGVNL 900
 QY 901 RKTIVNPEVEDEALGTAFAVQMPAHGFLFWCGLLDTRILEVQSDYSSVARTSIRASVTF 960
 Db 901 RKTIVNPEVEDEALGTAFAVQMPAHGFLFWCGLLDTRILEVQSDYSSVARTSIRASVTF 960
 QY 961 NRGFKAGRNRRKLFGLVLRKCHSLFDLDQVNSIQVCTNIYKILLQANRFACVLP 1020
 Db 961 NRGFKAGRNRRKLFGLVLRKCHSLFDLDQVNSIQVCTNIYKILLQANRFACVLP 1020
 QY 1021 FHQGVWKNPTFFLRVIDSTASLCYSILKAKNAGMSLGAKGAPLPSEAVQMLCHQAFLL 1080
 Db 1021 FHQGVWKNPTFFLRVIDSTASLCYSILKAKNAGMSLGAKGAPLPSEAVQMLCHQAFLL 1080
 QY 1081 KLTRHRTVYVPLGSLRTAQTOLSRKLPSTTLTALFMAANPALPSPFKITLD 1132
 Db 1081 KLTRHRTVYVPLGSLRTAQTOLSRKLPSTTLTALFMAANPALPSPFKITLD 1132

RESULT 2

AAW46957 standard; protein; 1132 AA.

AAW46957
 AC AAW46957;
 XX 13-AUG-1998 (first entry)
 DT 13-AUG-1998 (first entry)
 XX Human telomerase reverse transcriptase.
 DE Human telomerase reverse transcriptase.
 XX Human, telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
 KM cell proliferation; cancer; ageing; ribonucleoprotein.
 XX Homo sapiens.
 OS Homo sapiens.
 XX GB2317891-A.
 FN 08-APR-1998.
 PD 01-OCT-1997; 97GB-00020890.
 PE 01-OCT-1997; 97GB-00020890.
 XX 01-OCT-1996; 96US-0072443.
 PR 18-APR-1997; 97US-00844419.
 PR 25-APR-1997; 97US-00846017.
 PR 06-MAY-1997; 97US-00851843.
 PR 09-MAY-1997; 97US-00854050.
 PR 14-AUG-1997; 97US-00911312.
 PR 14-AUG-1997; 97US-00912351.
 PR 14-AUG-1997; 97US-00915503.
 XX (GERO-) GERON CORP.
 PA (UYTE-) UNIV TECHNOLOGY CORP.
 XX Cecch TR, Linsinger J, Nakamura T, Chapman KB, Morin GB, Harley CB;
 PI Andrews WH;
 XX WPI; 1998-171633/16.
 DR N-PSDB; AAV22379.
 XX Pure and recombinant human Telomerase Reverse Transcriptase and its
 PT variants - are useful in the diagnosis, prognosis and treatment of cell
 XX proliferation conditions especially cancer and ageing.
 PS Claim 3; Fig 17; 387p; English.

XX The present sequence represents human telomerase reverse transcriptase
 CC (hTERT) which is a ribonucleoprotein. The present invention also
 CC describes the following methods: (A) determining whether a test compound
 CC is a modulator of hTERT, by detecting the change in hTERT recombinant
 CC protein or polynucleotide, on administration of the compound; (B)
 CC preparation of recombinant telomerase by contacting a protein preparation
 CC of hTERT with a telomerase RNA component; (C) detection of the hTERT RNA or
 CC protein in a sample by binding a relevant probe to the sample and
 CC detecting the complex formed or in the case of RNA detection, amplifying
 CC the product and correlating the presence of complex or amplification
 CC product with presence of hTERT in the sample; and (D) increasing the
 CC proliferation of a vertebrate cell by increasing hTERT expression; and (E)
 CC the use of an agent that causes an increase in cell vertebrate cell
 CC proliferation to create a medicament that inhibits ageing. A protein
 CC preparation of hTERT and the polynucleotide encoding hTERT can be used in
 CC the manufacture of medicaments for inhibiting the effect of ageing or
 CC cancer. Inhibitors of telomerase activity can be used to treat conditions
 CC that are associated with high telomerase activity. A protein preparation
 CC of hTERT can also be used in the new methods

Sequence 1132 AA;

Query Match 99.8%; Score 5952; DB 2; Length 1132;

Best Local Similarity 99.8%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;

Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSILSHYREVLPATFVRRLGPQGMRLVQRGDPAPAFALVAQCLVCPM 60
 Db 1 MPRAPRCRAVRSILSHYREVLPATFVRRLGPQGMRLVQRGDPAPAFALVAQCLVCPM 60
 QY 61 DARPPPAAPSPFVQVCLKEIVARVQLRCERGAKNVAFGFALLDAGAGPEAATTSVR 120
 Db 61 DARPPPAAPSPFVQVCLKEIVARVQLRCERGAKNVAFGFALLDAGAGPEAATTSVR 120
 QY 121 SYLPNTVTDALRGSGAMGILLRRVGDVVLHLLARCAFLVAVAPSCAQVCGPPLVQLGA 180
 Db 121 SYLPNTVTDALRGSGAMGILLRRVGDVVLHLLARCAFLVAVAPSCAQVCGPPLVQLGA 180
 QY 181 ATQAPPPPHASGPRRLRCERAMNHSVRBAGVPLCLPAPGARRGGSASRSLPLKRRR 240
 Db 181 ATQAPPPPHASGPRRLRCERAMNHSVRBAGVPLCLPAPGARRGGSASRSLPLKRRR 240
 QY 241 GAAPBERTPVQGGSMANPGRTRGSDRGFCVSPAPPAEATSTLEGALSGTRHSPSVG 300
 Db 241 GAAPBERTPVQGGSMANPGRTRGSDRGFCVSPAPPAEATSTLEGALSGTRHSPSVG 300
 QY 301 RQHHAGPPSTSRPPRPMDTPCPVVAETKGLLYSSGDKQLRPSFLSSLRPSTLGARRL 360
 Db 301 RQHHAGPPSTSRPPRPMDTPCPVVAETKGLLYSSGDKQLRPSFLSSLRPSTLGARRL 360
 QY 361 VETTFILGSRPMPTGTRRLPLPCRYWQWRPLFLLGNHACCPYVLLKTHCPRAAVT 420
 Db 361 VETTFILGSRPMPTGTRRLPLPCRYWQWRPLFLLGNHACCPYVLLKTHCPRAAVT 420
 QY 421 PAAGVAREKPGQSAAPAEEDTDPRLVQLRQSSSPQVQYGFYRACLRLVPGWMS 480
 Db 421 PAAGVAREKPGQSAAPAEEDTDPRLVQLRQSSSPQVQYGFYRACLRLVPGWMS 480
 QY 481 RHNERPFLNNTKFTISLGNHAKLSLOELTWKMSVYDCMLRSPSGVCYPAEHLRETI 540
 Db 481 RHNERPFLNNTKFTISLGNHAKLSLOELTWKMSVYDCMLRSPSGVCYPAEHLRETI 540
 QY 541 LAKFLHMLMSYVVELLRSPFYVTEFTFOKNLFFYRSVMSKLSIGIRQLKVVQJRE 600
 Db 541 LAKFLHMLMSYVVELLRSPFYVTEFTFOKNLFFYRSVMSKLSIGIRQLKVVQJRE 600
 QY 601 LSEAEVRQREARPALITSLRFLFKPDGLRPIVNNDYVVGARTTRREKARRLTSRYKA 660
 Db 601 LSEAEVRQREARPALITSLRFLFKPDGLRPIVNNDYVVGARTTRREKARRLTSRYKA 660
 QY 661 LFSVINYERARRPGLGASVGLDDIHRAMRFVVRVAODPPFLYFVYVNTGAYDTI 720
 Db 661 LFSVINYERARRPGLGASVGLDDIHRAMRFVVRVAODPPFLYFVYVNTGAYDTI 720

Db 661 LFSVLNTERARRPGLLGASVGLGDDIHRAWRPFVLRVADPPPELVFKVADVGTGAYDTI 720
 Qy 721 PQRRLTEVIASIIKPNQNTYCVRRYAVVQRAAGHAKAKSVSTLTDQPTMRQFVAHL 780
 Db 721 PQRRLTEVIASIIKPNQNTYCVRRYAVVQRAAGHAKAKSVSTLTDQPTMRQFVAHL 780
 Qy 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHNAVIRKGSYVQCGIQQGSLSTL 840
 Db 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHNAVIRKGSYVQCGIQQGSLSTL 840
 Qy 841 LGSLLCYGDMENKLPAGIRRDGLLRLVDPFLVPLTHAKFPLRTLVGRVPEYGVNLT 900
 Db 841 LGSLLCYGDMENKLPAGIRRDGLLRLVDPFLVPLTHAKFPLRTLVGRVPEYGVNLT 900
 Qy 901 RKTIVNPFVDEALGGTAFFQMPAHGLFPMCGLLDTRLTLEQSPSSVARSISASYTF 960
 Db 901 RKTIVNPFVDEALGGTAFFQMPAHGLFPMCGLLDTRLTLEQSPSSVARSISASYTF 960
 Qy 961 NRGFKAGRMRRKLPFGLRLKCHSLFLDQVNSLQVTCTNIYKILLQAYRFHACVLQLP 1020
 Db 961 NRGFKAGRMRRKLPFGLRLKCHSLFLDQVNSLQVTCTNIYKILLQAYRFHACVLQLP 1020
 Qy 1021 FHQVWKNPFFELRVISDTASLCYSTLKAKNAGMSLGAKAGPLPSEAVQWLCHQAFLL 1080
 Db 1021 FHQVWKNPFFELRVISDTASLCYSTLKAKNAGMSLGAKAGPLPSEAVQWLCHQAFLL 1080
 Qy 1081 KLTRHRTVTVPLGLSLRTAQQLSRKLPSTTLTALAANAAPALPSDFKTIID 1132
 Db 1081 KLTRHRTVTVPLGLSLRTAQQLSRKLPSTTLTALAANAAPALPSDFKTIID 1132
 RESULT 3
 AAM90251
 ID AAM90251 standard; protein; 1132 AA.
 XX AAM90251;
 XX
 DT 24-MAY-1999 (first entry)
 XX
 DE Human catalytic telomerase sub-unit protein.
 XX
 KM Human; catalytic telomerase subunit; therapy; diagnosis; htc; assay;
 KM modulator; treatment; inhibit; cellular disorder; death; defect; cancer;
 KM ageing; antisense; neoplastic cell; telomerase-related condition;
 KM tumour cell.
 XX
 OS Homo sapiens.
 XX
 PN WO9859040-A2.
 XX
 PD 30-DEC-1998.
 XX
 PF 09-JUN-1998; 98WO-EP003468.
 XX
 PR 20-JUN-1997; 97DE-01026329.
 PR 26-MAR-1998; 98DE-01013274.
 PR 14-APR-1998; 98DE-01016496.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Hagen G, Siegmund H, Weichel W, Wlck M, Zubov D;
 XX
 DR WPI; 1999-081276/07.
 DR N-PSDB; AAV72117.
 XX
 PT New catalytically active subunit of human telomerase - used in the
 PT modulation of telomerase activity, particularly for treating cancer and
 PT ageing.
 XX
 PS Claim 2; Fig 2; 76pp; German.
 XX
 CC This sequence represents a novel human catalytic telomerase sub-unit
 CC (htc). This protein can be used in screening assays to identify

CC modulators of telomerase and/or other pathological processes involving telomerase,
 CC death, defects and/or ageing (also suitable for this are agents that
 CC particularly cancer and ageing (also suitable for this are agents that
 CC stimulate, inhibit or mimic the activity of the subunit). Antisense
 CC nucleic acids inhibit telomerase action (by binding to specific mRNA),
 CC particularly in neoplastic cells and may be expressed in vivo. Antibodies
 CC and fragments of the protein, used as probes or primers, are used to
 CC diagnose telomerase-related conditions (especially neoplasia) by (i)
 CC detecting abnormal levels of the subunit protein in body fluids or
 CC tissues or (ii) by measuring the amount of the encoding nucleic acid.
 CC Expression of the nucleic acid encoding the subunit mRNA is confined to
 CC tumour cells, in contrast to the ubiquitous expression of the telomerase
 CC RNA subunit
 XX
 SQ Sequence 1132 AA;
 Query Match 99.8%; Score 5952; DB 2; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MPRAFCRAVRSILRSHREVLPATFVRRLGPGQNRVYORCDPAFPALVAQCLVCM 60
 Db 1 MPRAFCRAVRSILRSHREVLPATFVRRLGPGQNRVYORCDPAFPALVAQCLVCM 60
 Qy 61 DARPPAPSPFROYSCLEIVARVLOLCERGANVLAQFALLDARGGPPAFTTSVR 120
 Db 61 DARPPAPSPFROYSCLEIVARVLOLCERGANVLAQFALLDARGGPPAFTTSVR 120
 Qy 121 SYLNTVTDALRSGAGMLLRVGDVYVHLARCALFLVAPSCAYQCGPLVQLGA 180
 Db 121 SYLNTVTDALRSGAGMLLRVGDVYVHLARCALFLVAPSCAYQCGPLVQLGA 180
 Qy 181 ATQARPPHAGRRRLGCRANMHSVREAGVBLGAPQARRRGSASRSLEPRPR 240
 Db 181 ATQARPPHAGRRRLGCRANMHSVREAGVBLGAPQARRRGSASRSLEPRPR 240
 Qy 241 GAAPERTPVGGSMAHPRTRGSDRGCVSPAPAEATSLGALSGRHSHPVG 300
 Db 241 GAAPERTPVGGSMAHPRTRGSDRGCVSPAPAEATSLGALSGRHSHPVG 300
 Qy 301 ROHHAGPSTSRPPRMDTPCPVVAETKAFLYSSQDKQLRPSFLSLRPSLTGARL 360
 Db 301 ROHHAGPSTSRPPRMDTPCPVVAETKAFLYSSQDKQLRPSFLSLRPSLTGARL 360
 Qy 361 VETIFLGSRRPMWGTFRRLPRLPQRYQWRPFLLELGNHAQCPGVLLKTHCPPLAAVT 420
 Db 361 VETIFLGSRRPMWGTFRRLPRLPQRYQWRPFLLELGNHAQCPGVLLKTHCPPLAAVT 420
 Qy 421 PAAGVCAREKPGSVAAPEEEDTPRLVQLRQHSPPQVYGFVACLRVLVPPGLMS 480
 Db 421 PAAGVCAREKPGSVAAPEEEDTPRLVQLRQHSPPQVYGFVACLRVLVPPGLMS 480
 Qy 481 RHNERREPLNTKXFLISLGRKAKLSLOELTWKSVRDCAMLRSPGVCPAAEHRLREBI 540
 Db 481 RHNERREPLNTKXFLISLGRKAKLSLOELTWKSVRDCAMLRSPGVCPAAEHRLREBI 540
 Qy 541 LAKEFLHMSVYVVELRSPFYETETFOKNRLEFPSPVWSLSIGIRHLLKRYQLAE 600
 Db 541 LAKEFLHMSVYVVELRSPFYETETFOKNRLEFPSPVWSLSIGIRHLLKRYQLAE 600
 Qy 601 LSEAEVQREARAPALLTSRLRFLPKPDGLRPIVNDVYVAGARTFREREAERLTSRYKA 660
 Db 601 LSEAEVQREARAPALLTSRLRFLPKPDGLRPIVNDVYVAGARTFREREAERLTSRYKA 660
 Qy 661 LFSVLNTERARRPGLLGASVGLGDDIHRAWRPFVLRVADPPPELVFKVADVGTGAYDTI 720
 Db 661 LFSVLNTERARRPGLLGASVGLGDDIHRAWRPFVLRVADPPPELVFKVADVGTGAYDTI 720
 Qy 721 PQRRLTEVIASIIKPNQNTYCVRRYAVVQRAAGHAKAKSVSTLTDQPTMRQFVAHL 780
 Db 721 PQRRLTEVIASIIKPNQNTYCVRRYAVVQRAAGHAKAKSVSTLTDQPTMRQFVAHL 780
 Qy 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHNAVIRKGSYVQCGIQQGSLSTL 840
 Db 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHNAVIRKGSYVQCGIQQGSLSTL 840

DB 781 QETSPLRDAVVIHQSSSLNEASSGLFDVFLRFMCHAVIRGKSYVOCGIPQGSILSTL 840
 QY 841 LGSICVGDMMENKLPAGIRRDGILLRLVDDPLVTPHLTHAKFLRTLVGVEYGCYNL 900
 DB 841 LGSICVGDMMENKLPAGIRRDGILLRLVDDPLVTPHLTHAKFLRTLVGVEYGCYNL 900
 QY 901 RKTIVNFPVEDEALGTAFAVQMPAHGLFPWCGILLDTRILEVQSDYSVARTSIRASVTF 960
 DB 901 RKTIVNFPVEDEALGTAFAVQMPAHGLFPWCGILLDTRILEVQSDYSVARTSIRASVTF 960
 QY 961 NRGFKAGRMNRKLPFGVLRKCHSLFLDLOVNSLOVCTNIYKILLQAVRFPAVLQLP 1020
 DB 961 NRGFKAGRMNRKLPFGVLRKCHSLFLDLOVNSLOVCTNIYKILLQAVRFPAVLQLP 1020
 QY 1021 FHQGVNPNPFFLRVISTDASLQSYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
 DB 1021 FHQGVNPNPFFLRVISTDASLQSYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
 QY 1081 KLTRHRVTYVPLIGSLRTAQTOLSRKLPCTTLTALBAANPALPSPDKTLLD 1132
 DB 1081 KLTRHRVTYVPLIGSLRTAQTOLSRKLPCTTLTALBAANPALPSPDKTLLD 1132

RESULT 4
 AAY28881
 ID AAY28881 standard; protein; 1132 AA.
 XX AAY28881;
 AC 17-JAN-2000 (first entry)
 DT
 XX Human telomerase reverse transcriptase protein.
 DE
 XX Human telomerase reverse transcriptase protein; hTERT; telomerase; hEST2;
 KM catalytic protein component; cell proliferative capacity; DNA primer;
 KM telomerase substrate; telomeric DNA synthesis; cell immortality;
 KM neoplastic phenotype; diagnostic application; prognostic application;
 KM telomerase related condition; cancer; therapeutic agent;
 KM telomerase expression; telomerase activity.
 KW
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 608
 FT /note= "Corresponds to cdc codon"
 FT
 XX WO9950279-A1.
 PN 07-OCT-1999.
 PD 31-MAR-1999; 99WO-US007160.
 XX 31-MAR-1999; 98US-00052919.
 PR 31-MAR-1998; 98US-00052919.
 XX (GERO-) GERON CORP.
 PA (UYTE-) UNIV TECHNOLOGY CORP.
 XX
 PI Ceeh TR, Ligner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
 PI Andrews WH;
 XX WPI; 1999-610834/52.
 DR N-PSDB; AA208150.
 XX
 PT Actinase polynucleotides for human telomerase reverse transcriptase used
 for diagnosing or treating cancer.
 XX
 PS Claim 2; Fig 2; 31p; English.
 XX The present sequence is human telomerase reverse transcriptase protein.
 CC This is the catalytic protein component of telomerase and is also
 CC referred to as hEST2. hTERT has the ability to extend a DNA primer that
 CC functions as a telomerase substrate for telomeric DNA synthesis. This

CC correlates with cell proliferative capacity, cell immortality, and the
 CC development of a neoplastic phenotype. Human TERT antisense
 CC oligonucleotides are useful for diagnostic or prognostic applications to
 CC telomerase related conditions, including cancer. They are also useful as
 CC therapeutic agents, for inhibition of telomerase expression and activity
 XX
 XX Sequence 1132 AA;
 Query Match 99.8%; Score 5952; DB 2; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MPARACRAVNSILRSHREVLPLATFRRRLPGQGMRLVQSGDPAAPALVACCLVCPW 60
 DB 1 MPARACRAVNSILRSHREVLPLATFRRRLPGQGMRLVQSGDPAAPALVACCLVCPW 60
 QY 61 DARPPAAPSPROYSCLELVARVLQRLCERGANXVLAFGFALLDGAAGGPEAFTTSVR 120
 DB 61 DARPPAAPSPROYSCLELVARVLQRLCERGANXVLAFGFALLDGAAGGPEAFTTSVR 120
 QY 121 STLEPNTVDALRGSGAKGLLRVGGDDVVLHLLARCALFVLVAASCAVQVGGPELYOLGA 180
 DB 121 STLEPNTVDALRGSGAKGLLRVGGDDVVLHLLARCALFVLVAASCAVQVGGPELYOLGA 180
 QY 121 STLEPNTVDALRGSGAKGLLRVGGDDVVLHLLARCALFVLVAASCAVQVGGPELYOLGA 180
 DB 121 STLEPNTVDALRGSGAKGLLRVGGDDVVLHLLARCALFVLVAASCAVQVGGPELYOLGA 180
 QY 181 ATQAPPPHAGSPRRRLCERAMNHSVREAGVPLGLPAPGARRRGSASRSLPJKRPRR 240
 DB 181 ATQAPPPHAGSPRRRLCERAMNHSVREAGVPLGLPAPGARRRGSASRSLPJKRPRR 240
 QY 241 GAAPPEERTPVQGGSWAHPGRTGSDRGFCVSPARPAAEATSLLEGALSTGRHSHPVG 300
 DB 241 GAAPPEERTPVQGGSWAHPGRTGSDRGFCVSPARPAAEATSLLEGALSTGRHSHPVG 300
 QY 301 RQNHAGPSTSRPPMPDPCPPVYAEKTHFLYSGDKEQRPSPFLSASLPSLTGARL 360
 DB 301 RQNHAGPSTSRPPMPDPCPPVYAEKTHFLYSGDKEQRPSPFLSASLPSLTGARL 360
 QY 361 VETIFLGSPPMWPGRPLRLPRLPORYWQMRPLELGNHAQCPYGVLLKTHCPRAAVT 420
 DB 361 VETIFLGSPPMWPGRPLRLPRLPORYWQMRPLELGNHAQCPYGVLLKTHCPRAAVT 420
 QY 421 PAAGVCAEKPQGSVAAPBEEDTDPRRLVOLLROSSPMOYGFPRALRLVPPGLWGS 480
 DB 421 PAAGVCAEKPQGSVAAPBEEDTDPRRLVOLLROSSPMOYGFPRALRLVPPGLWGS 480
 QY 481 RANERPFLENTKFFSLGKAKLSLOELTWKSVYDCAMLRSPVGCVPAAEHRREBI 540
 DB 481 RANERPFLENTKFFSLGKAKLSLOELTWKSVYDCAMLRSPVGCVPAAEHRREBI 540
 QY 541 LAKFLHMLSVYVVELLRSPFYVTEFTTQKNRLFYRPSVWSKLSIGIRGLKVCQJRE 600
 DB 541 LAKFLHMLSVYVVELLRSPFYVTEFTTQKNRLFYRPSVWSKLSIGIRGLKVCQJRE 600
 QY 601 LSEAEVROHREARPALNLSRLRFLPKPDGLPIVMDVVGARTFRREKRAERLSRVKA 660
 DB 601 LSEAEVROHREARPALNLSRLRFLPKPDGLPIVMDVVGARTFRREKRAERLSRVKA 660
 QY 661 LFSVLYNERARAPGLIGASVIGLDDIHRAMRTFVLRAAODPPPELYVYKVDVTAQDTI 720
 DB 661 LFSVLYNERARAPGLIGASVIGLDDIHRAMRTFVLRAAODPPPELYVYKVDVTAQDTI 720
 QY 721 PODRLTEVASTIKYQNTYCVARVAVVQKAAHGRKXFKSVSTLTLDQPMRQFVHL 780
 DB 721 PODRLTEVASTIKYQNTYCVARVAVVQKAAHGRKXFKSVSTLTLDQPMRQFVHL 780
 QY 781 QETSPLRDAVVIHQSSSLNEASSGLFDVFLRFMCHAVIRGKSYVOCGIPQGSILSTL 840
 DB 781 QETSPLRDAVVIHQSSSLNEASSGLFDVFLRFMCHAVIRGKSYVOCGIPQGSILSTL 840
 QY 841 LGSICVGDMMENKLPAGIRRDGILLRLVDDPLVTPHLTHAKFLRTLVGVEYGCYNL 900
 DB 841 LGSICVGDMMENKLPAGIRRDGILLRLVDDPLVTPHLTHAKFLRTLVGVEYGCYNL 900
 QY 901 RKTIVNFPVEDEALGTAFAVQMPAHGLFPWCGILLDTRILEVQSDYSVARTSIRASVTF 960
 DB 901 RKTIVNFPVEDEALGTAFAVQMPAHGLFPWCGILLDTRILEVQSDYSVARTSIRASVTF 960

Db 901 RKTIVNFPVDEALGGTAFAVQMPAHGLFPWCGLLDTRTLLEQVSDYSSTARSIRASTLTF 960
 QY 961 NRSEFKGRNRRRLFGVLRKCHSLFLDQVNSLQVCTNITYKILLQAYRTHACVLCQP 1020
 Db 961 NRSEFKGRNRRRLFGVLRKCHSLFLDQVNSLQVCTNITYKILLQAYRTHACVLCQP 1020
 QY 1021 FHOQVKNPPTFFLRVSDTASLQVNSLQVCTNITYKILLQAYRTHACVLCQP 1080
 Db 1021 FHOQVKNPPTFFLRVSDTASLQVNSLQVCTNITYKILLQAYRTHACVLCQP 1080
 QY 1081 KLTRHVTYVPLGLSLRTAQTOLSRKLPFTTLTALBAANPALPSDFKTLID 1132
 Db 1081 KLTRHVTYVPLGLSLRTAQTOLSRKLPFTTLTALBAANPALPSDFKTLID 1132
 RESULT 5
 ID AAY32090 standard; protein; 1132 AA.
 XX AAY32090;
 AC AAY32090;
 DT 17-JAN-2000 (first entry)
 XX Human telomerase reverse transcriptase (hTERT).
 DE Human telomerase reverse transcriptase (hTERT).
 KM Telomerase reverse transcriptase; human; hTERT; cell proliferation;
 KM cancer.
 XX Homo sapiens.
 OS Homo sapiens.
 PN MO9950386-A2.
 PD 07-OCT-1999.
 XX
 PF 31-MAR-1999; 99WO-US007097.
 XX
 PR 31-MAR-1998; 98US-00052864.
 PR 03-AUG-1998; 98US-00128354.
 PA (GERO-) GERON CORP.
 XX
 PI Morin GB;
 XX
 DR MPI; 1999-6:0842/52.
 DR N-PSDB; AAZ20279.
 PT
 XX New catalytic polypeptide and polynucleotide, useful for increasing
 PT catalytic activity in a cell.
 PS
 XX Claim 13; Fig 1; 24pp; English.
 CC The present sequence represents human telomerase reverse transcriptase
 CC (hTERT). Human telomerase is a target for diagnosing and treating diseases
 CC relating to cell proliferation and senescence, such as cancer, or for
 CC increasing the proliferative capacity of a cell. A claimed method for
 CC increasing the proliferative capacity of a vertebrate cell, especially a
 CC human or other mammalian cell, involves introducing into the cell a
 CC recombinant hTERT polynucleotide encoding an hTERT variant in which
 CC residues 192-323, 192-271, 200-271, 222-240, 415-450, 192-323
 CC and 415-450, or 192-271 and 415-450 of the present sequence are deleted.
 CC A claimed method of preparing recombinant telomerase involves contacting
 CC a recombinant hTERT deletion mutant (as above) with a telomerase RNA
 CC component such that the 2 proteins associate to form a complex capable of
 CC catalysing the addition of nucleotides to a telomerase substrate. A
 CC claimed method for reducing telomerase activity in a cell involves
 CC introducing a recombinant polynucleotide encoding an hTERT variant having
 CC a deletion of amino acids 192-450, 560-565, 637-660, 638-660, 748-764 or
 CC 1055-1071 of the present sequence
 XX
 XX Sequence 1132 AA;
 Query Match 99.8%; Score 5952; DB 2; Length 1132;

Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MPRAPCRAVSLIRSHRYREVLPLATFVRRLGPGQWMLVORGDPAAFRALVAOCLVCPW 60
 Db 1 MPRAPCRAVSLIRSHRYREVLPLATFVRRLGPGQWMLVORGDPAAFRALVAOCLVCPW 60
 QY 61 DARPAPAPSPFQVSCIKELVARYLQFLCERGANVLAFCGALLDGRGPPAFTTSVR 120
 Db 61 DARPAPAPSPFQVSCIKELVARYLQFLCERGANVLAFCGALLDGRGPPAFTTSVR 120
 QY 121 SYLNTVTDLIRGSGAMGLLRRYGDVVLVHLARCAFLVLAPEGAYQVCGPPLVQLG 180
 Db 121 SYLNTVTDLIRGSGAMGLLRRYGDVVLVHLARCAFLVLAPEGAYQVCGPPLVQLG 180
 QY 181 ATQARPPPHASGPPRRRLGGERAMNHSVREAGVPLGPAFGARRRGSGASRLPLPRPR 240
 Db 181 ATQARPPPHASGPPRRRLGGERAMNHSVREAGVPLGPAFGARRRGSGASRLPLPRPR 240
 QY 241 GAPEPERTVQGSMAHPERTGSPDRGCVVSPAPAEATSLGALSGTHSHSPVG 300
 Db 241 GAPEPERTVQGSMAHPERTGSPDRGCVVSPAPAEATSLGALSGTHSHSPVG 300
 QY 301 ROHAGPSTSRPBPWDTPCPVYAEYKFLYSQDKEQLRPSFLSLRPSLTGARRL 360
 Db 301 ROHAGPSTSRPBPWDTPCPVYAEYKFLYSQDKEQLRPSFLSLRPSLTGARRL 360
 QY 361 VETIFLGSRPWNMGTTPRLRLQRYWQMPPLLELIGNHAOCPPYVLLKTHCPILAAAT 420
 Db 361 VETIFLGSRPWNMGTTPRLRLQRYWQMPPLLELIGNHAOCPPYVLLKTHCPILAAAT 420
 QY 421 PAAGVCAREKPGQSVAAPEEDTDPRLVLQLEQSHSPQVQVGFVACLRPLVPLGMS 480
 Db 421 PAAGVCAREKPGQSVAAPEEDTDPRLVLQLEQSHSPQVQVGFVACLRPLVPLGMS 480
 QY 481 RHNERPRLNTKRFISLGKXAKLSLOELTWKMSVRDCAWLRSPGVCVPAEBRLREI 540
 Db 481 RHNERPRLNTKRFISLGKXAKLSLOELTWKMSVRDCAWLRSPGVCVPAEBRLREI 540
 QY 541 LAKEFLHMLSVVYVELRSPFYVETTFPOKRLFFRPSGWSLQSIGRQHLKRVQLE 600
 Db 541 LAKEFLHMLSVVYVELRSPFYVETTFPOKRLFFRPSGWSLQSIGRQHLKRVQLE 600
 QY 601 LSEAEVQOHRERAPALITSRRLRPIPKPDGLRPIVNDVYVAGARTFRERKAEHLTSRYKA 660
 Db 601 LSEAEVQOHRERAPALITSRRLRPIPKPDGLRPIVNDVYVAGARTFRERKAEHLTSRYKA 660
 QY 661 LFSVLYNERARRRPGLLGASVLDLIDHRAWRTVLRADPPELTFYKVDVTGAYDT 720
 Db 661 LFSVLYNERARRRPGLLGASVLDLIDHRAWRTVLRADPPELTFYKVDVTGAYDT 720
 QY 721 PODRLTEVIAIILKPONTYCVRRYAVVOKAAGHAKAKFSHVSTLTDLPYMRQFVAHL 780
 Db 721 PODRLTEVIAIILKPONTYCVRRYAVVOKAAGHAKAKFSHVSTLTDLPYMRQFVAHL 780
 QY 781 QETSPLRDVAVTIOSSSLNBAASGLFDVLRPMCHNANIRKGSYVQCGIIRQGSILSTL 840
 Db 781 QETSPLRDVAVTIOSSSLNBAASGLFDVLRPMCHNANIRKGSYVQCGIIRQGSILSTL 840
 QY 841 LCLSLCGDMENKLPAGIRRDGLLRIVYDPLVTPPLTAKTFLRLTVGVEYGVNVL 900
 Db 841 LCLSLCGDMENKLPAGIRRDGLLRIVYDPLVTPPLTAKTFLRLTVGVEYGVNVL 900
 QY 901 RKTIVNFPVDEALGGTAFAVQMPAHGLFPWCGLLDTRTLLEQVSDYSSTARSIRASTLTF 960
 Db 901 RKTIVNFPVDEALGGTAFAVQMPAHGLFPWCGLLDTRTLLEQVSDYSSTARSIRASTLTF 960
 QY 961 NRSEFKGRNRRRLFGVLRKCHSLFLDQVNSLQVCTNITYKILLQAYRTHACVLCQP 1020
 Db 961 NRSEFKGRNRRRLFGVLRKCHSLFLDQVNSLQVCTNITYKILLQAYRTHACVLCQP 1020
 QY 1021 FHOQVKNPPTFFLRVSDTASLQVNSLQVCTNITYKILLQAYRTHACVLCQP 1080
 Db 1021 FHOQVKNPPTFFLRVSDTASLQVNSLQVCTNITYKILLQAYRTHACVLCQP 1080

```

Db      1021 FHQGVKNKPTFLKRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLC HQAFLL 1080
Qy      1081 KLTRHRVTYVPLIGSLTAQTOLSRKLPPTTLTALLEANPALPSPDKTILD 1132
Db      1081 KLTRHRVTYVPLIGSLTAQTOLSRKLPPTTLTALLEANPALPSPDKTILD 1132

RESULT 6
AA43621
ID      AA43621 standard; protein; 1132 AA.
XX
AC      AA43621;
XX
DT      26-JAN-2000 (first entry)
XX
DE      A human telomerase reverse transcriptase (TRT) polypeptide.
XX
KM      Human, telomerase reverse transcriptase; TRT, T lymphocyte activation;
KM      dendritic cell; telomerase activity; cancer cell; proliferating cell;
KM      immunological destruction; telomerase; cancer; proliferation disease.
XX
OS      Homo sapiens.
XX
PN      W09950392-A1.
XX
PD      07-OCT-1999.
XX
PF      30-MAR-1999; 99WO-US006898.
XX
PR      31-MAR-1998; 98US-0112006P.
XX
PA      (GERO-) GERON CORP.
XX
PI      Gaeta FCA;
XX
DR      WPI: 1999-610845/52.
DR      N-PSDB; AA230154.
XX
PT      Eliciting an in vivo immune response for prevention and treatment of
PT      cancers.
XX
PS      Claim 3; Fig 1; 26pp; English.
XX
CC      The present sequence represents a human telomerase reverse transcriptase
CC      (TRT) polypeptide. The protein is used in the method of the invention.
CC      The specification describes a method for activating a T lymphocyte,
CC      comprising contacting the T lymphocyte with a dendritic cell that
CC      expresses a TRT peptide in the context of a MHC class I or MHC class II
CC      molecule. The protein causes induction of an in vivo immunological
CC      response to telomerase activity. Cancer cells are characterized by
CC      expression of endogenous TRT gene and the presence of detectable
CC      telomerase activity. Therefore, by eliciting a specific immune response
CC      to TRT or to TRT-expressing cells, it is possible to selectively target
CC      proliferating cells for immunological destruction. The method is used for
CC      eliciting an in vivo immune response to telomerase by activating a T
CC      lymphocyte, and is useful for prevention and treatment of cancers and
CC      other proliferation diseases/conditions
XX
SQ      Sequence 1132 AA;
Query Match      99.8%; Score 5952; DB 2; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MPAPRCRAVRSLSRSHREVLPATFVRRLGPGGMLVQGGPAAARALVAQCLVCPW 60
Db      1 MPAPRCRAVRSLSRSHREVLPATFVRRLGPGGMLVQGGPAAARALVAQCLVCPW 60
Qy      61 DARPPAPSPFQVSCUKELVAVTLQRLCERGAQNVAFGFAILDGARGGPPEAFTTSVR 120
Db      61 DARPPAPSPFQVSCUKELVAVTLQRLCERGAQNVAFGFAILDGARGGPPEAFTTSVR 120
Qy      121 SYLPNTVTDALRGSGAMGLLRVGGDVVLVHLARCALFVLVAPSCAYQVCGPPLVQLGA 180
Db      121 SYLPNTVTDALRGSGAMGLLRVGGDVVLVHLARCALFVLVAPSCAYQVCGPPLVQLGA 180

Db      121 SYLPNTVTDALRGSGAMGLLRVGGDVVLVHLARCALFVLVAPSCAYQVCGPPLVQLGA 180
Qy      181 ATQAPPPPHASGPRRRRLGGERAMNHSVEAGVPLGLPAPGARRRRGSASRLPLPKRRR 240
Db      181 ATQAPPPPHASGPRRRRLGGERAMNHSVEAGVPLGLPAPGARRRRGSASRLPLPKRRR 240
Qy      241 GAAPERTPVQGGMAHPGRTGSGDRGFQVSPAPAEATSLGALSGTRSHSPVG 300
Db      241 GAAPERTPVQGGMAHPGRTGSGDRGFQVSPAPAEATSLGALSGTRSHSPVG 300
Qy      301 RQHHAGPSTSRPPRPMDTQCPVYAEIKHFLYSSGDKQLRPSFLLSLRPSLTGAARL 360
Db      301 RQHHAGPSTSRPPRPMDTQCPVYAEIKHFLYSSGDKQLRPSFLLSLRPSLTGAARL 360
Qy      361 VETITLGSPPWPGTPRRPLRPLPQRYWQMRPLFLELLGNHACQPGVLTCTCPRAAVT 420
Db      361 VETITLGSPPWPGTPRRPLRPLPQRYWQMRPLFLELLGNHACQPGVLTCTCPRAAVT 420
Qy      421 PAAGVCAKPKPGSVAAAEEDTDRLVOLLRQSSPMQYGFVRACTLRLLVPGLWGS 480
Db      421 PAAGVCAKPKPGSVAAAEEDTDRLVOLLRQSSPMQYGFVRACTLRLLVPGLWGS 480
Qy      481 RHNERPFLNTRKFTSLGKHAQLSTQELTWKSVDCAMLRSPGVGVPAAEHRLREI 540
Db      481 RHNERPFLNTRKFTSLGKHAQLSTQELTWKSVDCAMLRSPGVGVPAAEHRLREI 540
Qy      541 LAKFLHMLSVYVVELLSFFVYETTFQKRLFFRPSVMSKLSIGIRCHLKKVQURE 600
Db      541 LAKFLHMLSVYVVELLSFFVYETTFQKRLFFRPSVMSKLSIGIRCHLKKVQURE 600
Qy      601 LSEAEVRQREARPALTLRLRFLPKPDGLRIVMDVYVGARTRRERKARLTSRYKA 660
Db      601 LSEAEVRQREARPALTLRLRFLPKPDGLRIVMDVYVGARTRRERKARLTSRYKA 660
Qy      661 LPSVINYERARRPGLLGASVGLDDIHRAMRFVLRVAODPEPLYEVKQDVTAAYDTI 720
Db      661 LPSVINYERARRPGLLGASVGLDDIHRAMRFVLRVAODPEPLYEVKQDVTAAYDTI 720
Qy      721 PODRLTEVIASIIKQNTYCVARYAVQKAAHGVKAKFKSHVSTLTDLQPYMQFVAHL 780
Db      721 PODRLTEVIASIIKQNTYCVARYAVQKAAHGVKAKFKSHVSTLTDLQPYMQFVAHL 780
Qy      781 QETSPRLDAVVEQSSSLNEASGLFDVFLRPMCHAVRIRKGSVYQCGIPQGSILSTL 840
Db      781 QETSPRLDAVVEQSSSLNEASGLFDVFLRPMCHAVRIRKGSVYQCGIPQGSILSTL 840
Qy      841 LCSLCYGDMENTLFGAIRRDGILLRVDDFLVTEHLTHAKFTLTVRGVEYCVNLT 900
Db      841 LCSLCYGDMENTLFGAIRRDGILLRVDDFLVTEHLTHAKFTLTVRGVEYCVNLT 900
Qy      901 RCTVYNFVEDALAGTAVQMPAGLFPWCGLLDPTLVEQSYSSYARSSTAASVTF 960
Db      901 RCTVYNFVEDALAGTAVQMPAGLFPWCGLLDPTLVEQSYSSYARSSTAASVTF 960
Qy      961 NRGFAAGRMRRKLGVALRKCHSLFDLQVNSLQVCTNIIKYILLQAYRRHACVLCQP 1020
Db      961 NRGFAAGRMRRKLGVALRKCHSLFDLQVNSLQVCTNIIKYILLQAYRRHACVLCQP 1020
Qy      1021 FHQGVKNKPTFLKRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLC HQAFLL 1080
Db      1021 FHQGVKNKPTFLKRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLC HQAFLL 1080
Qy      1081 KLTRHRVTYVPLIGSLTAQTOLSRKLPPTTLTALLEANPALPSPDKTILD 1132
Db      1081 KLTRHRVTYVPLIGSLTAQTOLSRKLPPTTLTALLEANPALPSPDKTILD 1132

RESULT 7
AA26580
ID      AA26580 standard; protein; 1132 AA.
XX
AC      AA26580;

```

XX 13-SEP-1999 (first entry)
 XX Human telomerase reverse transcriptase (hTERT) enzyme.
 XX Telomerase reverse transcriptase; TERT; mouse; telomere length assay;
 XX immunogen; enzyme; telomerase-mediated DNA replication; human.
 XX Homo sapiens.
 XX MO9927113-A1.
 XX 03-JUN-1999.
 XX 25-NOV-1998; 98MO-US025211.
 XX 26-NOV-1997; 97US-00979742.
 XX 16-MAR-1998; 98US-00042460.
 XX (GERO-) GERON CORP.
 XX (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
 XX Morin GB, Allsopp R, Depinho R, Greenberg R;
 XX WPI; 1999-347722/29.
 XX Mouse telomerase reverse transcriptase (mTERT) enzyme proteins and
 XX nucleic acids.
 XX Disclosure; Fig 3; 135pp; English.
 XX The invention relates to a mouse telomerase reverse transcriptase (mTERT)
 XX enzyme. Compositions containing mTERT can be used in telomere length
 XX assays. Isolated mTERT is useful as an immunogen for the production of
 XX monoclonal or polyclonal antibodies. The method is useful for assessing
 XX the degree of purification and identification of new mTERT species, such
 XX as an mTERT allele, homolog or isoform, or to screen for modulators
 XX (antagonists and agonists) of telomerase-mediated DNA replication.
 XX Antagonists and agonists of mTERT can be used to modify the activity of
 XX other telomerase enzymes such as human TERT (hTERT). The present sequence
 XX represents a human TERT enzyme
 XX
 XX Sequence 1132 AA;
 XX
 XX Query Match 99.8%; Score 5952; DB 2; Length 1132;
 XX Best Local Similarity 99.8%; Pred. No. 0;
 XX Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX 1 MPAPPCRAVRSILRSYREVLPLATFVRLGPGQRLVQSGDPAFAFRLVAQCLVCVPM 60
 XX 1 MPAPPCRAVRSILRSYREVLPLATFVRLGPGQRLVQSGDPAFAFRLVAQCLVCVPM 60
 XX 61 DAAPPAPABSFROVSCLELVARVQLRCERGAQNYLAFGALLDQARGPPEAFTTSVR 120
 XX 61 DAAPPAPABSFROVSCLELVARVQLRCERGAQNYLAFGALLDQARGPPEAFTTSVR 120
 XX 121 SYLPLNTVTALRGSGAWGLLRVGGDVVHLARGLFVLAAPGAYVCGEPLOYGA 180
 XX 121 SYLPLNTVTALRGSGAWGLLRVGGDVVHLARGLFVLAAPGAYVCGEPLOYGA 180
 XX 181 ATGAPPPPHASGERRRLGGERAMNHSVRBAGVPLGPAFGARRRGSGASRSJLPKRRR 240
 XX 181 ATGAPPPPHASGERRRLGGERAMNHSVRBAGVPLGPAFGARRRGSGASRSJLPKRRR 240
 XX 241 GAAPPEERTPVGGGSAHAGRTRGSDRGFCVSPAPRAEATSLGALSGTRHSHPSVG 300
 XX 241 GAAPPEERTPVGGGSAHAGRTRGSDRGFCVSPAPRAEATSLGALSGTRHSHPSVG 300
 XX 301 RQHHAAPPSTSRPPRMDTPCPVYATGAFVSSGDKQLRPSFLSLSLRSLTGARRL 360
 XX 301 RQHHAAPPSTSRPPRMDTPCPVYATGAFVSSGDKQLRPSFLSLSLRSLTGARRL 360
 XX 361 VETIFLGSRRPMFGTFRRLRLPLQRYWQMRPLFLELLGNHAQCPGVILKTHCPDAAVT 420

Db 361 VETIFLGSRRPMFGTFRRLRLPLQRYWQMRPLFLELLGNHAQCPGVILKTHCPDAAVT 420
 Qy 421 PAACVCAAREKPGQSVAAPEEDTDPRRLVOLLQOHSSPMQVYGFPAACLRRLVPEGLWS 480
 Db 421 PAACVCAAREKPGQSVAAPEEDTDPRRLVOLLQOHSSPMQVYGFPAACLRRLVPEGLWS 480
 Qy 481 RHNERRFLRNTKKFISIGKAKLSLOELTWKMSVRDCAWLRSPGVCVPAARLRBEI 540
 Db 481 RHNERRFLRNTKKFISIGKAKLSLOELTWKMSVRDCAWLRSPGVCVPAARLRBEI 540
 Qy 541 LAKFLHMLMSVYVELLRSPFYVTEFTFQKRLFFRPSYWSKLSIGIRQHLKRYQLRE 600
 Db 541 LAKFLHMLMSVYVELLRSPFYVTEFTFQKRLFFRPSYWSKLSIGIRQHLKRYQLRE 600
 Qy 601 LSEAEVROHREARPAULTSRFLPKPDGLRPLVNMMDYVVGARTPREKAEALTSRVKA 660
 Db 601 LSEAEVROHREARPAULTSRFLPKPDGLRPLVNMMDYVVGARTPREKAEALTSRVKA 660
 Qy 661 LFSVLNTERARRRPGLGASVIGLDIHRAWRTEFLVRAQDPPEELYFVKVDVTGAYDTI 720
 Db 661 LFSVLNTERARRRPGLGASVIGLDIHRAWRTEFLVRAQDPPEELYFVKVDVTGAYDTI 720
 Qy 721 PQRRLTEVIAISIIKPPQTYCVRRYAVVQKAHGHVRAKFSHVSTLIDQPYRQFVAHL 780
 Db 721 PQRRLTEVIAISIIKPPQTYCVRRYAVVQKAHGHVRAKFSHVSTLIDQPYRQFVAHL 780
 Qy 781 QETSPFLDAVYIEOSSSLNEASSGLFDFVFLRFMCHAVRIRGKSYVQCGIPQGSILSTL 840
 Db 781 QETSPFLDAVYIEOSSSLNEASSGLFDFVFLRFMCHAVRIRGKSYVQCGIPQGSILSTL 840
 Qy 841 LCSCICYDMENKLPAGIRDPGLLRVDDPLVLTPTHTAKTLRLTLVNGVPEYGCVMNL 900
 Db 841 LCSCICYDMENKLPAGIRDPGLLRVDDPLVLTPTHTAKTLRLTLVNGVPEYGCVMNL 900
 Qy 901 RKTIVNPEVDEALGTAFAVQMPAHGLFPWCGLLDRLTEVOSDYSYARTSIRASVTE 960
 Db 901 RKTIVNPEVDEALGTAFAVQMPAHGLFPWCGLLDRLTEVOSDYSYARTSIRASVTE 960
 Qy 961 NRGFKAGNNRRKLPGLVRLKCHSLFLDQVNSLQTVCTNIYKILLQAYRFAVCYLQLP 1020
 Db 961 NRGFKAGNNRRKLPGLVRLKCHSLFLDQVNSLQTVCTNIYKILLQAYRFAVCYLQLP 1020
 Qy 1021 FHQGVWKNPPEFLRVISDTASLCYSTILKAKNAQMSLGAKGAAGLPSEAVQMTCHOAFL 1080
 Db 1021 FHQGVWKNPPEFLRVISDTASLCYSTILKAKNAQMSLGAKGAAGLPSEAVQMTCHOAFL 1080
 Qy 1081 KLTRHRVTYVPLGSLRTAQTLRSKLPSTTLTALBAANPALPSPDKTILD 1132
 Db 1081 KLTRHRVTYVPLGSLRTAQTLRSKLPSTTLTALBAANPALPSPDKTILD 1132
 XX
 XX RESULT 8
 XX AAG64859
 XX ID AAG64859 standard; protein; 1132 AA.
 XX
 XX AAG64859;
 XX
 XX 21-SEP-2001 (first entry)
 XX
 XX Heart muscle cell differentiation related protein SEQ ID NO: 31.
 XX Heart muscle cell; human; cell differentiation; heart disease.
 XX Homo sapiens.
 XX OS
 XX MO200148151-A1.
 XX 05-JUL-2001.
 XX 27-DEC-2000; 2000WO-JP009323.
 XX 28-DEC-1999; 99UP-00372826.

PR 28-FEB-2000; 2000MO-JP001148.
 PR 02-NOV-2000; 2000MO-JP007741.
 XX
 PA (KYOM) KYOMA HAKKO KOGYO KK.
 XX
 PI Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;
 PI Yamada Y;
 XX
 DR WPI; 2001-425656/45.
 DR N-PSDB; AAA46235.
 XX
 PT Cells capable of differentiating into cardiomyocytes and originating in
 PT bone marrow or umbilical blood cells for study of cardiomyocyte
 PT differentiation and treatment of heart disease.
 XX
 PS Claim 87; Page 143-147; 183pp; Japanese.
 CC The present invention provides cells originating in the human bone marrow
 CC or umbilical blood cells which are capable of differentiating into
 CC cardiomyocytes. These cells are useful in the treatment of diseases
 CC involving heart muscle degeneration, such as myocardial infarction, and
 CC the study of cardiomyocyte differentiation. The present sequence is a
 CC protein described in the exemplification of the invention
 XX
 SQ Sequence 1132 AA;

Query Match 99.8%; Score 5952; DB 4; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAARRAARSLRSHYREVLPLATFVRRLGQWRMLVORGPAPRAVAQCIVCM 60
 DB 1 MPRAARRAARSLRSHYREVLPLATFVRRLGQWRMLVORGPAPRAVAQCIVCM 60
 QY 61 DARRPPAPSPFRCVSCLELVARVLQRLCERGAKNVAFGAFALDAGRGPPAFTTSVR 120
 DB 61 DARRPPAPSPFRCVSCLELVARVLQRLCERGAKNVAFGAFALDAGRGPPAFTTSVR 120
 QY 121 SYLPNTVTDLRSGGANGLLIRYGDVVLHLLARCALFVLVAPSCAYQCGPPLVQLGA 180
 DB 121 SYLPNTVTDLRSGGANGLLIRYGDVVLHLLARCALFVLVAPSCAYQCGPPLVQLGA 180
 QY 121 SYLPNTVTDLRSGGANGLLIRYGDVVLHLLARCALFVLVAPSCAYQCGPPLVQLGA 180
 DB 121 SYLPNTVTDLRSGGANGLLIRYGDVVLHLLARCALFVLVAPSCAYQCGPPLVQLGA 180
 QY 181 ATGARPPPHASGPRRLGGERAMNHSVREAGVPLGLPAGARRGGASRLPLPRPR 240
 DB 181 ATGARPPPHASGPRRLGGERAMNHSVREAGVPLGLPAGARRGGASRLPLPRPR 240
 QY 241 GAAPERTPTVGGGSMWHPGRTGSDRGCVVSPAPAEATSLGALSGTRHSHPSVG 300
 DB 241 GAAPERTPTVGGGSMWHPGRTGSDRGCVVSPAPAEATSLGALSGTRHSHPSVG 300
 QY 301 ROHHAGPSTSRPPRPMDTCCPPYATKTFYSSGKELDRSFLSLSPBLTGARL 360
 DB 301 ROHHAGPSTSRPPRPMDTCCPPYATKTFYSSGKELDRSFLSLSPBLTGARL 360
 QY 361 VETIFLGSRRPMTGTPRLPLPQRYQMRLPFLTELLGNHACCPYGLLTKHCPRAAYT 420
 DB 361 VETIFLGSRRPMTGTPRLPLPQRYQMRLPFLTELLGNHACCPYGLLTKHCPRAAYT 420
 QY 421 PAAGVCARERPOGSAVAPEEDTDPRRLVOLLROHSSPMQVYGFVACLRRLVPGIWS 480
 DB 421 PAAGVCARERPOGSAVAPEEDTDPRRLVOLLROHSSPMQVYGFVACLRRLVPGIWS 480
 QY 481 RHNEERFLRTTKKFIISGAKAKLSLOELTWMSVPCDAMLRSPGVGCVAPEHRLREI 540
 DB 481 RHNEERFLRTTKKFIISGAKAKLSLOELTWMSVPCDAMLRSPGVGCVAPEHRLREI 540
 QY 541 LAKFLHMLSVYVELLRSPFYVETTFQKNRLFFYPYSWSKIOSIGIRQHLKRYOLRE 600
 DB 541 LAKFLHMLSVYVELLRSPFYVETTFQKNRLFFYPYSWSKIOSIGIRQHLKRYOLRE 600
 QY 601 LSEAEVQOHRRAPALTSRLRFIPKPDGLRPIVNMVYVGARFRREKRAEPLTSVKA 660
 DB 601 LSEAEVQOHRRAPALTSRLRFIPKPDGLRPIVNMVYVGARFRREKRAEPLTSVKA 660

QY 661 LFSVLYNERARRPGLLGASVGLDIDIRAWRTFVLRYVARAOPPELYEVKDYTGAYDTI 720
 DB 661 LFSVLYNERARRPGLLGASVGLDIDIRAWRTFVLRYVARAOPPELYEVKDYTGAYDTI 720
 QY 721 PODRLTEVIASIIKPONTYCVRRYAVQKAAHGVKAKSKHVSITLDLOPYMEQFVAHL 780
 DB 721 PODRLTEVIASIIKPONTYCVRRYAVQKAAHGVKAKSKHVSITLDLOPYMEQFVAHL 780
 QY 781 QETSPLRDAVVIEQSSINENASGLFDVFLRPMCHAVRINKSVQCGIPOSISLTL 840
 DB 781 QETSPLRDAVVIEQSSINENASGLFDVFLRPMCHAVRINKSVQCGIPOSISLTL 840
 QY 841 LCSLCYGMENKLFAGIRBDGLLRLVDDFLVTPHLLTHAKTFLRLVGVPEYGVNL 900
 DB 841 LCSLCYGMENKLFAGIRBDGLLRLVDDFLVTPHLLTHAKTFLRLVGVPEYGVNL 900
 QY 901 RKTYYNPFVEDEALGTFVQMPAHGLFPMCGILLDPTLEVOQDYSYARTSIRASVTF 960
 DB 901 RKTYYNPFVEDEALGTFVQMPAHGLFPMCGILLDPTLEVOQDYSYARTSIRASVTF 960
 QY 961 NRGFGAGNMRRKLFVGLRLKCHSLFDLOVNSIQVCTNIIKILLQAVRFHACVQLP 1020
 DB 961 NRGFGAGNMRRKLFVGLRLKCHSLFDLOVNSIQVCTNIIKILLQAVRFHACVQLP 1020
 QY 1021 FHOQVWKNPTFFLRYISDTASLCISILKAKNAGSLGAKGAPLPSAVOMLCHQAFLL 1080
 DB 1021 FHOQVWKNPTFFLRYISDTASLCISILKAKNAGSLGAKGAPLPSAVOMLCHQAFLL 1080
 QY 1081 KLTRHRTVYVPLGSLRTAQTQLSRKLPQTTLTALEAANPALPDEFTIID 1132
 DB 1081 KLTRHRTVYVPLGSLRTAQTQLSRKLPQTTLTALEAANPALPDEFTIID 1132

RESULT 9
 AAG64329
 ID AAG64329 standard; protein; 1132 AA.
 XX
 AC AAG64329;
 XX
 DT 24-SEP-2001 (first entry)
 XX
 DE Human protein #2.
 XX
 KM Angiogenesis; cardiac; cell differentiating agent; bone marrow;
 XX heart muscle cell; heart disease; human.
 XX
 OS Homo sapiens.
 XX
 PN MO200148149-A1.
 XX
 PD 05-JUL-2001.
 XX
 PF 28-FEB-2000; 2000MO-JP001148.
 XX
 PR 28-DEC-1999; 99JP-00372826.
 XX
 PA (KYOM) KYOMA HAKKO KOGYO KK.
 XX
 PI Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K;
 PI Yamada Y;
 XX
 DR WPI; 2001-418252/44.
 DR N-PSDB; AAA49601.
 XX
 PT New adult bone marrow-originated cells capable of differentiating into
 PT heart muscle cells, applicable as remedies for various heart diseases
 PT particularly with damaged heart muscle accompanying degeneration.
 XX
 PS Disclosure; Page 128-134; 158pp; Japanese.
 CC The present invention relates to cells isolated from bone marrow, which
 CC are capable of at least differentiating into heart muscle cells. The
 CC cells are applicable as remedies for various heart diseases particularly

CC with damaged heart muscle accompanying degeneration. The present sequence
 CC was used to illustrate the present invention
 XX
 SQ Sequence 1132 AA;
 Query Match 99.8%; Score 5952; DB 4; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPPCRAVRSLSRSHYREVLPATFVRLRGDQRLVQDPAFPALVAQCICVCPW 60
 DB 1 MPAPPCRAVRSLSRSHYREVLPATFVRLRGDQRLVQDPAFPALVAQCICVCPW 60

QY 61 DAPPPAASPFRVSGSLKELVAVLQRLGERGKAVLAFGALLGARGGPEAFTSVR 120
 DB 61 DAPPPAASPFRVSGSLKELVAVLQRLGERGKAVLAFGALLGARGGPEAFTSVR 120

QY 121 SYLNTVTDALRSGAMGILLRRVGDVIVHLIARCAFLVAPSCAYQVCPPLVQLGA 180
 DB 121 SYLNTVTDALRSGAMGILLRRVGDVIVHLIARCAFLVAPSCAYQVCPPLVQLGA 180

QY 181 ATQARPPHASPGRRLGGERAMNHSVREAGVPLGIPAGARRGSGASRLPLKRRR 240
 DB 181 ATQARPPHASPGRRLGGERAMNHSVREAGVPLGIPAGARRGSGASRLPLKRRR 240

QY 241 GAAPPEERTPVGGSWAHPRTRGSDRGFCVSPAPAEATSLGALSGTRHSHPSVG 300
 DB 241 GAAPPEERTPVGGSWAHPRTRGSDRGFCVSPAPAEATSLGALSGTRHSHPSVG 300

QY 301 RQHHAPPESTSPRRPMDTCCPPVVAETGFLYSSGDKEQLRPSLILSLRSLTGARRL 360
 DB 301 RQHHAPPESTSPRRPMDTCCPPVVAETGFLYSSGDKEQLRPSLILSLRSLTGARRL 360

QY 361 VETIFLGSRRPMGTPRLPRLPORWQYRPLFLELIGNHACPPGVLLKTCPLRAAVT 420
 DB 361 VETIFLGSRRPMGTPRLPRLPORWQYRPLFLELIGNHACPPGVLLKTCPLRAAVT 420

QY 421 PAAGVCAKPKPOGSVAPEEDTDPRLVQLLRQSSPWQVGYRACILRLVPPGLWGS 480
 DB 421 PAAGVCAKPKPOGSVAPEEDTDPRLVQLLRQSSPWQVGYRACILRLVPPGLWGS 480

QY 481 RHNERFELNKKFSLSGHAKLSLOELFWKMSVDCALRRSPVGCYPAAEHLREI 540
 DB 481 RHNERFELNKKFSLSGHAKLSLOELFWKMSVDCALRRSPVGCYPAAEHLREI 540

QY 541 LAKFLHMLSVYVELLRSPFYVTEFTFOKRLFFYRPSVMSKLSIGIRQLKRVQLE 600
 DB 541 LAKFLHMLSVYVELLRSPFYVTEFTFOKRLFFYRPSVMSKLSIGIRQLKRVQLE 600

QY 601 LSAEVRQREARPAALTSRLRIPKPDGLRPIVMNDIVGARTRRERARLTSRVKA 660
 DB 601 LSAEVRQREARPAALTSRLRIPKPDGLRPIVMNDIVGARTRRERARLTSRVKA 660

QY 661 LFSVLNFERARRPGLGASVLGIDDIHRAMRTFVLRAQDPPPELYEVKVDVTGAYDTI 720
 DB 661 LFSVLNFERARRPGLGASVLGIDDIHRAMRTFVLRAQDPPPELYEVKVDVTGAYDTI 720

QY 721 PQDRLTEVVASITKPNNTYCVRRYAVVQAAAGHVRKAFKSHVSLTLDQPMRFVHL 780
 DB 721 PQDRLTEVVASITKPNNTYCVRRYAVVQAAAGHVRKAFKSHVSLTLDQPMRFVHL 780

QY 781 QETSPRLDAVVEOSSSLNEASSGLPDLVFLRPMCHAAVRIKSKSVQCGIPQSSITSL 840
 DB 781 QETSPRLDAVVEOSSSLNEASSGLPDLVFLRPMCHAAVRIKSKSVQCGIPQSSITSL 840

QY 841 LSGLCYGDMENTKLPAGIRRDGLLRVLVDFFLLVTHLTAKEFLTLTVRGVPEYCVNL 900
 DB 841 LSGLCYGDMENTKLPAGIRRDGLLRVLVDFFLLVTHLTAKEFLTLTVRGVPEYCVNL 900

QY 901 RKVVNFPEDEALGDTAFVCMPAHGLPFMCGLLDTRTLEQSSYSSYARTSPASVTF 960
 DB 901 RKVVNFPEDEALGDTAFVCMPAHGLPFMCGLLDTRTLEQSSYSSYARTSPASVTF 960

QY 960 KRIIVNFVEDELGGTAFVQMPAHGLPFMCGLLDTRTLEQSSYSSYARTSPASVTF 960
 DB 960 KRIIVNFVEDELGGTAFVQMPAHGLPFMCGLLDTRTLEQSSYSSYARTSPASVTF 960

QY 961 NRGFAGRNMRRLPGVLRKCHSLFLDLQVNSLQVCTNITYKILLLOAYRFPACVLOLP 1020
 DB 961 NRGFAGRNMRRLPGVLRKCHSLFLDLQVNSLQVCTNITYKILLLOAYRFPACVLOLP 1020

QY 1021 FHOQVKNPFFLRVISDTSALCYSLIKAKNAGMSLGARCAAGPLDSEAVQWLCHQAFLL 1080
 DB 1021 FHOQVKNPFFLRVISDTSALCYSLIKAKNAGMSLGARCAAGPLDSEAVQWLCHQAFLL 1080

QY 1081 KLTRHRVTYVPLIGSLRTAQTOLSRKLPQTTLTALANANPALPSPFKIILD 1132
 DB 1081 KLTRHRVTYVPLIGSLRTAQTOLSRKLPQTTLTALANANPALPSPFKIILD 1132

RESULT 10
 AAB99930
 ID AAB99930 standard; protein; 1132 AA.
 XX
 AC AAB99930;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE Human telomerase protein sequence SEQ ID NO:31.
 XX
 KW Differentiation; heart muscle cell; cytokine; transcription factor;
 KW proliferation; surface antigen; heart disease; cardiomyocyte;
 KW bone marrow; umbilical blood cell; heart muscle degeneration;
 KW myocardial infarction.
 XX
 OS Homo sapiens.
 XX
 FN W0200148150-A1.
 XX
 PD 05-JUL-2001.
 XX
 PF 02-NOV-2000; 2000WO-JP007741.
 XX
 PR 28-DEC-1999; 99JP-00372826.
 XX
 PR 28-FEB-2000; 2000WO-JP001148.
 XX
 PA (XYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;
 PI Yamada Y;
 XX
 DR WPI, 2001-42665/45.
 XX
 DR N-PSDB; AAB44366.
 XX
 PT Cells capable of differentiating into cardiomyocytes and originating in
 PT bone marrow or umbilical blood cells for study of cardiomyocyte
 PT differentiation and treatment of heart disease.
 XX
 PS Claim 146; Page 137-141; 187pp; Japanese.
 CC
 CC The present invention describes cells originating in bone marrow or
 CC umbilical blood cells which are capable of differentiating into
 CC cardiomyocytes. Also described are: (1) cardiomyocytes produced by the
 CC differentiation of the cells; (2) a method for carrying out the
 CC differentiation into cardiomyocytes, regulated by a promotional and/or
 CC inhibitory factor; (3) a method for the differentiation of the cells into
 CC cell types other than cardiomyocytes; (4) drug compositions promoting the
 CC formation of heart muscle and regeneration of heart tissue which contain
 CC the cells; (5) a method for the production of antibodies which recognise
 CC the cells, especially antibodies which recognise a surface antigen on the
 CC cells; (6) a method for screening factors which promote the proliferation
 CC of the cells; (7) a method for immortalising the cells by expressing
 CC telomerase in them; (8) drug compositions for the treatment of heart
 CC disease which contain the immortalised cells; and (9) cell-free
 CC supernatant from the culture of the cells and its use in promoting their
 CC differentiation into cardiomyocytes. The cells are used in the treatment
 CC of diseases involving heart muscle degeneration, such as myocardial
 CC infarction and in the study of cardiomyocyte differentiation. AHA4351 to
 CC AHA4409 and AAB99915 to AAB99915 represent sequences used in the
 CC exemplification of the present invention

XX	Sequence 1132 AA;	99.8%; Score 5952; DB 4; Length 1132;	
5Q	Query Match	Best Local Similarity 99.8%; Pred. No. 0;	
	Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;		
QY	1 MPRAPRCAVRSILRSIRREVLPATFVRRLGPGQWMLVGRGPPAFAFRAVACLVCPM 60		
DB	1 MPRAPRCAVRSILRSIRREVLPATFVRRLGPGQWMLVGRGPPAFAFRAVACLVCPM 60		
QY	61 DARRPPAPSPFRQVSCIKELVARVLRICRGAKNVLAFFALDDGARGPPPAFTTSVR 120		
DB	61 DARRPPAPSPFRQVSCIKELVARVLRICRGAKNVLAFFALDDGARGPPPAFTTSVR 120		
QY	121 SYLENTVTDALRSGAGWLLIRYGDVYLHLLARCALFVLVAPSCAYQVCGPPLYLQGA 180		
DB	121 SYLENTVTDALRSGAGWLLIRYGDVYLHLLARCALFVLVAPSCAYQVCGPPLYLQGA 180		
QY	181 ATQARPPPHASGPPRRILGCEBAMNHSVREAGVPLGLPAPGARRGGSASSLPLRPFR 240		
DB	181 ATQARPPPHASGPPRRILGCEBAMNHSVREAGVPLGLPAPGARRGGSASSLPLRPFR 240		
QY	241 GAAPERTPTVQGSMAHPGRTRGSDRGFCVSPAPAEATSLGALSGRHSHPSVG 300		
DB	241 GAAPERTPTVQGSMAHPGRTRGSDRGFCVSPAPAEATSLGALSGRHSHPSVG 300		
QY	301 RQHHAGPPTSRPRPMDTGPPIYATKHFIVSSGCKEQLRPSFLLSRLPSTGARL 360		
DB	301 RQHHAGPPTSRPRPMDTGPPIYATKHFIVSSGCKEQLRPSFLLSRLPSTGARL 360		
QY	361 VETIFLSRPMMPGTPPRLPRLPQRYWQMRPLFLELLGNAGCPYGLLKTGCPLEAAVT 420		
DB	361 VETIFLSRPMMPGTPPRLPRLPQRYWQMRPLFLELLGNAGCPYGLLKTGCPLEAAVT 420		
QY	421 PAAGVCARERKQGSVAAPBEEDTDPRRLVOLLROHSSPMQVYGFVRACLRRLVPGIWS 480		
DB	421 PAAGVCARERKQGSVAAPBEEDTDPRRLVOLLROHSSPMQVYGFVRACLRRLVPGIWS 480		
QY	481 RHNERRLRTKKKTSISGKAKLSLQELTWMQSRDCAMLRSPGVCVPAEHLRBEI 540		
DB	481 RHNERRLRTKKKTSISGKAKLSLQELTWMQSRDCAMLRSPGVCVPAEHLRBEI 540		
QY	541 LAKEHLMSVYVVELLSPEFYVTEITFOKNRLEFYRPSVSKLSIGIRQHLKRYQRE 600		
DB	541 LAKEHLMSVYVVELLSPEFYVTEITFOKNRLEFYRPSVSKLSIGIRQHLKRYQRE 600		
QY	601 LSEFVQCHREARPAALTSLRFLPKPDGLRPIYNNMYYVAGATPREKRAERLTSRVKA 660		
DB	601 LSEFVQCHREARPAALTSLRFLPKPDGLRPIYNNMYYVAGATPREKRAERLTSRVKA 660		
QY	661 LFSVLANERARRPGLASVGLDDIRAWRTFVLRAQDPPELTVFVKVDTGANDTI 720		
DB	661 LFSVLANERARRPGLASVGLDDIRAWRTFVLRAQDPPELTVFVKVDTGANDTI 720		
QY	721 PODRLTEVIAIIIPQNTYCYRARAAYVQKAAGHVRKAFKSHVSTLLDLPYMRQFVAHL 780		
DB	721 PODRLTEVIAIIIPQNTYCYRARAAYVQKAAGHVRKAFKSHVSTLLDLPYMRQFVAHL 780		
QY	781 QETPFLDAVAVIBOSSSLNEASSGLFVPLRFPMCHAVIRGKSYVOCOSIPQSSISLT 840		
DB	781 QETPFLDAVAVIBOSSSLNEASSGLFVPLRFPMCHAVIRGKSYVOCOSIPQSSISLT 840		
QY	841 LCSICYDMMENKLFAGIRDDGLLRVDDFLVPHLTHAKTFRLTVRGVPEYGCVVNL 900		
DB	841 LCSICYDMMENKLFAGIRDDGLLRVDDFLVPHLTHAKTFRLTVRGVPEYGCVVNL 900		
QY	901 RKTIVNPFVEDEALGTAFAVQMPAHGLFPMCGILLDRRTLEVQDYSYARTSIRASVTF 960		
DB	901 RKTIVNPFVEDEALGTAFAVQMPAHGLFPMCGILLDRRTLEVQDYSYARTSIRASVTF 960		
QY	961 NRGFKAQNMNRKLFVGLRLKCHSLFLDLQVNSLQVCTNITYKILLQAYRFAACVQLP 1020		
DB	961 NRGFKAQNMNRKLFVGLRLKCHSLFLDLQVNSLQVCTNITYKILLQAYRFAACVQLP 1020		
DB	961 NRGFKAQNMNRKLFVGLRLKCHSLFLDLQVNSLQVCTNITYKILLQAYRFAACVQLP 1020		
QY	1021 FHQYWKNPTEFPLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSAVOMLCHQAFLL 1080		
DB	1021 FHQYWKNPTEFPLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSAVOMLCHQAFLL 1080		
QY	1081 KLTRHRVTVYVPLGSLRTAQOLSRKLPQTTLTLEAAMPALPSPDFKTIID 1132		
DB	1081 KLTRHRVTVYVPLGSLRTAQOLSRKLPQTTLTLEAAMPALPSPDFKTIID 1132		
DB	1081 KLTRHRVTVYVPLGSLRTAQOLSRKLPQTTLTLEAAMPALPSPDFKTIID 1132		
RESULT 11			
AAB82765			
ID	AAB82765 standard; protein; 1132 AA.		
XX			
AC	AAB82765;		
XX			
DT	29-OCT-2001 (first entry)		
XX			
DE	Human telomerase reverse transcriptase.		
XX			
XX	Telomerase reverse transcriptase; hTERT; human; cancer; tumour;		
KW	cytotoxic T lymphocyte; major histocompatibility complex;		
KX	human leucocyte antigen; HLA-A2.1; vaccine.		
XX			
OS	Homo sapiens.		
XX			
PH	Key	Location/Qualifiers	
FT	Peptide	13..21	/note="HLA-A2.1 binding motif"
FT	Peptide	23..31	/note="HLA-A2.1 binding motif"
FT	Peptide	76..84	/note="HLA-A2.1 binding motif"
FT	Peptide	96..104	/note="HLA-A2.1 binding motif"
FT	Peptide	140..148	/note="HLA-A2.1 binding motif"
FT	Peptide	152..160	/note="HLA-A2.1 binding motif"
FT	Peptide	346..354	/note="HLA-A2.1 binding motif"
FT	Peptide	353..361	/note="HLA-A2.1 binding motif"
FT	Peptide	371..379	/note="HLA-A2.1 binding motif"
FT	Peptide	388..396	/note="HLA-A2.1 binding motif"
FT	Peptide	407..415	/note="HLA-A2.1 binding motif"
FT	Peptide	487..495	/note="HLA-A2.1 binding motif"
FT	Peptide	540..548	/note="HLA-A2.1 binding motif"
FT	Peptide	548..556	/note="HLA-A2.1 binding motif"
FT	Peptide	555..563	/note="HLA-A2.1 binding motif"
FT	Peptide	572..580	/note="HLA-A2.1 binding motif"
FT	Peptide	705..713	/note="HLA-A2.1 binding motif"
FT	Peptide	724..732	/note="HLA-A2.1 binding motif"
FT	Peptide	772..780	/note="HLA-A2.1 binding motif"
FT	Peptide	797..805	/note="HLA-A2.1 binding motif"
FT	Peptide	812..820	/note="HLA-A2.1 binding motif"
FT	Peptide	836..844	/note="HLA-A2.1 binding motif"
FT	Peptide		/note="HLA-A2.1 binding motif"

FT	Pepptide	863..877 /note= "HLA-A2.1 binding motif"
FT	Pepptide	863..873 /label= p865
FT	Pepptide	/note= "HLA-A2.1 binding motif"
FT	Pepptide	883..891 /note= "HLA-A2.1 binding motif"
FT	Pepptide	926..934 /note= "HLA-A2.1 binding motif"
FT	Pepptide	934..942 /note= "HLA-A2.1 binding motif"
FT	Pepptide	969..977 /note= "HLA-A2.1 binding motif"
FT	Pepptide	988..996 /note= "HLA-A2.1 binding motif"
FT	Pepptide	1072..1080 /note= "HLA-A2.1 binding motif"
FT	Pepptide	1079..1087 /note= "HLA-A2.1 binding motif"
FT	Pepptide	1095..1103 /note= "HLA-A2.1 binding motif"
FT	Pepptide	1122..1130 /note= "HLA-A2.1 binding motif"
XX		
PN	WO200160391-A1.	
PD	23-AUG-2001.	
PE	15-FEB-2001; 2001WO-US005143.	
PR	15-FEB-2000; 2000US-0182685P. 15-FEB-2001; 2001US-00182685.	
PA	(REGC) UNIV CALIFORNIA.	
PI	Zanetti M;	
XX	WPI; 2001-536552/59.	
PT	Vaccine for initiating and enhancing a cytotoxic T lymphocyte response, for treating cancers or tumors or for inducing immune response against tumors, comprises a telomerase reverse transcriptase peptide.	
PS	Disclosure; Fig 5; 52pp; English.	
XX		
CC	The present sequence is that of human telomerase reverse transcriptase (hTERT). The sequence was analysed for 9-mer peptide sequences containing known binding motifs for the human leukocyte antigen HLA-A2.1 molecule. From an initial panel of about 30 candidate peptides, 2 sequences, denoted p540 (see AAB82772) and p865 (see AAB82773), were examined. The majority of healthy individuals as well as patients with prostate cancer immunised in vitro against these 2 HLA-A2.1 restricted peptides developed hTERT-specific cytotoxic T lymphocytes (CTL). The cancer patients' CTL specifically lysed a variety of HLA-A2+ cancer cell lines such as prostate, breast, colon, lung and melanoma, demonstrating immunological recognition of endogenously-processed hTERT peptides. In vivo immunisation of HLA-A2.1 transgenic mice generated a specific CTL response against both hTERT peptides. The induction of CTL responses in vitro and in vivo, and the susceptibility to lysis of tumour cells of various origins by hTERT CTL, suggest that hTERT could serve as a universal cancer vaccine for humans. Thus, a claimed universal vaccine for treating tumours of any origin comprises at least 1 hTERT peptide in an amount effective for initiating and enhancing a CTL response against cancer cells. The peptide is 7-15 amino acid residues in length and may be modified to enhance binding to the major histocompatibility complex. Also claimed is a method for inducing and enhancing a CTL response against cancer cells, involving harvesting blood leucocytes, pulsing with hTERT, and contacting cancer cells with the pulsed leucocytes. A method for targeting CTL to tumour mammal, especially a cancer patient	
XX		
Sequence 1132 AA;		

```

Db 1021 FHQVWKNPFFLIVISDTASLCYSILKAKAGMSLGAKGAGLPSEAVQWLC HQAFLL 1080
Qy 1081 KLTTRHRTVYVPLGSLRTAQTOLSRKLGTTTLTALEAANPALPSDFKTIID 1132
Db 1081 KLTTRHRTVYVPLGSLRTAQTOLSRKLGTTTLTALEAANPALPSDFKTIID 1132

RESULT 12
ID AAE29226 standard; protein; 1132 AA.
AC AAE29226;
XX
XX 27-JAN-2003 (first entry)
XX
XX Human telomerase reverse transcriptase (TERT).
XX
XX Carbohydrate antigen; alpha(1,3)galactosyltransferase; alpha1,3GT; TERT;
XX transgenic; alpha(1,2)fucosyltransferase; alpha1,2FT; human; enzyme;
XX telomerase reverse transcriptase.
XX
XX Homo sapiens.
XX
XX MO200274948-A2.
XX
XX 26-SEP-2002.
XX
XX 21-MAR-2002; 2002WO-CA000378.
XX
XX 21-MAR-2001; 2001US-0277811P.
XX
XX (GERO-) GERON CORP.
XX
XX Denning C, Clark AJ, Schiff JM;
XX
XX WP1; 2002-759895/82.
XX
XX DR N-PSDB; AAD46821.
XX
XX Mammalian cells, useful for producing animal tissues with carbohydrate
XX antigens that are compatible for transplantation into human patients.
XX
XX Disclosure; Page 34; 71pp; English.
XX
XX The invention relates to animal tissues with carbohydrate antigens that
XX are compatible for transplantation into human patients. The mammalian
XX cell is inactivated homozygously for expression of alpha(1,3)galactosyl-
XX transferase (alpha1,3GT) gene and comprises a transgene for alpha(1,2)-
XX fucosyltransferase (alpha1,2FT). It is useful for producing animal tissue
XX with carbohydrate antigens that are compatible for transplantation into
XX human patients. The present sequence is human telomerase reverse
XX transcriptase (TERT) used in the invention
XX
XX Sequence 1132 AA:
XX
Qy Query Match 99.8%; Score 5952; DB 5; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 1 MPRAPRCAVARSILSRHYREVLPLATFVRRLGPGGWLTVGRGPAARALVAQIVVPM 60
1 MPRAPRCAVARSILSRHYREVLPLATFVRRLGPGGWLTVGRGPAARALVAQIVVPM 60
Qy 61 DABPPAPSPFQVSCKEIVARVQLRCERGANVLAFAFALIDGARGPPAFTTSVR 120
61 DABPPAPSPFQVSCKEIVARVQLRCERGANVLAFAFALIDGARGPPAFTTSVR 120
Db 61 DABPPAPSPFQVSCKEIVARVQLRCERGANVLAFAFALIDGARGPPAFTTSVR 120
Qy 121 SYLENVTYTDALRGSGANGLLIRVGDVYLHLLARCLFVLVAPSCAYQVCGPPLVQLGA 180
121 SYLENVTYTDALRGSGANGLLIRVGDVYLHLLARCLFVLVAPSCAYQVCGPPLVQLGA 180
Db 121 SYLENVTYTDALRGSGANGLLIRVGDVYLHLLARCLFVLVAPSCAYQVCGPPLVQLGA 180
Qy 181 ATOARPPHAGSPRRRLGCEERAMNHSVEAGVPLGLPAPGARRRGGASSLPLPKRPRR 240
181 ATOARPPHAGSPRRRLGCEERAMNHSVEAGVPLGLPAPGARRRGGASSLPLPKRPRR 240

Db 181 ATOARPPHAGSPRRRLGCEERAMNHSVEAGVPLGLPAPGARRRGGASSLPLPKRPRR 240
Qy 241 GAAPPEPRTPVQGGWMAHGRTRGSDRGFCVVSAPRAEEXTSLGALSGTRHSPVSG 300
241 GAAPPEPRTPVQGGWMAHGRTRGSDRGFCVVSAPRAEEXTSLGALSGTRHSPVSG 300
Db 241 GAAPPEPRTPVQGGWMAHGRTRGSDRGFCVVSAPRAEEXTSLGALSGTRHSPVSG 300
Qy 301 ROHHAAGPSTSRPPRPMDTPCPPVYAEFKHPLVSSGDKEQLRPSFLSLGSLRSLTGARRL 360
301 ROHHAAGPSTSRPPRPMDTPCPPVYAEFKHPLVSSGDKEQLRPSFLSLGSLRSLTGARRL 360
Db 301 ROHHAAGPSTSRPPRPMDTPCPPVYAEFKHPLVSSGDKEQLRPSFLSLGSLRSLTGARRL 360
Qy 361 VETITFGSPKMWGPRRLPLRPLRQYWMORPLFELLNHACQCPGVILKTHCPRAAVT 420
361 VETITFGSPKMWGPRRLPLRPLRQYWMORPLFELLNHACQCPGVILKTHCPRAAVT 420
Db 361 VETITFGSPKMWGPRRLPLRPLRQYWMORPLFELLNHACQCPGVILKTHCPRAAVT 420
Qy 421 PAAGVCAREKPGGSVAAPSEEDTDPRLLVQLRQHSFMYGYGFYRACLRLVPPGLWGS 480
421 PAAGVCAREKPGGSVAAPSEEDTDPRLLVQLRQHSFMYGYGFYRACLRLVPPGLWGS 480
Db 421 PAAGVCAREKPGGSVAAPSEEDTDPRLLVQLRQHSFMYGYGFYRACLRLVPPGLWGS 480
Qy 481 RNNRRFLRNTKKTSLGKHAQLSTQELTWKMSVDCMLARSBGVGVPAEHLREBEI 540
481 RNNRRFLRNTKKTSLGKHAQLSTQELTWKMSVDCMLARSBGVGVPAEHLREBEI 540
Db 481 RNNRRFLRNTKKTSLGKHAQLSTQELTWKMSVDCMLARSBGVGVPAEHLREBEI 540
Qy 541 LAKFLHMLMSVYVVELLSFFYVETTFQKNRLFEPYRPSVMSKQSIGIRQHLKRVQURE 600
541 LAKFLHMLMSVYVVELLSFFYVETTFQKNRLFEPYRPSVMSKQSIGIRQHLKRVQURE 600
Db 541 LAKFLHMLMSVYVVELLSFFYVETTFQKNRLFEPYRPSVMSKQSIGIRQHLKRVQURE 600
Qy 601 LSEAEVQRQREARPALTLRLAFIRKPDGLRPIVMDVYVGAARTRRKRAEHLTSRYKA 660
601 LSEAEVQRQREARPALTLRLAFIRKPDGLRPIVMDVYVGAARTRRKRAEHLTSRYKA 660
Db 601 LSEAEVQRQREARPALTLRLAFIRKPDGLRPIVMDVYVGAARTRRKRAEHLTSRYKA 660
Qy 661 LFSVLYNERARPPGLGASVGLDDIHRAMRTFVLRVAQDPPPELTVKVDVGAAYDTI 720
661 LFSVLYNERARPPGLGASVGLDDIHRAMRTFVLRVAQDPPPELTVKVDVGAAYDTI 720
Db 661 LFSVLYNERARPPGLGASVGLDDIHRAMRTFVLRVAQDPPPELTVKVDVGAAYDTI 720
Qy 721 PODRLTEVIASIIKQNTYCVARYAVVQKAAGHVRKAFKSHVSTLTDLOPYMROFVAHL 780
721 PODRLTEVIASIIKQNTYCVARYAVVQKAAGHVRKAFKSHVSTLTDLOPYMROFVAHL 780
Db 721 PODRLTEVIASIIKQNTYCVARYAVVQKAAGHVRKAFKSHVSTLTDLOPYMROFVAHL 780
Qy 781 QETSPERDAVVEEGSSSLNEASSGLFDVFLRMCHHAVIRGKSVVQCGIPOGSLISTL 840
781 QETSPERDAVVEEGSSSLNEASSGLFDVFLRMCHHAVIRGKSVVQCGIPOGSLISTL 840
Db 781 QETSPERDAVVEEGSSSLNEASSGLFDVFLRMCHHAVIRGKSVVQCGIPOGSLISTL 840
Qy 841 LCSLCYGMENKLFAGIRRDGLRLVDDFLVTLPHLTHAKTFRTLVRGVPEYGCYVNL 900
841 LCSLCYGMENKLFAGIRRDGLRLVDDFLVTLPHLTHAKTFRTLVRGVPEYGCYVNL 900
Db 841 LCSLCYGMENKLFAGIRRDGLRLVDDFLVTLPHLTHAKTFRTLVRGVPEYGCYVNL 900
Qy 901 RKTIVNFPVEDALAGTAFAVQMPAHGLFPWCGLLDRTTLEVOGSYSYARTSTAATF 960
901 RKTIVNFPVEDALAGTAFAVQMPAHGLFPWCGLLDRTTLEVOGSYSYARTSTAATF 960
Db 901 RKTIVNFPVEDALAGTAFAVQMPAHGLFPWCGLLDRTTLEVOGSYSYARTSTAATF 960
Qy 961 NRGFKAGRMRRKLGVLRLKCHSLFDLOVNSLQTVCTNIYKILLDAVYFHACVLDLP 1020
961 NRGFKAGRMRRKLGVLRLKCHSLFDLOVNSLQTVCTNIYKILLDAVYFHACVLDLP 1020
Db 961 NRGFKAGRMRRKLGVLRLKCHSLFDLOVNSLQTVCTNIYKILLDAVYFHACVLDLP 1020
Qy 1021 FHQVWKNPFFLIVISDTASLCYSILKAKAGMSLGAKGAGLPSEAVQWLC HQAFLL 1080
1021 FHQVWKNPFFLIVISDTASLCYSILKAKAGMSLGAKGAGLPSEAVQWLC HQAFLL 1080
Db 1021 FHQVWKNPFFLIVISDTASLCYSILKAKAGMSLGAKGAGLPSEAVQWLC HQAFLL 1080
Qy 1081 KLTTRHRTVYVPLGSLRTAQTOLSRKLGTTTLTALEAANPALPSDFKTIID 1132
1081 KLTTRHRTVYVPLGSLRTAQTOLSRKLGTTTLTALEAANPALPSDFKTIID 1132
Db 1081 KLTTRHRTVYVPLGSLRTAQTOLSRKLGTTTLTALEAANPALPSDFKTIID 1132

RESULT 13
ID AAU72735 standard; protein; 1132 AA.
AC AAU72735;
XX
XX 09-APR-2002 (first entry)
XX
XX Human telomerase reverse transcriptase (TERT).
XX

```

KM Telomerase reverse transcriptase; TERT; cytosolic; apoptosis;
 KM cell growth inhibitor; antisense oligonucleotide; antisense technology.
 XX Homo sapiens.
 XX
 XX W0200186198-A1.
 XX
 XX PD 22-NOV-2001.
 XX
 XX PF 15-MAY-2001; 2001WO-05015774.
 XX
 XX PR 16-MAY-2000; 2000US-00572423.
 XX PR 07-DEC-2000; 2000US-00733294.
 XX
 XX PA (ISIS-) ISIS PHARM INC.
 XX
 XX PI Monia BP, Gaarde WA, Freier SM, Wanciewicz E;
 XX
 XX WPI: 2002-075321/10.
 XX
 XX DR N-PSDB; AAS96607.
 XX
 XX PT New compound targeted to nucleic acid molecule encoding telomerase
 XX PT transcriptase (TERT), which specifically hybridizes with and inhibits
 XX PT expression of TERT, useful for modulating apoptosis and inhibiting cell
 XX PT growth.
 XX
 XX PS Disclosure; Page 100-105; 154pp; English.
 XX
 XX CC The invention describes a compound, 8-50 nucleobases in length targeted
 XX CC to a nucleic acid molecule encoding human TERT (telomerase reverse
 XX CC transcriptase), where the compound specifically hybridizes with and
 XX CC inhibits the expression of TERT. A series of oligonucleotides were
 XX CC designed to target different regions of the human TERT RNA. These were 20
 XX CC nucleotides in length and composed of a central gap region consisting of
 XX CC ten 2'-deoxynucleotides, flanked on both sides (5' and 3' directions) by
 XX CC five-nucleotide wings. The wings were composed of 2'-methoxyethyl (2'-
 XX CC MOE) nucleotides. The compounds were analyzed for their effect on human
 XX CC TERT mRNA levels by reverse transcriptase (RT)-polymerase chain reaction
 XX CC (PCR). The compound is useful for inhibiting the expression of TERT in
 XX CC cells or tissues, for treating a human having disease or condition
 XX CC associated with TERT, for modulating apoptosis, for inhibiting cell
 XX CC growth (preferably, cancer cell growth), in antisense therapy and for
 XX CC diagnostics and therapeutics. This is the amino acid sequence of human
 XX CC telomerase reverse transcriptase (TERT), described in the method of the
 XX CC invention
 XX
 XX SQ Sequence 1132 AA;
 XX
 XX Query Match 99.8%; Score 5952; DB 5; Length 1132;
 XX Best Local Similarity 99.8%; Pred. No. 0;
 XX Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MPAPRCRAVRSLSRSHYREVLPATFVRLGPOGRLVQRGDPAPAFALVAQCLVCPW 60
 Db 1 MPAPRCRAVRSLSRSHYREVLPATFVRLGPOGRLVQRGDPAPAFALVAQCLVCPW 60
 QY 61 DAPPPAAPSFRQVSLKELVARVLOQLCERGAKNVLAFFALDGAAGPPEAFTTSVR 120
 Db 61 DAPPPAAPSFRQVSLKELVARVLOQLCERGAKNVLAFFALDGAAGPPEAFTTSVR 120
 QY 121 SYLNTVTALRSGAGMGLLRVVDVLAHLARCALFVLAAPSACAYOVGPPLYOLGA 180
 Db 121 SYLNTVTALRSGAGMGLLRVVDVLAHLARCALFVLAAPSACAYOVGPPLYOLGA 180
 QY 181 ATGAPPPAASGPRRLGGERAMNHSVREAGVPLGIPAGARRGSGASRSLLPKRPRR 240
 Db 181 ATGAPPPAASGPRRLGGERAMNHSVREAGVPLGIPAGARRGSGASRSLLPKRPRR 240
 QY 241 GAAPERTPTVGGGSAHAGRTGPDRCFCVSPAPRAEETSLEGLSGTRSHHPSVG 300
 Db 241 GAAPERTPTVGGGSAHAGRTGPDRCFCVSPAPRAEETSLEGLSGTRSHHPSVG 300
 QY 301 RGHAGPSTSRPPRFMDTPCPVVAETKGLFLYSSGDKQLRPSFLSLRPSLTGARRL 360

Db 301 RGHAGPSTSRPPRFMDTPCPVVAETKGLFLYSSGDKQLRPSFLSLRPSLTGARRL 360
 QY 361 VETIFLGSRRPMPGTPRRLPLPQRYWQKRPLELLGNAGCCPYGLTKHCPPLAAVT 420
 Db 361 VETIFLGSRRPMPGTPRRLPLPQRYWQKRPLELLGNAGCCPYGLTKHCPPLAAVT 420
 QY 421 PAAGVCAKRPQGSVAAPBEEDTDPRRLVOLLQOHSSPMQVYGFVPAACLRRLVPGIWS 480
 Db 421 PAAGVCAKRPQGSVAAPBEEDTDPRRLVOLLQOHSSPMQVYGFVPAACLRRLVPGIWS 480
 QY 481 RHNRFRFLRNTKPFISLGKAKLSLOELTKMSVRCAMLRSPGVCVPAASHRREEL 540
 Db 481 RHNRFRFLRNTKPFISLGKAKLSLOELTKMSVRCAMLRSPGVCVPAASHRREEL 540
 QY 541 LAKFLHMLSVYVELLSFFVYTTTFQKRLFFRRPSVSKLOSTIGRQHLKRYOLRE 600
 Db 541 LAKFLHMLSVYVELLSFFVYTTTFQKRLFFRRPSVSKLOSTIGRQHLKRYOLRE 600
 QY 601 LSEAEVROHREARPAITLSRLFPKPDGLRPVNMNDYVGARTPPREKAEELTSRVKA 660
 Db 601 LSEAEVROHREARPAITLSRLFPKPDGLRPVNMNDYVGARTPPREKAEELTSRVKA 660
 QY 661 LFSVLANERARRPDLGASVLDGDIHRAMRTFVLSRAODPPELFFVKVDYTGAYDTI 720
 Db 661 LFSVLANERARRPDLGASVLDGDIHRAMRTFVLSRAODPPELFFVKVDYTGAYDTI 720
 QY 721 PQRRLTVIASIIPQNTYCVRRYAVQKAAHGVKAPKSHYSTLTLDQPMKRFVANH 780
 Db 721 PQRRLTVIASIIPQNTYCVRRYAVQKAAHGVKAPKSHYSTLTLDQPMKRFVANH 780
 QY 781 QETSPLDAVIEQSSSLNEASSGLFDFVFLRFMCHAVIRKGSYVQCGIPQGSILSTL 840
 Db 781 QETSPLDAVIEQSSSLNEASSGLFDFVFLRFMCHAVIRKGSYVQCGIPQGSILSTL 840
 QY 841 LCSCICYDMENKLPAGIRPQGLLRLVDPDLVTPHLTAKTFLRLTVNGVPEYGCVANL 900
 Db 841 LCSCICYDMENKLPAGIRPQGLLRLVDPDLVTPHLTAKTFLRLTVNGVPEYGCVANL 900
 QY 901 RKTVMNPFVDEALGTAFAFQMPAHGLFPCGILLRLTEVQSDVSYARTSIRASVTF 960
 Db 901 RKTVMNPFVDEALGTAFAFQMPAHGLFPCGILLRLTEVQSDVSYARTSIRASVTF 960
 QY 961 NRGFKAGNNRRKLPGLVRLKCHSLFLDQVNSLQVTCNTIYKILLQAVRFHACVLOLP 1020
 Db 961 NRGFKAGNNRRKLPGLVRLKCHSLFLDQVNSLQVTCNTIYKILLQAVRFHACVLOLP 1020
 QY 1021 FHOQVMKNPFPLRIVISDTASLCYSILKAKNAGMSIAGKGAAPLSEBAVOMCHQAPFL 1080
 Db 1021 FHOQVMKNPFPLRIVISDTASLCYSILKAKNAGMSIAGKGAAPLSEBAVOMCHQAPFL 1080
 QY 1081 KLTSHRYTVPLLSLRTAQTQSRKLPGLTTLTALBAANPALPSDFKTLTD 1132
 Db 1081 KLTSHRYTVPLLSLRTAQTQSRKLPGLTTLTALBAANPALPSDFKTLTD 1132
 RESULT 14
 ABR42384
 ID ABR42384 standard; protein; 1132 AA.
 XX
 XX ABR42384;
 XX
 XX 11-AUG-2003 (first entry)
 XX
 XX Human telomerase reverse transcriptase.
 XX
 XX Telomerase reverse transcriptase; TERT; enzyme; RNA interference;
 XX short interfering RNA; siRNA; cancer; tumour; cytosolic; contraceptive;
 XX immunosuppressive; antifertility; fungicide; antiparasitic;
 XX antiinflammatory; human; gene therapy.
 XX
 XX Homo sapiens.
 XX OS

PN W02003035667-A2.
 XX
 PD 01-MAY-2003.
 XX
 PE 16-OCT-2002; 2002W0-US033065.
 XX
 XX 22-OCT-2001; 2001US-0345326P.
 PR 20-FEB-2002; 2002US-0359196P.
 XX 22-MAY-2002; 2002US-0383195P.
 PA (UVRP) UNIV ROCHESTER.
 PI Rowley PT.
 XX
 XX WPI; 2003-403336/38.
 DR N-PSDB; ACCS8039.
 XX
 PT Novel double-stranded short interfering RNA having sense and antisense
 PT nucleic acids which are complementary to each other and to target nucleic
 PT acid e.g., telomerase RNA or mRNA encoding telomerase reverse
 PT transcriptase.
 PS
 PS Disclosure; Fig 4; 37pp; English.
 XX
 CC The present sequence is the protein sequence of human telomerase reverse
 CC transcriptase (TERT). The invention relates to the discovery that double-
 CC stranded interfering RNAs, such as short interfering RNAs (siRNA), which
 CC target telomerase RNA or TERT mRNA are capable of inhibiting telomerase
 CC activity. Inhibition of telomerase in cancer cells leads to telomere
 CC shortening, end-to-end chromosomal fusion, and apoptosis. Interference of
 CC telomerase activity can also be used for treatment of infertility, for
 CC contraception or sterilisation, for immunosuppression, for treatment of
 CC yeast, parasite and fungal infections, and in anti-inflammatory therapies.
 CC As telomerase is active in a limited number of cell types, e.g. tumor
 CC cells, germ-line cells, certain stem cells of the haematopoietic system, T
 CC and B cells, sun-damaged skin, and proliferative cervix, most normal
 CC cells are not affected by telomerase RNA interference therapy
 CC
 XX
 SQ Sequence 1132 AA:

Query Match 99.8%; Score 5952; DB 6; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVSLRSHRYEVLPLATFYRRRLGPGQMRLVGSDPAFRALVAQGLVCPW 60
 Db 1 MPRAPRCRAVSLRSHRYEVLPLATFYRRRLGPGQMRLVGSDPAFRALVAQGLVCPW 60
 QY 61 DARPPAAPSPRQVSCLEKELVAVLQRLCERGANVLAFGALLDGAARGGPPAFTTSVR 120
 Db 61 DARPPAAPSPRQVSCLEKELVAVLQRLCERGANVLAFGALLDGAARGGPPAFTTSVR 120
 QY 121 SYLNTVTDALRGSGAGMLLRVGGDPLVHLRLCALFLVVAHSCAYVCGPPLVQLGA 180
 Db 121 SYLNTVTDALRGSGAGMLLRVGGDPLVHLRLCALFLVVAHSCAYVCGPPLVQLGA 180
 QY 181 ATOARPPPHASGPRRLGCEERAMNHSVREAGVPLGLPARARRGGASRLPLPKPRR 240
 Db 181 ATOARPPPHASGPRRLGCEERAMNHSVREAGVPLGLPARARRGGASRLPLPKPRR 240
 QY 241 GAABEPRTPVQGSMAHPTGRGSDRGFCVSPAPAPAEATLDEALGSTRSHSVG 300
 Db 241 GAABEPRTPVQGSMAHPTGRGSDRGFCVSPAPAPAEATLDEALGSTRSHSVG 300
 QY 301 RQHAGPSTSRPPRPMWTPCPVYAEKTHFLYSGDKEQURPSFLLSLRLTGARRL 360
 Db 301 RQHAGPSTSRPPRPMWTPCPVYAEKTHFLYSGDKEQURPSFLLSLRLTGARRL 360
 QY 361 VETIFLGRPMWPGTFRRLPLPQRYWQMRPLFELLNHAQCPYVILKTHCLRAVLT 420
 Db 361 VETIFLGRPMWPGTFRRLPLPQRYWQMRPLFELLNHAQCPYVILKTHCLRAVLT 420
 QY 421 PAAGVCAEKPGQGVAAPEEEDTPRRVLQRLRHSSPMQYGVFVACLRRLVPPGLMGS 480

Db 421 PAAGVCAEKPGQGVAAPEEEDTPRRVLQRLRHSSPMQYGVFVACLRRLVPPGLMGS 480
 QY 481 RENERRPLNRTKKFISLGGHAKLSLOELTWKMSVYDCAMLRSPGVGCVPAAEHRLREI 540
 Db 481 RENERRPLNRTKKFISLGGHAKLSLOELTWKMSVYDCAMLRSPGVGCVPAAEHRLREI 540
 QY 541 LAKFLHMLMSVYVALLSPFYVTTTQXNRPLFYRSPVSKLSIDIRHILKRVQURE 600
 Db 541 LAKFLHMLMSVYVALLSPFYVTTTQXNRPLFYRSPVSKLSIDIRHILKRVQURE 600
 QY 601 LSEAEVRQREARPPALITSRLRFIPKPDGLP2IVMDYVVGARTRFRREKRAERLTSRYKA 660
 Db 601 LSEAEVRQREARPPALITSRLRFIPKPDGLP2IVMDYVVGARTRFRREKRAERLTSRYKA 660
 QY 661 LFSVINYERARRPPGLIGASVIGLDDIHRAMRTFVLRYAODPPBLFYVKVDVTAADTI 720
 Db 661 LFSVINYERARRPPGLIGASVIGLDDIHRAMRTFVLRYAODPPBLFYVKVDVTAADTI 720
 QY 721 PODRLTEVIASTIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
 Db 721 PODRLTEVIASTIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
 QY 781 QETSPLRDAVVIQSSSINEASSGLFDVFLRFMCHAVIRKSYVQCGIIPQGSILSTL 840
 Db 781 QETSPLRDAVVIQSSSINEASSGLFDVFLRFMCHAVIRKSYVQCGIIPQGSILSTL 840
 QY 841 LLSLCGDMENLTPAGIRRDGILLRLVDDPLLYTHLTHAKTEFLTVRGVEYGCYVNL 900
 Db 841 LLSLCGDMENLTPAGIRRDGILLRLVDDPLLYTHLTHAKTEFLTVRGVEYGCYVNL 900
 QY 901 RKTVMNFPVEDALGTAFAVQMPAHGLPFWCGILLDTLRLVQSDYSYARTSIRASVTF 960
 Db 901 RKTVMNFPVEDALGTAFAVQMPAHGLPFWCGILLDTLRLVQSDYSYARTSIRASVTF 960
 QY 961 NRGFAGRNMRKLLFGVRLKCHSLFLDIQVNSLQTVCTNITKILLQAYRHHACVLOLP 1020
 Db 961 NRGFAGRNMRKLLFGVRLKCHSLFLDIQVNSLQTVCTNITKILLQAYRHHACVLOLP 1020
 QY 1021 FHOQWKQNTFFLRVYISDTASLCYSILKXKXGMSIGAKGAGPLSEAVQWLCHQAFLL 1080
 Db 1021 FHOQWKQNTFFLRVYISDTASLCYSILKXKXGMSIGAKGAGPLSEAVQWLCHQAFLL 1080
 QY 1081 KLTRHRVTVVPLIGSLRTAQOLSRKLPQTLTALBAANPALPSDFKTIID 1132
 Db 1081 KLTRHRVTVVPLIGSLRTAQOLSRKLPQTLTALBAANPALPSDFKTIID 1132

RESULT 15
 ABR42063
 ID ABR42063 standard; protein; 1132 AA.
 XX
 XX ABR42063:
 DT 28-JUL-2003 (first entry)
 XX
 XX Human telomerase reverse transcriptase.
 DE
 XX Telomerase reverse transcriptase; TERT; enzyme; RNA interference;
 KM short interfering RNA; siRNA; cancer; tumour; cytostatic; contraceptive;
 KM immunosuppressive; anti-infertility; fungicide; antiparasitic;
 KM anti-inflammatocty; human; gene therapy.
 OS Homo sapiens.
 XX
 XX W02003034985-A2.
 PN
 XX
 PD 01-MAY-2003.
 XX
 XX 16-OCT-2002; 2002W0-US033146.
 PF
 XX 22-OCT-2001; 2001US-0345326P.
 PR 20-FEB-2002; 2002US-0359196P.
 PR

PR 22-MAY-2002; 2002US-0383195P.
 XX (UTRP) UNIV ROCHESTER.
 XX Rowley PT;
 XX WPI: 2003-403289/38.
 DR N-PSDB; ACC57552.
 XX
 PT Novel nucleic acid encoding or comprising interfering RNAs which target
 PT telomerase RNA, useful for inhibiting telomerase activity for treating
 PT cancer, infertility and disorders of the immune system.
 XX
 PS Disclosure; Fig 4; 52pp; English.
 XX
 CC The present sequence is that of human telomerase reverse transcriptase
 CC (TERT). The invention relates to the discovery that double-stranded
 CC interfering RNAs, such as short interfering RNAs (siRNA), which target
 CC telomerase RNA or TERT mRNA are capable of inhibiting telomerase
 CC activity. Inhibition of telomerase in cancer cells leads to telomere
 CC shortening, end-to-end chromosomal fusion, and apoptosis. Interference of
 CC telomerase activity can also be used for treatment of infertility, for
 CC contraception or sterilisation, for immunosuppression, for treatment of
 CC yeast, parasite and fungal infections, and in anti-inflammatory therapies.
 CC As telomerase is active in a limited number of cell types, e.g. tumour
 CC cells, germ-line cells, certain stem cells of the haematopoietic system, T
 CC and B cells, sun-damaged skin, and proliferative cervix, most normal
 CC cells are not affected by telomerase RNA interference therapy
 XX
 SQ Sequence 1132 AA:
 Query Match 99.8%; Score 5952; DB 6; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MPBAPCRARSLRSHYSEVLEPLATFVRRLPGQWRLVORDPAPFALVQCVCVW 60
 DB 1 MPBAPCRARSLRSHYSEVLEPLATFVRRLPGQWRLVORDPAPFALVQCVCVW 60
 QY 61 DARRPAPASFRQVSLKELVARVLOQLCEGAKNVLAPFALLDGAAGPPEATTSYR 120
 DB 61 DARRPAPASFRQVSLKELVARVLOQLCEGAKNVLAPFALLDGAAGPPEATTSYR 120
 QY 121 SYLPNTVTALRSGAGMLLRVGDVTVHLARCALVVAAPCAVYVCGPPLYOGA 180
 DB 121 SYLPNTVTALRSGAGMLLRVGDVTVHLARCALVVAAPCAVYVCGPPLYOGA 180
 QY 181 ATGARRPPHAGSGRRRLGGERAMNHSVRAGVPLGLPAGARRGSGASRSLPLKRRPR 240
 DB 181 ATGARRPPHAGSGRRRLGGERAMNHSVRAGVPLGLPAGARRGSGASRSLPLKRRPR 240
 QY 241 GAAPBBERLPVGGGVAHPGRTGSPDRGFCVSPAPRAEATSLGALSGTRHSHPSVG 300
 DB 241 GAAPBBERLPVGGGVAHPGRTGSPDRGFCVSPAPRAEATSLGALSGTRHSHPSVG 300
 QY 301 ROHHAGPPSTRPRPMDTPCPPVVAETGHLFYSQGXQLRPSFLSLRSLTGARRL 360
 DB 301 ROHHAGPPSTRPRPMDTPCPPVVAETGHLFYSQGXQLRPSFLSLRSLTGARRL 360
 QY 361 VETIFLGSSRRPMGTPRRLPLRQRYWQRPFLFELIGNHAQCPYVLKTHCPRAAVT 420
 DB 361 VETIFLGSSRRPMGTPRRLPLRQRYWQRPFLFELIGNHAQCPYVLKTHCPRAAVT 420
 QY 421 PAAGVAREKPGQSVAAPEEDTPRRLVQLRQSSPMQYVGFRACLRLRVPGLWGS 480
 DB 421 PAAGVAREKPGQSVAAPEEDTPRRLVQLRQSSPMQYVGFRACLRLRVPGLWGS 480
 QY 481 RHNERFLNKKFSLIGHAKLSLOELTWMKSVDCAMLRSPGVCPAAEHRLREI 540
 DB 481 RHNERFLNKKFSLIGHAKLSLOELTWMKSVDCAMLRSPGVCPAAEHRLREI 540
 QY 541 LAKFLHMLMSVYVVELLSFFVYETTFPQKRLFRYPSWSKLSIGIRQLKRVQURE 600
 DB 541 LAKFLHMLMSVYVVELLSFFVYETTFPQKRLFRYPSWSKLSIGIRQLKRVQURE 600

DB 541 LAKFLHMLMSVYVVELLSFFVYETTFPQKRLFRYPSWSKLSIGIRQLKRVQURE 600
 QY 601 LSEAEVROHREARPAALLTSRLRFLPKPDGLRPIVNDYVVGARTFRERKAEELTSRYKA 660
 DB 601 LSEAEVROHREARPAALLTSRLRFLPKPDGLRPIVNDYVVGARTFRERKAEELTSRYKA 660
 QY 661 LFSVANTERARPGILLASVGLGDDIHRAMRTFLRACDPPPELTFVAVDVTGAADTI 720
 DB 661 LFSVANTERARPGILLASVGLGDDIHRAMRTFLRACDPPPELTFVAVDVTGAADTI 720
 QY 721 PODRLTEVIASIIKQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
 DB 721 PODRLTEVIASIIKQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
 QY 781 QETSELDVAVIEOSSSLNEASSGLFDVFLRFMCHAVRIRGKSVYOCOGIPGSLITSL 840
 DB 781 QETSELDVAVIEOSSSLNEASSGLFDVFLRFMCHAVRIRGKSVYOCOGIPGSLITSL 840
 QY 841 LCSLCYGMENKLPAGIRRDGLLRLVDLPLVPLTHAKTFLRLTVRGVPEYGVNVL 900
 DB 841 LCSLCYGMENKLPAGIRRDGLLRLVDLPLVPLTHAKTFLRLTVRGVPEYGVNVL 900
 QY 901 RKTVMNPPVEDALGTAFAVQMPAHGLFPCGGLLDRTLEVSQVSSYARTSIRASLTF 960
 DB 901 RKTVMNPPVEDALGTAFAVQMPAHGLFPCGGLLDRTLEVSQVSSYARTSIRASLTF 960
 QY 961 NRGFKAGNNRKLFGVRLKCHSLFLDQVNSIQVCTNIYKILLQAVRFACVQLP 1020
 DB 961 NRGFKAGNNRKLFGVRLKCHSLFLDQVNSIQVCTNIYKILLQAVRFACVQLP 1020
 QY 1021 FHQGVKNPFFLRVISDTASLCYSIIKAKNAGKSGAKGAAPLPSEAVQWLCHOAFL 1080
 DB 1021 FHQGVKNPFFLRVISDTASLCYSIIKAKNAGKSGAKGAAPLPSEAVQWLCHOAFL 1080
 QY 1081 KLTHRTVYVPLIGSLTFAOTLSRKLPGTTLTALLEANAPALPSPFKITLD 1132
 DB 1081 KLTHRTVYVPLIGSLTFAOTLSRKLPGTTLTALLEANAPALPSPFKITLD 1132
 RESULT 16
 ID ABB56676 standard; protein; 1132 AA.
 XX ABB56676;
 XX 25-MAR-2003 (first entry)
 DE Human telomerase reverse transcriptase protein SEQ ID NO:2.
 XX Human; telomerase reverse transcriptase; enzyme; hTERT; chromosome 5;
 KW vulnereary; anticulcer; epithelial cell migration promoter; wound;
 KW epithelial cell; keratinocyte; epidermal; mucosal.
 OS Homo sapiens.
 PN WO200291999-A2.
 XX 21-NOV-2002.
 PD 09-MAY-2002; 2002WO-US014867.
 PF 09-MAY-2001; 2001US-0289903P.
 PR (GERO-) GERON CORP.
 PA Jiang X, Chiu C, Harley CB;
 PI WPI: 2003-120591/11.
 DR N-PSDB; AB222474.
 XX Composition for treating wounds and enhancing epithelialization of a skin
 PT surface, comprises vector encoding telomerase reverse transcriptase or

PT telomerized epithelial cells on a microparticle or a matrix.
 XX
 PS Disclosure; Page 32; 68pp; English.

XX
 CC The present invention describes a pharmaceutical composition (I) comprising a vector encoding telomerase reverse transcriptase (TERT) in an excipient or device, or comprises telomerized epithelial cells on a microparticle or a matrix suitable for topical administration or administration to a wound site. (I) has a vulnary and anticancer activities and can be used to promote epithelial cell migration. (I) is useful for treating a wound and enhancing epithelialization of a skin surface. The wound is especially a skin wound including acute lesion such as traumatic lesion, burn, or surgical incision, chronic lesion such as chronic venous ulcer, diabetic ulcer or compression ulcer and the wound is further monitored for closure. The telomerase activity or TERT expression is increased in epithelial cells at the site of treatment and also in fibroblasts or endothelial cells at the site of treatment. The epithelial cells are especially keratinocytes. A polynucleotide encoding TERT is useful for the preparation of a medicament for treatment of a wound or an epithelial surface in a human or animal. An epithelial cell with increased telomerase activity or increased expression of TERT is useful for preparation of a medicament for the treatment of a wound in a human or animal. (I) is also useful for treating wounds of other epithelial surfaces including mucosal surfaces such as bronchus, mouth, nose, oesophagus, stomach, or intestine. The present sequence represents human TERT (hTERT), which is given in the exemplification of the present invention. hTERT is located to chromosome 5

XX
 SO Sequence 1133 AA:

Query Match 99.8%; Score 5952; DB 6; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAPRCAVRSLLRSHYREYLPATFVRRLGPGQWRLVORGDPARALVAOCLVCPV 60
 DB 1 MPRAPRCAVRSLLRSHYREYLPATFVRRLGPGQWRLVORGDPARALVAOCLVCPV 60
 QY 61 DARPAPAPSFQVYSCUKELVAVLQRLCERGANVLAFAFPALDAGRGPPAFTTSVR 120
 DB 61 DARPAPAPSFQVYSCUKELVAVLQRLCERGANVLAFAFPALDAGRGPPAFTTSVR 120
 QY 121 SYLPTNTVDALRGSGAGLLRRVGDVIVHLLARCLFVLVAPSCAYVCGPPLVQLGA 180
 DB 121 SYLPTNTVDALRGSGAGLLRRVGDVIVHLLARCLFVLVAPSCAYVCGPPLVQLGA 180
 QY 181 ATQARPPPHASGPRRLRCERAMNHSVREAGVPLGLPAPGARRRGSGASRLPLPKPRR 240
 DB 181 ATQARPPPHASGPRRLRCERAMNHSVREAGVPLGLPAPGARRRGSGASRLPLPKPRR 240
 QY 241 GAAPERTPTVYGQSGMAHPGRTGSPDRGFCVSPAPPAEATSLLEALGTRSHSVG 300
 DB 241 GAAPERTPTVYGQSGMAHPGRTGSPDRGFCVSPAPPAEATSLLEALGTRSHSVG 300
 QY 241 GAAPERTPTVYGQSGMAHPGRTGSPDRGFCVSPAPPAEATSLLEALGTRSHSVG 300
 DB 241 GAAPERTPTVYGQSGMAHPGRTGSPDRGFCVSPAPPAEATSLLEALGTRSHSVG 300
 QY 301 ROHAGPSTGRPRPMDPCPPYATKHFVLSGGKEQLRPSFLLSRPSITGARRL 360
 DB 301 ROHAGPSTGRPRPMDPCPPYATKHFVLSGGKEQLRPSFLLSRPSITGARRL 360
 QY 361 VETIFIGSRPWPMPGTPRRLPLPQRYWQMRPLFELLIGNHACPYGLLKTGCPRAAVT 420
 DB 361 VETIFIGSRPWPMPGTPRRLPLPQRYWQMRPLFELLIGNHACPYGLLKTGCPRAAVT 420
 QY 421 PAAGVCAKREKQGVAAPEEDTDPRRLVOLLROHSSPMOYGVVACLRVLPGLMGS 480
 DB 421 PAAGVCAKREKQGVAAPEEDTDPRRLVOLLROHSSPMOYGVVACLRVLPGLMGS 480
 QY 481 RHNERRFLRNTKFTSLGKHAHLSLOELTWMSVRCAMLRSPGVGCVPAAEHRLREI 540
 DB 481 RHNERRFLRNTKFTSLGKHAHLSLOELTWMSVRCAMLRSPGVGCVPAAEHRLREI 540
 QY 541 LAKFLHMLMSYVVELLSFYVYETTTQKRLFFYRSVWSKIOSIGIOHKLRYOLRE 600
 DB 541 LAKFLHMLMSYVVELLSFYVYETTTQKRLFFYRSVWSKIOSIGIOHKLRYOLRE 600

QY 601 LSEAVERQHRARPALTLSTRFLIPKPDGLSPIVMQYVGAFTFRRKRAERLTSRYKA 660
 DB 601 LSEAVERQHRARPALTLSTRFLIPKPDGLSPIVMQYVGAFTFRRKRAERLTSRYKA 660
 QY 661 LFSVINYERARPGILGASVILGDDIHRAMTFVLVRVRAQPPPELYFKVDYGAVDTI 720
 DB 661 LFSVINYERARPGILGASVILGDDIHRAMTFVLVRVRAQPPPELYFKVDYGAVDTI 720
 QY 721 PODRLTEVIASIKPONTVCYRRVAVVQKAHGRKAFKSHVSTLTDLPYMRQFVAHL 780
 DB 721 PODRLTEVIASIKPONTVCYRRVAVVQKAHGRKAFKSHVSTLTDLPYMRQFVAHL 780
 QY 781 QETSPDLDAVVIQSSSLNEASSGLFDVFLRPMCHAVRIRKSGYVCCGIPQSSILSTL 840
 DB 781 QETSPDLDAVVIQSSSLNEASSGLFDVFLRPMCHAVRIRKSGYVCCGIPQSSILSTL 840
 QY 841 LCSLCYGMENKLPAGIRDDGLLRVDDPILMTPHATFRLTVRGVEYGVNVL 900
 DB 841 LCSLCYGMENKLPAGIRDDGLLRVDDPILMTPHATFRLTVRGVEYGVNVL 900
 QY 901 RKTIVNFVEDEALGTAFCVQMPAHGLFPMCGLLDTRTLEVOSSDYSSARTSIRASVTF 960
 DB 901 RKTIVNFVEDEALGTAFCVQMPAHGLFPMCGLLDTRTLEVOSSDYSSARTSIRASVTF 960
 QY 961 NEGFPAGRNMRKLFVLRKCHSLFDLOVNSLQVCTNINIKILLQAYRFAVCVQLP 1020
 DB 961 NEGFPAGRNMRKLFVLRKCHSLFDLOVNSLQVCTNINIKILLQAYRFAVCVQLP 1020
 QY 1021 FHOQVWKQPTFLRATISDTASLCYSILKAKNAGMSLAKGAAGPLPSBAVOMLCHQAFLL 1080
 DB 1021 FHOQVWKQPTFLRATISDTASLCYSILKAKNAGMSLAKGAAGPLPSBAVOMLCHQAFLL 1080
 QY 1081 KLTRHRTVYVPLLSLRTAQQLSRKLPQTITLTALEAANPALPSDFKTIID 1132
 DB 1081 KLTRHRTVYVPLLSLRTAQQLSRKLPQTITLTALEAANPALPSDFKTIID 1132

RESULT 17
 ABR58045
 ID ABR58045 standard; protein; 1132 AA.
 XX
 AC ABR58045;
 XX
 DT 29-AUG-2003 (first entry)
 XX
 DE Human telomerase reverse transcriptase.
 XX
 KW Enzyme; human; telomerase reverse transcriptase; adipogenic capacity;
 KW primary preadipocyte cell; adipogenesis; obesity; adipocytokine;
 XX
 OS Homo sapiens.
 XX
 PN WO2003031640-A2.
 XX
 PD 17-APR-2003.
 XX
 PF 07-OCT-2002; 2002WO-US031635.
 XX
 PR 06-OCT-2001; 2001US-0327650P.
 XX
 PR 06-OCT-2001; 2001US-0327651P.
 XX
 PA (BOST-) BOSTON MEDICAL CENT CORP.
 XX
 PI Kirkland J, Tchekonia T;
 XX
 DR WPI; 2003-421278/39.
 XX
 DR N-PSDB; ACC44482.
 XX
 PT New primary preadipocyte strain expressing telomerase reverse transcriptase, useful in research applications, screening assays, clinical applications, and in the administration of therapeutic agents.

PT particularly for obesity.
XX
XX Disclosure; Page 13; 53pp; English.
XX
CC The invention relates to the generation of primary preadipocyte cell
CC strains that express telomerase reverse transcriptase (TERT, the
CC catalytic subunit of telomerase), and maintain and/or enhance replicative
CC potential and maintain adipogenic capacity of the cell. This sequence
CC represents the TERT protein. The cell strain can be used in research to
CC study all aspect of adipogenesis, especially in relation to researching
CC treatments for e.g. obesity. The cell can also be used to identify
CC adipogenesis modulators for use as therapeutic agents such as hormones,
CC growth factors, cytokines, enzymes, cholesterol binding proteins,
CC cholesterol removing proteins or their combinations. Alternatively, the
CC therapeutic agent may be an adipocytokine, preferably adiponectin, or
CC insulin
XX
XX Sequence 1132 AA;
Query Match. 99.8%; Score 5952; DB 6; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MPRAAPCRVRSLSLRSHREVLPLATFVRSLGPGKRLVQSGDPAFAFALVQCLVCPM 60
Db 1 MPRAAPCRVRSLSLRSHREVLPLATFVRSLGPGKRLVQSGDPAFAFALVQCLVCPM 60
QY 61 DAPPPAPASFRVQSCLELVAVRLQRLCERGAKNVLAFGALLDAGRGPEAFTTSVR 120
Db 61 DAPPPAPASFRVQSCLELVAVRLQRLCERGAKNVLAFGALLDAGRGPEAFTTSVR 120
QY 121 SYLPTVTALNRSGAWGILLRRVGDVYLHLLACALFVLAAPCAVQCPPLVQGA 180
Db 121 SYLPTVTALNRSGAWGILLRRVGDVYLHLLACALFVLAAPCAVQCPPLVQGA 180
QY 181 ATQAPPPHAGSGRRRLGGERAMNSVRAGVPLGLPAGARRGSGASRSLLPKPRR 240
Db 181 ATQAPPPHAGSGRRRLGGERAMNSVRAGVPLGLPAGARRGSGASRSLLPKPRR 240
QY 241 GAAPBEERPPVGGGWAHPGRTGSDRGFCVSPAPAPAEATSLGALSGTRHSPVG 300
Db 241 GAAPBEERPPVGGGWAHPGRTGSDRGFCVSPAPAPAEATSLGALSGTRHSPVG 300
QY 301 ROHHAGPSTSRPPRPMWPCPPVVAETGHLFYSSGDKEQLRPSLLSLRSLTGARRL 360
Db 301 ROHHAGPSTSRPPRPMWPCPPVVAETGHLFYSSGDKEQLRPSLLSLRSLTGARRL 360
QY 361 VETIFLGSRRPMWGPTRRLPLPQRYWQNRPLFELLGNAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRRPMWGPTRRLPLPQRYWQNRPLFELLGNAQCPYGVLLKTHCPRAAVT 420
QY 421 PAAGVABRKPGSVAPAEEDTDPRRLVQLRQSSPMQVGFYACLRRLVPPGLMG 480
Db 421 PAAGVABRKPGSVAPAEEDTDPRRLVQLRQSSPMQVGFYACLRRLVPPGLMG 480
QY 481 RHNERFLNRTKFKLSLGKAKLSLOELTWKMSVDCAMLRSPGVGCVPAAEHRLREI 540
Db 481 RHNERFLNRTKFKLSLGKAKLSLOELTWKMSVDCAMLRSPGVGCVPAAEHRLREI 540
QY 541 LAKFLHMLSVYVVELRFFVYETTPQKRLFFYRPSWSKLSIGIRHLKRVQRE 600
Db 541 LAKFLHMLSVYVVELRFFVYETTPQKRLFFYRPSWSKLSIGIRHLKRVQRE 600
QY 601 LSEAEVRQREARPALITSLRFLPKDGLRPIVMDVVGARTREKRAERLTSRYKA 660
Db 601 LSEAEVRQREARPALITSLRFLPKDGLRPIVMDVVGARTREKRAERLTSRYKA 660
QY 661 LRSVLYNEARPPGLIGASVLGLDIHRAWRTFVLRAODPPRLVYKVDVGAADTI 720
Db 661 LRSVLYNEARPPGLIGASVLGLDIHRAWRTFVLRAODPPRLVYKVDVGAADTI 720
QY 721 PDRLEVIASIIKQNTYCVRRYAVVOKAAGHVRKAFKSHVSTLTDQPYMRQFVAHL 780
Db 721 PDRLEVIASIIKQNTYCVRRYAVVOKAAGHVRKAFKSHVSTLTDQPYMRQFVAHL 780

Db 721 PDRLEVIASIIKQNTYCVRRYAVVOKAAGHVRKAFKSHVSTLTDQPYMRQFVAHL 780
QY 781 QETSPRLDAVAVIEOSSSLNASSGLPDLFLRPMCHAVRIRGSHYVQCGIIPGGSILSTL 840
Db 781 QETSPRLDAVAVIEOSSSLNASSGLPDLFLRPMCHAVRIRGSHYVQCGIIPGGSILSTL 840
QY 841 LCSLCYDMDENKLPAGIRRDGILLRLVDDPLVTPHLTHAKTLRLVRCVPEYGVNL 900
Db 841 LCSLCYDMDENKLPAGIRRDGILLRLVDDPLVTPHLTHAKTLRLVRCVPEYGVNL 900
QY 901 RKTVMNPFVDEALGGAFAVQMPAHGIFPWCGLLDTREIVOSDYSVARTSRASVTF 960
Db 901 RKTVMNPFVDEALGGAFAVQMPAHGIFPWCGLLDTREIVOSDYSVARTSRASVTF 960
QY 961 NRGFKARNRRKLPGLRLKCHSLPDLQVNSLQTCVNIYKILLQAVRPAVYLQLP 1020
Db 961 NRGFKARNRRKLPGLRLKCHSLPDLQVNSLQTCVNIYKILLQAVRPAVYLQLP 1020
QY 1021 FHQGVKNPFFPLRVISDTASLCYSIIKANAQMSIGAKGAPLPSEAVQMLCHQAFLL 1080
Db 1021 FHQGVKNPFFPLRVISDTASLCYSIIKANAQMSIGAKGAPLPSEAVQMLCHQAFLL 1080
QY 1081 KLTRHRTVYPLGSLRTAQTOLSRKLPGLTFLALEAANPALPSPFKTILD 1132
Db 1081 KLTRHRTVYPLGSLRTAQTOLSRKLPGLTFLALEAANPALPSPFKTILD 1132
RESULT 18
ADD21420
ID ADD21420 standard; protein; 1132 AA.
XX
AC ADD21420;
XX
DT 15-JAN-2004 (first entry)
XX
XX Human TERT protein related to continual cell growth.
XX
KW continual growth; cultured cell; cyclin dependent kinase; cdk4; cdk2;
KW cdk6; activating mutation; cell growth; cell division; cell cycle;
KW cancer-causing agent; continual growth-induced cell; enzyme; TERT;
KW telomerase; human.
XX
OS Homo sapiens.
XX
XX WO2003044169-A2.
XX
PN 30-MAY-2003.
XX
PD 15-NOV-2002; 2002MO-US036729.
XX
PF 15-NOV-2001; 2001US-0334760P.
XX
PR (ITEM) UNITV TEMPLE.
XX
FA Reddy PE, Rane SG, Mettus RV;
XX
PI Reddy PE, Rane SG, Mettus RV;
XX
PI WPI; 2003-449813/42.
XX
DR
XX
PT A composition for reversibly inducing continual growth in normal cells
PT comprises a cyclin dependent kinase protein (e.g. cdk4, cdk2 or cdk6) or
PT its active fragment, derivative, homolog or analog, having an activating
PT mutation.
XX
PS Claim 16; Page 135-138; 77pp; English.
XX
CC This invention relates to a novel composition for inducing a reversible
CC state of a continual growth in cultured cells and comprises at least one
CC compound comprising a cyclin dependent kinase (cdk)4, cdk2 or cdk6
CC protein having an activating mutation. Growth and division of living
CC cells involve a regular series of events and processes that comprise the
CC cell cycle. Cyclin dependent kinases cdk2, cdk4 and cdk6 are involved in
CC the control of G1, the point at which cells irreversibly commit to DNA
CC synthesis and thus enter the cell cycle. The invention is useful in

CC reversibly inducing continual growth in normal cells and may allow the
 CC screening of cancer-causing agents with the continual growth-induced
 CC cells. The present sequence is that of the human TERT protein, the
 CC catalytic subunit of telomerase, related to the invention. Note: Due to
 CC an error in the specification or sequence listing, the Seq ID numbers
 CC given in the disclosure do not correspond to those given in the sequence
 CC listing. It is therefore unclear which Seq ID number corresponds to which
 CC sequence and exactly which sequence is being claimed.

XX
 SQ Sequence 1132 AA;

Query Match 99.8%; Score 5952; DB 7; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPBAPCRARSLRLSHVREVLPLATFVRRLGPGQRLVORGDPAPAFALVACLVCPWM 60
 Db 1 MPBAPCRARSLRLSHVREVLPLATFVRRLGPGQRLVORGDPAPAFALVACLVCPWM 60
 QY 61 DARPAPAPSPFROVSCIKELVARVLQRLCERGANVLAFGFALLDAGRGPPAFTSVR 120
 Db 61 DARPAPAPSPFROVSCIKELVARVLQRLCERGANVLAFGFALLDAGRGPPAFTSVR 120
 QY 121 SYLPNTTDLRSGGAMGLLRVGDVYLHLLARCLFVLVAPSGAYVCGPPLYLQGA 180
 Db 121 SYLPNTTDLRSGGAMGLLRVGDVYLHLLARCLFVLVAPSGAYVCGPPLYLQGA 180
 QY 181 ATQARPPHAGSPRRRLCERAMNHSVREAGVPLGLPAPGARRRGSSASRLPLKRRPR 240
 Db 181 ATQARPPHAGSPRRRLCERAMNHSVREAGVPLGLPAPGARRRGSSASRLPLKRRPR 240
 QY 241 GAAPERTITVGGGSAHPGRTGSPRGCVVSPAPAEALSLRGALSGTHSHPSVG 300
 Db 241 GAAPERTITVGGGSAHPGRTGSPRGCVVSPAPAEALSLRGALSGTHSHPSVG 300
 QY 301 ROHHAGPSTSRPRPMDTCPPIYATETKAFILVSSGGKEQLRPSFLSLRPLTGARRL 360
 Db 301 ROHHAGPSTSRPRPMDTCPPIYATETKAFILVSSGGKEQLRPSFLSLRPLTGARRL 360
 QY 361 VETIFLGSPPMPCGTFRRLPLPQRYWQMRPLFELIIGNAQCPCYVLLKTHCPLEAAT 420
 Db 361 VETIFLGSPPMPCGTFRRLPLPQRYWQMRPLFELIIGNAQCPCYVLLKTHCPLEAAT 420
 QY 421 PAAGVCAKEKPGQSVAPBEEDTPRRLVQLRHSSPMQVGVFVRACLRLVPPGLMGS 480
 Db 421 PAAGVCAKEKPGQSVAPBEEDTPRRLVQLRHSSPMQVGVFVRACLRLVPPGLMGS 480
 QY 481 RHNERRLRLNTKFLISLGHAKLSLOELTWKMSVRCAMLRSPGVGCVAEHRRLREEL 540
 Db 481 RHNERRLRLNTKFLISLGHAKLSLOELTWKMSVRCAMLRSPGVGCVAEHRRLREEL 540
 QY 541 LAKFLHMLMSYVVELLSRFYVTTETTFQKRLFFRPSWSKLSQSIGIQLKRVOLRE 600
 Db 541 LAKFLHMLMSYVVELLSRFYVTTETTFQKRLFFRPSWSKLSQSIGIQLKRVOLRE 600
 QY 601 LSEAEVCHREARPALTSRLRFIPKPGRLPIYNNVYVAGARFRREKAEARLTSVKA 660
 Db 601 LSEAEVCHREARPALTSRLRFIPKPGRLPIYNNVYVAGARFRREKAEARLTSVKA 660
 QY 661 LFSVLNTERARPGILGASVGLDDIRAMTFVLARVAOCPPELFFVKVDVGAYDTI 720
 Db 661 LFSVLNTERARPGILGASVGLDDIRAMTFVLARVAOCPPELFFVKVDVGAYDTI 720
 QY 721 PODLLEVIASIIIPONTVCVRRYAVVOKAHGVRKAFKSHVSTLIDLPYMQFVAHL 780
 Db 721 PODLLEVIASIIIPONTVCVRRYAVVOKAHGVRKAFKSHVSTLIDLPYMQFVAHL 780
 QY 781 QETSLRDVAVYIEGSSLINEASSGLFDVFLRFMCHAVAIRIGKSYVOCGIPQSSILSTL 840
 Db 781 QETSLRDVAVYIEGSSLINEASSGLFDVFLRFMCHAVAIRIGKSYVOCGIPQSSILSTL 840
 QY 841 LCSLCYGMENKLPAGIRDDGLLRVNDLFLVPHLTHAKTFLRLTVRGVPEYGVNVL 900

Db 841 LCSLCYGMENKLPAGIRDDGLLRVNDLFLVPHLTHAKTFLRLTVRGVPEYGVNVL 900
 QY 901 RKTIVNPFVEDEALGTAIVQMPAHGLFPMCGLLDTRTLEVSQSYASRTASVTF 960
 Db 901 RKTIVNPFVEDEALGTAIVQMPAHGLFPMCGLLDTRTLEVSQSYASRTASVTF 960
 QY 961 NRGFGAGNNRRKIFGVIRLKGSLFDLPQVNSIQYCTNTYKILLQAVRFAVCVQLP 1020
 Db 961 NRGFGAGNNRRKIFGVIRLKGSLFDLPQVNSIQYCTNTYKILLQAVRFAVCVQLP 1020
 QY 1021 FHQGVWKNPTEFLVISTASTLCYSILKAKAGMSLAKAGAGPLPEAVQMLCHOAFLL 1080
 Db 1021 FHQGVWKNPTEFLVISTASTLCYSILKAKAGMSLAKAGAGPLPEAVQMLCHOAFLL 1080
 QY 1081 KLTRRRVTVVPLGSLRTAQOLSRKLPGTTTLALEAANPALPSDEKTIID 1132
 Db 1081 KLTRRRVTVVPLGSLRTAQOLSRKLPGTTTLALEAANPALPSDEKTIID 1132
 Db 1081 KLTRRRVTVVPLGSLRTAQOLSRKLPGTTTLALEAANPALPSDEKTIID 1132
 RESULT 19
 ADH72743
 ID ADH72743 standard; protein, 1132 AA.
 AC
 XX ADH72743;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Human protein of the invention SEQ ID NO:19.
 XX
 XX stem cell; cardiatic; hepatotropic; nephrotropic; cytosolic; neotropic;
 KW neuroprotective; antiarthritic; antidiabetic; antiarteriosclerotic;
 KW heart failure; leukaemia; neurodegenerative disease; diabetes;
 KW arteriosclerosis; skeletal muscle; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003027281-A2.
 XX
 PD 03-APR-2003.
 XX
 PF 20-SEP-2002; 2002WO-TP009702.
 XX
 PR 20-SEP-2001; 2001JP-00286332.
 XX
 PR 09-MAY-2002; 2002JP-00133575.
 XX
 PA (KYOM) KYOMA HAKKO KOGYO KK.
 PA (TAMA/) TAMA K.
 PA (ANDO/) ANDO K.
 PI Tamaki T, Ando K, Akatsuka A, Nakamura Y, Hotta T, Sakurada K;
 XX
 XX WPI; 2003-371925/35.
 XX
 DR Pluripotent stem cells originating in skeletal muscle interstitial
 XX tissue, useful in drugs for regenerating tissues and cells e.g. in
 PT treating heart failure, leukaemia, neurodegenerative diseases, and
 PT diabetes.
 PS Disclosure; SEQ ID NO 19; 29pp; Japanese.
 XX
 XX The invention relates to novel pluripotent stem cells originating from a
 CC skeletal muscle interstitial tissue. A cell of the invention has
 CC cardiatic, hepatotropic, nephrotropic, cytosolic, neotropic,
 CC neuroprotective, antiarthritic, antidiabetic, and antiarteriosclerotic
 CC activity. The cells are useful in drugs for regenerating tissues and
 CC cells e.g. in treating heart failure, leukaemia, neurodegenerative
 CC diseases, diabetes and arteriosclerosis. The pluripotent stem cells were
 CC isolated from rat skeletal muscles after analysis of the various
 CC components by culturing and staining, as well as by other biochemical
 CC analysis. The present sequence is used in the exemplification of the
 CC invention.
 XX
 XX Sequence 1132 AA;

Query Match 99.8%; Score 5952; DB 7; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSILRSHREVLPLATFVRRLGPGQRLVORGDPAAFRALVAQCLVCVPM 60
 DB 1 MPAPRCRAVRSILRSHREVLPLATFVRRLGPGQRLVORGDPAAFRALVAQCLVCVPM 60

QY 61 DAPPPAASFFOVSCIKELVARVLOQLCEGAKXVLAFGFLLDAGAGPPEAFTTSVR 120
 DB 61 DAPPPAASFFOVSCIKELVARVLOQLCEGAKXVLAFGFLLDAGAGPPEAFTTSVR 120

QY 121 SYLPNTVTALRSGAGMGLLRVGDVIVHLIARCALFVLAFCAYVCCPPLYOLGA 180
 DB 121 SYLPNTVTALRSGAGMGLLRVGDVIVHLIARCALFVLAFCAYVCCPPLYOLGA 180

QY 181 ATQAPRPPHAGSRRLGGERAMNHSVRACVPLGIPAGARRGGSASRLPLKPRR 240
 DB 181 ATQAPRPPHAGSRRLGGERAMNHSVRACVPLGIPAGARRGGSASRLPLKPRR 240

QY 241 GAAPERTPVGGGSAHFGRTGSPDRGFCVSPAPAEATSLGALSGTRHSHPSVG 300
 DB 241 GAAPERTPVGGGSAHFGRTGSPDRGFCVSPAPAEATSLGALSGTRHSHPSVG 300

QY 301 ROHHAGPPTSPRPPEWDTPCPPVAETKHFYSSGDKQLRPSFLSSLRPSLTGARRL 360
 DB 301 ROHHAGPPTSPRPPEWDTPCPPVAETKHFYSSGDKQLRPSFLSSLRPSLTGARRL 360

QY 361 VETIFLGSRRPMGTRRLPRLPORWQVRPLFLELIGNHACCPGVLLKTCPRRAVT 420
 DB 361 VETIFLGSRRPMGTRRLPRLPORWQVRPLFLELIGNHACCPGVLLKTCPRRAVT 420

QY 421 PAAGVAREKPOGSVAPEEEDTPRRIVOLLROHSSPMQVYGFVACLRRLVPEGLWS 480
 DB 421 PAAGVAREKPOGSVAPEEEDTPRRIVOLLROHSSPMQVYGFVACLRRLVPEGLWS 480

QY 481 RHNERFLNKKETSLGKAKLSLOELTWKSVDCAMLRSPGVCPAAHEHLREI 540
 DB 481 RHNERFLNKKETSLGKAKLSLOELTWKSVDCAMLRSPGVCPAAHEHLREI 540

QY 541 LAKFLHMLSVYVVELRSPFYVETTFQKRLFPYRPSWSKLSIGIRHOLKRVQRE 600
 DB 541 LAKFLHMLSVYVVELRSPFYVETTFQKRLFPYRPSWSKLSIGIRHOLKRVQRE 600

QY 601 LSEAEVRQREARPALITSLRFLFKPDGLRPIVNDYVVGARTRRRKAERLTSRYKA 660
 DB 601 LSEAEVRQREARPALITSLRFLFKPDGLRPIVNDYVVGARTRRRKAERLTSRYKA 660

QY 661 LPSVLYERARRPGLGASVGLDDIHRAMRTFVLRVADPPPELYEVKVDVAGAYDTI 720
 DB 661 LPSVLYERARRPGLGASVGLDDIHRAMRTFVLRVADPPPELYEVKVDVAGAYDTI 720

QY 721 PODRLTEVASTIKQNTYCVARVAVVOKAHGHVKAFKSHVSTLTDLOPYMKQFVAHL 780
 DB 721 PODRLTEVASTIKQNTYCVARVAVVOKAHGHVKAFKSHVSTLTDLOPYMKQFVAHL 780

QY 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRPMCHAVRIGKSVQCGIPQSSILSTL 840
 DB 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRPMCHAVRIGKSVQCGIPQSSILSTL 840

QY 841 LCSLCYGMENKLFAGIRRDGILLRLVDPFLVTHLTHAKTFLRTLVGVPBEYGVNLT 900
 DB 841 LCSLCYGMENKLFAGIRRDGILLRLVDPFLVTHLTHAKTFLRTLVGVPBEYGVNLT 900

QY 901 RTIVNFPVEDALGGTAFVQMPAHGLFPWCGLLDITTELEVQSSYATSTIRASVTF 960
 DB 901 RTIVNFPVEDALGGTAFVQMPAHGLFPWCGLLDITTELEVQSSYATSTIRASVTF 960

QY 961 NRGFGAGNMRRKLFGLVRLKCHSLFLDQVNSIQTVCTNIYKLLILQAYRFAHCYQLP 1020
 DB 961 NRGFGAGNMRRKLFGLVRLKCHSLFLDQVNSIQTVCTNIYKLLILQAYRFAHCYQLP 1020

QY 1021 FHQQWKNPPEFLVISDTASLCYSILKARNAGSLGAKGAGPLPSEAYOWICHOAFLL 1080
 DB 1021 FHQQWKNPPEFLVISDTASLCYSILKARNAGSLGAKGAGPLPSEAYOWICHOAFLL 1080

QY 1081 KLTSHRVTVYVPLGSLRTAQTOLSRKLGTTTLALEAANPALPSPFKTILD 1132
 DB 1081 KLTSHRVTVYVPLGSLRTAQTOLSRKLGTTTLALEAANPALPSPFKTILD 1132

RESULT 20
 ADG70114
 ID ADG70114 standard; protein: 1132 AA.
 XX
 AC ADG70114;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE hTERT protein.
 XX
 KW cytosolic; gene therapy; reverse transcriptase-inhibitor; HIV-1;
 KW human telomerase reverse transcriptase; hTERT; chimeric; catalytic site;
 KW unregulated cellular growth; cancer; tumor.
 XX
 OS Homo sapiens.
 XX
 FN MO2003095605-A2.
 XX
 PD 20-NOV-2003.
 XX
 PF 14-APR-2003; 2003MO-EP003874.
 XX
 PR 08-MAY-2002; 2002US-0378820P.
 XX
 PA (PHAA) PHARMACIA ITAL SPA.
 XX
 PI Moll J, Schnuchel A, Stouten P;
 XX
 DR WPI, 2004-012095/01.
 XX
 DR N-PSDE; ADG70113.
 XX
 PT New HIV-1 Reverse Transcriptase and human Telomerase Reverse
 PT Transcriptase proteins and nucleic acids, useful in gene therapy or for
 PT treating or preventing unregulated cellular growth, e.g. cancer cell or
 PT tumor growth.
 XX
 PS Example 1; SEQ ID NO 4; 141pp; English.
 XX
 CC The invention relates to the isolation of compounds that bind and inhibit
 CC the activity of HIV-1 reverse transcriptase (RT) or human telomerase
 CC reverse transcriptase (hTERT). The method involves determining these
 CC compounds using a HIV-1 RT/hTERT chimeric construct containing the
 CC catalytic sites of each enzyme. The nucleic acid is useful for treating
 CC or preventing unregulated cellular growth, including cancer cell and
 CC tumor growth. It is also useful in gene therapy. Compounds that inhibit
 CC telomerase activity can be used to treat cancer. The vectors of the
 CC invention can be used to amplify DNA or RNA encoding HIV-RT/hTERT and/or
 CC express DNA which encodes HIV-RT/hTERT. This sequence corresponds to the
 CC human TERT protein.
 XX
 SQ Sequence 1132 AA;

Query Match 99.8%; Score 5952; DB 8; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSILRSHREVLPLATFVRRLGPGQRLVORGDPAAFRALVAQCLVCVPM 60
 DB 1 MPAPRCRAVRSILRSHREVLPLATFVRRLGPGQRLVORGDPAAFRALVAQCLVCVPM 60

QY 61 DAPPPAASFFOVSCIKELVARVLOQLCEGAKXVLAFGFLLDAGAGPPEAFTTSVR 120
 DB 61 DAPPPAASFFOVSCIKELVARVLOQLCEGAKXVLAFGFLLDAGAGPPEAFTTSVR 120

QY	12	SYLBNPTATDRLRGSGAWGLILRRYGDVYLHLLRCAFLFYLVASCAQYQVGPPLYQGA	180
Db	121	SYLBNPTATDRLRGSGAWGLILRRYGDVYLHLLRCAFLFYLVASCAQYQVGPPLYQGA	180
QY	181	ATQARPPPHASGPPRRLLGCERAMNHSYEAQVPLGLPAPGARRRGGSASRLPLPKRPRR	240
Db	181	ATQARPPPHASGPPRRLLGCERAMNHSYEAQVPLGLPAPGARRRGGSASRLPLPKRPRR	240
QY	241	GAABEPBTPVQGSMAHPGRTBPSRQGFVVSAPARAEEATLEGALESTBHSHSVQ	300
Db	241	GAABEPBTPVQGSMAHPGRTBPSRQGFVVSAPARAEEATLEGALESTBHSHSVQ	300
QY	301	ROHHAGEPSTSRPRPMDTPCPVYAETKHFLLYSSGDKQLRPSFLLSLRPSLTGARRL	360
Db	301	ROHHAGEPSTSRPRPMDTPCPVYAETKHFLLYSSGDKQLRPSFLLSLRPSLTGARRL	360
QY	361	VEITFLSRPMPGTPRRLRPLPORVOMRPLFLELLGNHACQCYGVLLKTHGCLRAVY	420
Db	361	VEITFLSRPMPGTPRRLRPLPORVOMRPLFLELLGNHACQCYGVLLKTHGCLRAVY	420
QY	421	PAQVCAREKQGSVAABEEDTDPRRLVOLLROHSSPWOYUYGVRACTLRRLVPPGLWS	480
Db	421	PAQVCAREKQGSVAABEEDTDPRRLVOLLROHSSPWOYUYGVRACTLRRLVPPGLWS	480
QY	481	RHNRRRLRNKKFLISGKHNKLSQELTWKMSYRDCMYLRRSGVGVCPARAEBRLBEI	540
Db	481	RHNRRRLRNKKFLISGKHNKLSQELTWKMSYRDCMYLRRSGVGVCPARAEBRLBEI	540
QY	541	LAKELHMLMSYVVELLRSPFYVTEETTFQKORLFFYRPSVMSKLSIGIRGHLRVOLRE	600
Db	541	LAKELHMLMSYVVELLRSPFYVTEETTFQKORLFFYRPSVMSKLSIGIRGHLRVOLRE	600
QY	601	LSEAEVQOHRARPLLTSRLRFLPKRPGCAPIYMMQDVGAARPPRKRARELRLSRKA	660
Db	601	LSEAEVQOHRARPLLTSRLRFLPKRPGCAPIYMMQDVGAARPPRKRARELRLSRKA	660
QY	661	LFSVLNTERARPGILGASVLGLDDIHRAMRTFVLVRAAODRPRELYVKKVDVGAYDTI	720
Db	661	LFSVLNTERARPGILGASVLGLDDIHRAMRTFVLVRAAODRPRELYVKKVDVGAYDTI	720
QY	721	POBLRTEVIAIIRKQNTYCYRRAVAVOKAANGHYRKAFKSHVSTLTDLOXYMOQFAVHL	780
Db	721	POBLRTEVIAIIRKQNTYCYRRAVAVOKAANGHYRKAFKSHVSTLTDLOXYMOQFAVHL	780
QY	781	QETSPRLDAVYIEOSSSLNEASSGFLFVFLRPMCNAHVARIGKSYVQCGIPOSILSTL	840
Db	781	QETSPRLDAVYIEOSSSLNEASSGFLFVFLRPMCNAHVARIGKSYVQCGIPOSILSTL	840
QY	841	LCSLCYGMEMKULPAGIRRDGLILRLVDDFLILPHLTHACTFLRTLVRGPREVGCYVNL	900
Db	841	LCSLCYGMEMKULPAGIRRDGLILRLVDDFLILPHLTHACTFLRTLVRGPREVGCYVNL	900
QY	901	RKTUVNFEVDEALGTAFAVQMPAHGLPMMCGLLDTTLEVOQSYSSEYASTISRASVTF	960
Db	901	RKTUVNFEVDEALGTAFAVQMPAHGLPMMCGLLDTTLEVOQSYSSEYASTISRASVTF	960
QY	961	NRGFRAGNNRRKULFGVIRLKCBSIFLDLOVNSLQTVCTNIYKILLOAYRFFHACVLOLF	1020
Db	961	NRGFRAGNNRRKULFGVIRLKCBSIFLDLOVNSLQTVCTNIYKILLOAYRFFHACVLOLF	1020
QY	1021	FHQQVWKRPTEFLRVIDSTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVOMLGHQAFLL	1080
Db	1021	FHQQVWKRPTEFLRVIDSTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVOMLGHQAFLL	1080
QY	1081	KLTRRRVTVVPLLSGLRTAQOTLSKRLPGTTLTAAEAAANPALBDFETIILD	1132
Db	1081	KLTRRRVTVVPLLSGLRTAQOTLSKRLPGTTLTAAEAAANPALBDFETIILD	1132

AC ADG90599;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human TERT SEQ ID NO:2.
XX
XX human; immune response; telomerase reverse transcriptase; TERT;
XX cytosolic; immunostimulant; cancer; cytotoxic T cell response.
XX
XX Homo sapiens.
XX
XX WO2004002408-A2.
XX
XX 08-JAN-2004.
XX
XX 24-JUN-2003; 2003WO-US019844.
XX
XX 27-JUN-2002; 2002US-03932955.
XX
XX (GERO-) GERON CORP.
XX
XX Majumdar A, Ferber IA, Frolkis M, Wang Z,
XX
XX WPI; 2004-071946/07.
XX
XX N-PSDB; ADG90598.
XX
XX
XX Eliciting an immune response in a mammal specific for its own telomerase
XX reverse transcriptase (TERT), useful for treating or preventing cancer,
XX comprises administering a composition containing TERT of another
XX mammalian species.
XX
XX
XX Claim 66; SEQ ID NO 2; 44pp; English.
XX
XX
XX The invention relates to a novel method for eliciting an immune response
XX in a mammalian subject that is specific for its own telomerase reverse
XX transcriptase (TERT), comprising administering an immunogenic composition
XX containing a protein with at least 20 consecutive amino acids of TERT of
XX another mammalian species, or a nucleic acid encoding the protein. A
XX composition of the invention has cytostatic, and immunostimulant
XX activity. The protein or the nucleic acid encoding the protein is useful
XX in the manufacture of a medicament for the treatment of cancer in a human
XX or for eliciting a cytotoxic T cell response in a human.
XX
XX Sequence 1132 AA;

```
Query Match      99.8%;  Score 5952;  DB 8;  Length 1132;
Best Local Similarity 99.8%;  Pred. No. 0;
Matches 1130;  Conservative 1;  Mismatches 1;  Indels 0;  Gaps 0;
```

QY	1	MPAPACRAVRSLTSHREYVPLTTPRRLGPGCWLYORGDAAPRALVACIYCVPM	60
Db	1	MPAPACRAVRSLTSHREYVPLTTPRRLGPGCWLYORGDAAPRALVACIYCVPM	60
QY	61	DAPPAPASPROVSCIKELVARVQLRCERAKNVLAFCGALLDGARGPPEAFTTSVR	120
Db	61	DAPPAPASPROVSCIKELVARVQLRCERAKNVLAFCGALLDGARGPPEAFTTSVR	120
QY	121	SYLPNTVTALRGSGWGLLRVBDVPLHLARCLFVLVAPSCAYVCGPPLYOLGA	180
Db	121	SYLPNTVTALRGSGWGLLRVBDVPLHLARCLFVLVAPSCAYVCGPPLYOLGA	180
QY	181	ATGAPRPFAHSGRRRLGGERAMNHSVBEAGVPLGAPGARRRGSAASLSLIPKAPRR	240
Db	181	ATGAPRPFAHSGRRRLGGERAMNHSVBEAGVPLGAPGARRRGSAASLSLIPKAPRR	240
QY	241	GAAPPEPRIVGGGSAWHGRTGCGSDGFCVWSPARAEATLSLEALGSTRHSHPVG	300
Db	241	GAAPPEPRIVGGGSAWHGRTGCGSDGFCVWSPARAEATLSLEALGSTRHSHPVG	300
QY	301	ROHHAGPSTSRPRPMDTPCPPTVTAETKHFLYSSGDKGEOIRBSFLLSLRPSLTGARRL	360
Db	301	ROHHAGPSTSRPRPMDTPCPPTVTAETKHFLYSSGDKGEOIRBSFLLSLRPSLTGARRL	360

[illegible]

QY 361 VETIFGSRPMWPGTBRRLPRLPORWQMRPFLLELGNHACPGVLLKTHCPRAAVT 420
 DB 361 VETIFGSRPMWPGTBRRLPRLPORWQMRPFLLELGNHACPGVLLKTHCPRAAVT 420
 QY 421 PAAGVCAKREKPGSVAAPEEDTDRRLVQLRCHSSPMQVGFYACLRRLVPPGLMGS 480
 DB 421 PAAGVCAKREKPGSVAAPEEDTDRRLVQLRCHSSPMQVGFYACLRRLVPPGLMGS 480
 QY 481 RHNERFRLNTKFFISLGHAKLSLOELTWKMSVDCAMLRSPBGVCVPAAEHLREBI 540
 DB 481 RHNERFRLNTKFFISLGHAKLSLOELTWKMSVDCAMLRSPBGVCVPAAEHLREBI 540
 QY 541 LAKFLHMLMSYVVELLRSFYVETTFEQKRLFFYRPSVSKLOSIGIRHLKRVQURE 600
 DB 541 LAKFLHMLMSYVVELLRSFYVETTFEQKRLFFYRPSVSKLOSIGIRHLKRVQURE 600
 QY 601 LSEAEVROREARPAALLTSRLRFIPKPDGLPIVNDYVYGARTRRREKARELTSRYKA 660
 DB 601 LSEAEVROREARPAALLTSRLRFIPKPDGLPIVNDYVYGARTRRREKARELTSRYKA 660
 QY 661 LFSVLYNEARBPGLLGASVLDLDIRAMRTFVLVRAODEPPELVFVKVDVIGAYDTI 720
 DB 661 LFSVLYNEARBPGLLGASVLDLDIRAMRTFVLVRAODEPPELVFVKVDVIGAYDTI 720
 QY 721 PODRLTEVIASIIKQNTYCVRRYAVVQKAAGHVRKAKFKSHVSTLTDLQPYMQFVAHL 780
 DB 721 PODRLTEVIASIIKQNTYCVRRYAVVQKAAGHVRKAKFKSHVSTLTDLQPYMQFVAHL 780
 QY 781 QETSPRLDVAVLEOSSSINEASSGLPDVFLRFMCHAVRIGKSVVQCGIPQGSIIITL 840
 DB 781 QETSPRLDVAVLEOSSSINEASSGLPDVFLRFMCHAVRIGKSVVQCGIPQGSIIITL 840
 QY 841 LQSLCGDMENKLPAGIRRDGLLRLVDLFLVTLPHLTHAKFTLTLVRGVPEXCVNL 900
 DB 841 LQSLCGDMENKLPAGIRRDGLLRLVDLFLVTLPHLTHAKFTLTLVRGVPEXCVNL 900
 QY 901 RKTVNFPEPBDALGTAFAVQMPAGLPPWCGLLDPTLEVOQSYSSYATSTRASVTF 960
 DB 901 RKTVNFPEPBDALGTAFAVQMPAGLPPWCGLLDPTLEVOQSYSSYATSTRASVTF 960
 QY 961 NNGFKAQRMRERKLFQVLRKCHSLFLDQVNSLQTVGCNIIYKILLQAYEFHACVQLP 1020
 DB 961 NNGFKAQRMRERKLFQVLRKCHSLFLDQVNSLQTVGCNIIYKILLQAYEFHACVQLP 1020
 QY 1021 FHQCVKAFETPFLRVIISDTASLCYSILKAKNAGSLAKGAAGPLPSAVOMLCHQAFLL 1080
 DB 1021 FHQCVKAFETPFLRVIISDTASLCYSILKAKNAGSLAKGAAGPLPSAVOMLCHQAFLL 1080
 QY 1081 KLTRHRVTVPPLGSLRTAQOTLSRKLPGTTLTALEAANPALPSDFKTIID 1132
 DB 1081 KLTRHRVTVPPLGSLRTAQOTLSRKLPGTTLTALEAANPALPSDFKTIID 1132
 RESULT 22
 AD182172
 ID AD182172 standard; protein; 1132 AA.
 AC AD182172;
 XX
 DT 22-APR-2004 (first entry)
 DE Human telomerase reverse transcriptase.
 XX
 KW Human; embryonic stem cell; pluripotent stem cell; abnormal cell growth;
 OS Homo sapiens.
 XX
 PN US2003224411-A1.
 XX
 PD 04-DEC-2003.
 PF 13-MAR-2003; 2003US-00388578.

XX 13-MAR-2003; 2003US-00388578.
 PR
 XX (STAN/) STANTON L W.
 PA (BRAN/) BRANDENBERGER R.
 PA (GOLD/) GOLD J D.
 PA (IRVI/) IRVING J M.
 PA (MAND/) MANDALAM R.
 PA (MOKM/) MOK M.
 PA (SHEL/) SHELTON D.
 XX
 PI Stanton LM, Brandenberger R, Gold JD, Irving JM, Mandalam R;
 PI Mok M, Shelton D;
 DR WPI: 2004-119701/12.
 DR N-PSDB; AD182171.
 XX
 PT Assessing culture of undifferentiated primate pluripotent stem cells by
 PT detecting expression of markers e.g., Zic family member 3, other than
 PT human telomerase reverse transcriptase/octamer binding transcription
 PT factor.
 PS
 PS Claim 1; SEQ ID NO 2; 106bp; English.
 XX
 CC The invention relates to assessing a culture of undifferentiated primate
 CC pluripotent stem cells (pPS, e.g. embryonic stem cells), involving
 CC detecting expression of markers (MR1) e.g. Zic family member 3 (ZIC3), as
 CC given in specification, other than human telomerase reverse transcriptase
 CC (hTERT) or octamer binding transcription factor (Oct)3/4, or a marker
 CC (MR2) such as, cripto or podocalyxin-like protein and hTERT and/or Oct3/4
 CC or second marker chosen from (MR2). Also included are maintaining (M2)
 CC pPS cells in a pluripotent state (involves causing them to express one of
 CC the following markers (MR3) at a higher level, FOXO1A, ZIC3, hypothetical
 CC protein FLJ20582, Forkhead box H1 (FOXH1), Zinc finger protein, Hsa12,
 CC KOBAR-zinc finger protein SZFI-1 or zinc finger protein of cerebellum
 CC ZIC2, or any other marker (MR4) chosen from PHD protein Jde-1 (Jade-1),
 CC Kruppel-like zinc finger protein (ZNF300), etc., as given in the
 CC specification), causing pPS cells to differentiate into a particular
 CC tissue type by causing them to express one of the markers chosen from
 CC (MR3) or (MR4) (or markers chosen from GATA binding protein 3 (GATA3),
 CC core promoter element binding protein (CPEB3), etc., as given in the
 CC specification), maintaining pPS cells in a pluripotent state (involves
 CC culturing pPS cells or their progeny in the presence of a normally
 CC secreted protein that is encoded by a gene that down-regulated upon
 CC differentiation of human embryonic stem (hES) cells, chosen from
 CC Fibrillin 3 gene, LEFT B gene, ZIC3 gene, EphA1 gene, etc., as given in
 CC the specification), causing pPS cells to differentiate (involves
 CC culturing pPS cells or their progeny in the presence of a normally
 CC secreted protein that is encoded by a gene that up-regulated upon
 CC differentiation of hES cells, chosen from p31 protein gene, Tax
 CC interaction protein 1 gene, KIA0853 protein gene, keratin 19 (KRT 19)
 CC gene, etc., as given in the specification), causing an encoding sequence
 CC to be preferentially expressed in undifferentiated pPS cells, causing an
 CC encoding sequence to be preferentially expressed in differentiated cells,
 CC sorting (M4) differentiated cells from less differentiated cells
 CC (involves separating cells expressing a surface marker chosen from any
 CC one of MR1 from cells not expressing the marker), causing pPS cells to
 CC proliferate without differentiation, identifying genes that are up or
 CC down regulated during differentiation of pPS cells, and a kit (I) for
 CC assessing a culture of pPS cells by M1. The method (M1) is useful for
 CC assessing culture of undifferentiated primate pluripotent stem cells and
 CC for assessing the growth characteristics of a cell population. The cell
 CC population has been obtained by culturing cells from human blastocyst or
 CC from a human patient suspected of having a clinical condition related to
 CC abnormal cell growth. The method further involves determining whether the
 CC cell population is pluripotent from the marker expression and assessing
 CC whether the patient has a malignancy from the marker expression. The
 CC present sequence is a protein whose expression is down regulated in
 CC pluripotent stem cells.
 XX
 SO Sequence 1132 AA;

Query Match

99.8%; Score 5952; DB 8; Length 1132;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0;
Gaps 0

QY	1	MPRARCAVRELLSHREVLPLATFVRRLPGQHRILYQRBDAFPAFLVQCLVYCM	60
Db	1	MPRARCAVRELLSHREVLPLATFVRRLPGQHRILYQRBDAFPAFLVQCLVYCM	60
QY	61	DARPPAPSPFQVSCIKELVARVLOQLCERGAKVLAEGFALLDGAAGGPEAFTSVR	120
Db	61	DARPPAPSPFQVSCIKELVARVLOQLCERGAKVLAEGFALLDGAAGGPEAFTSVR	120
QY	121	SYLPMTVTDALRGSGAWGILLRRVGDVULHLLARCALFVLYAPSCAYVCGCPPLYOLGA	180
Db	121	SYLPMTVTDALRGSGAWGILLRRVGDVULHLLARCALFVLYAPSCAYVCGCPPLYOLGA	180
QY	181	ATQAPRPHASGPRRRLGGERAMNHSVRAGVPLGIPAGCARRGGSASRLPLKRPBR	240
Db	181	ATQAPRPHASGPRRRLGGERAMNHSVRAGVPLGIPAGCARRGGSASRLPLKRPBR	240
QY	241	GAAPPERTPVQGGWAHPGTRGSDRGFCVSPAPRAPEATLSLEGALSGTRHSHPSVG	300
Db	241	GAAPPERTPVQGGWAHPGTRGSDRGFCVSPAPRAPEATLSLEGALSGTRHSHPSVG	300
QY	301	QOHAGPSTSPRPMDPCPPVAETGHLFYLSGQDKQLPSFLSLSLRSLTGARL	360
Db	301	QOHAGPSTSPRPMDPCPPVAETGHLFYLSGQDKQLPSFLSLSLRSLTGARL	360
QY	361	VETTLGSSPMMGTPRRPLRLPORYWQMRPLFLELGNHAOCPPGVLLKTHCPRAAYT	420
Db	361	VETTLGSSPMMGTPRRPLRLPORYWQMRPLFLELGNHAOCPPGVLLKTHCPRAAYT	420
QY	421	PAAGCABEKPQGSVAAPREEDTDRLRLVQLLRHSSPMQVYGFPARCLRLVPPGLMGS	480
Db	421	PAAGCABEKPQGSVAAPREEDTDRLRLVQLLRHSSPMQVYGFPARCLRLVPPGLMGS	480
QY	481	RHNERPLRNTKFTSLGHAULTLOELTWKNSVBDCAWLRRSPGVGCYPAAEHRLREBI	540
Db	481	RHNERPLRNTKFTSLGHAULTLOELTWKNSVBDCAWLRRSPGVGCYPAAEHRLREBI	540
QY	541	LAKPLHLMXSVYVVLRLSFFVYETTPQKNLLEFRPSWKLQSIGRQHLKXVQLE	600
Db	541	LAKPLHLMXSVYVVLRLSFFVYETTPQKNLLEFRPSWKLQSIGRQHLKXVQLE	600
QY	601	LSEAEVRQREARPALTSRLRFLIEKPDOLRPIVMNDYVVGARTRRERKARLTSRYXA	660
Db	601	LSEAEVRQREARPALTSRLRFLIEKPDOLRPIVMNDYVVGARTRRERKARLTSRYXA	660
QY	661	LFSVINYRABRBPGLLGASVLGLDDIHAMRFFVLRYAQDPPBELYFVKUVDTGAYDTI	720
Db	661	LFSVINYRABRBPGLLGASVLGLDDIHAMRFFVLRYAQDPPBELYFVKUVDTGAYDTI	720
QY	721	PODRLTEVIASIIKQONTYCVARYAVWQZAAHGHRKAFKSHSVTLTDLOQPMROFVAHL	780
Db	721	PODRLTEVIASIIKQONTYCVARYAVWQZAAHGHRKAFKSHSVTLTDLOQPMROFVAHL	780
QY	781	QETSLRBAVYIEGSSSLNEASSGLFDVFLRPMCHNAVRIRGKSYVQCGIPIQGSILSTL	840
Db	781	QETSLRBAVYIEGSSSLNEASSGLFDVFLRPMCHNAVRIRGKSYVQCGIPIQGSILSTL	840
QY	841	LCSLGYGMENTLFAGIRRDGILLRVDFLLVTBHLTHAKFTLTVRGVEYCYVNL	900
Db	841	LCSLGYGMENTLFAGIRRDGILLRVDFLLVTBHLTHAKFTLTVRGVEYCYVNL	900
QY	901	RKTYVNFVEEDBALGGTAFVQMPAAGLFPWCGLLDTRLLEVQSSYSASARISIASLTF	960
Db	901	RKTYVNFVEEDBALGGTAFVQMPAAGLFPWCGLLDTRLLEVQSSYSASARISIASLTF	960
QY	961	NRGFAGANMERKLGVLRLKCHSLFDLDQVNSLQTVCNIIKILLQAYRFAVLOLP	1020
Db	961	NRGFAGANMERKLGVLRLKCHSLFDLDQVNSLQTVCNIIKILLQAYRFAVLOLP	1020
QY	1021	FHQQWKNPFFLRVISTJASLCYSLIKAKNAGMSLGAAGAAGPLSEAVQMLCHQAPLL	1080

Db 1021 FHQGVKNPPTFLEFVSDTSLCSILKAKNAGSLGKGAAGLPSFAVOMLCHQATLL 1096

QY 1081 KLTENRVTYVYPLGSLRTAQTQSLRKLPGTTLTALAAANPALPSDFKTIID 1132

Db 1081 KLTENRVTYVYPLGSLRTAQTQSLRKLPGTTLTALAAANPALPSDFKTIID 1132

RESULT 23
AAW61350
ID AAW61350 standard; protein; 1154 AA

CC This polypeptide comprises human telomerase protein 2 (TP2), a novel
CC protein of the telomerase complex. Its amino acid sequence was deduced
CC from a composite (see AA027876) of isolated cDNA clones 32 (see AA027872)
CC and TP2-15 (see AA027875), obtained from a human colon tumour cell line
CC LIM163 cDNA. Expressing TP2 in a cell is used to increase telomerase
CC activity and thus proliferation for treatment of e.g. HIV infection, AIDS
CC and ageing disorders, while expressing an inactive mutant of TP2 (or
CC molecule antisense to the gene) is used to decrease telomerase activity.
CC e.g. for treatment of cancer. TP2 polypeptides can also be used to screen
CC for agents that inhibit TP2 activity or its binding to TRP1 (see
CC AA061347) or telomerase RNA, potentially useful therapeutically, also to
CC raise specific antibodies useful in immunoassays and therapeutically as
CC inhibitors. Also contemplated are transgenic animals in which the TP2
CC gene has been inactivated or is overexpressed. TP2 polypeptides are
CC administered i.v., s.c. or orally, or they are delivered from engineered
CC cells or gene therapy vectors. (Updated on 25-MAR-2003 to correct PR
CC field.)

Query Match 99.8%; Score 5952; DB 2; Length 1154;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 61 DARPPAASFRQVCLKEIVARVLQRLCERGAKNVLAFGPALLDGAAGPEEAFITTSVR 120
 DB 83 DARPPAASFRQVCLKEIVARVLQRLCERGAKNVLAFGPALLDGAAGPEEAFITTSVR 142
 QY 121 SYLENTVTDALGSGAKGILLRRVDDVLVHLLACALFVVAAPCAVQVGGPELYOUGA 180
 DB 143 SYLENTVTDALGSGAKGILLRRVDDVLVHLLACALFVVAAPCAVQVGGPELYOUGA 202
 QY 181 ATOQAPPPHASPGRRLGGERAMNSVREAVPLGLPAPGARRRRGSASRLPJKPERR 240
 DB 203 ATOQAPPPHASPGRRLGGERAMNSVREAVPLGLPAPGARRRRGSASRLPJKPERR 262
 QY 241 GAAPBERTPVQGSWAPHRTRGPSDRGFCVSPAPPAEATSLGALSGTRISHSPVG 300
 DB 263 GAAPBERTPVQGSWAPHRTRGPSDRGFCVSPAPPAEATSLGALSGTRISHSPVG 322
 QY 301 RQHHAGPSTSPRPMDPCPPVYAEKHFLLYSGGDEKOLRPSLILSLRPSLTGARL 360
 DB 323 RQHHAGPSTSPRPMDPCPPVYAEKHFLLYSGGDEKOLRPSLILSLRPSLTGARL 382
 QY 361 VETIFLGSRRPMMPGTERRLLPRLPQRYWQWRPLLELLGNHACPYGVILLKTHCPILAAVT 420
 DB 383 VETIFLGSRRPMMPGTERRLLPRLPQRYWQWRPLLELLGNHACPYGVILLKTHCPILAAVT 442
 QY 421 PAAGVAREKPGQSVAAPEEDTDPRLVOLLROHSSPMOYGYFVRACTLRRLVPPGLMGS 480
 DB 443 PAAGVAREKPGQSVAAPEEDTDPRLVOLLROHSSPMOYGYFVRACTLRRLVPPGLMGS 502
 QY 481 RHNERFLNTKKFTSLGKAKLSLOELTWKMSVDCAMLRSPGCVPAAREHRLREI 540
 DB 503 RHNERFLNTKKFTSLGKAKLSLOELTWKMSVDCAMLRSPGCVPAAREHRLREI 562
 QY 541 LAKFLHMLSVYVVELLRSPFYVETTTQKNLFFRPSWSKLOSIGIOLHKLKRVQRE 600
 DB 563 LAKFLHMLSVYVVELLRSPFYVETTTQKNLFFRPSWSKLOSIGIOLHKLKRVQRE 622
 QY 601 LSAEVRORREARPALITSLRFLPIKPDGLRPIVMNDYVVGARTPRREKAERLTSRYKA 660
 DB 623 LSAEVRORREARPALITSLRFLPIKPDGLRPIVMNDYVVGARTPRREKAERLTSRYKA 682
 QY 661 LFSVLNVERARPPGLIGASVIGLDIHRAMRTFVLVRADBPPLVYVVDVGTAVYTI 720
 DB 683 LFSVLNVERARPPGLIGASVIGLDIHRAMRTFVLVRADBPPLVYVVDVGTAVYTI 742
 QY 721 PODRLTEVIASTIKPONTYCVARVAVVOKAAGHVRKAFKSVSTLTLOPYMRQFVAHL 780
 DB 743 PODRLTEVIASTIKPONTYCVARVAVVOKAAGHVRKAFKSVSTLTLOPYMRQFVAHL 802
 QY 781 OETSPLRDAVIEOSSSLNEASSGLEDFVFLRPMCHAVRIRKSYVQCQGIPOGSIISTL 840
 DB 803 OETSPLRDAVIEOSSSLNEASSGLEDFVFLRPMCHAVRIRKSYVQCQGIPOGSIISTL 862
 QY 841 LGSICGDMENKLFAGIRDDGILLRLVDFELLVTBHLTHAKFTLETLVRGVPEVGCYVNL 900
 DB 863 LGSICGDMENKLFAGIRDDGILLRLVDFELLVTBHLTHAKFTLETLVRGVPEVGCYVNL 922
 QY 901 RKTUVNFPEDDEALGTAFCVQMPAHGLFPWCGILLDRILEVOSDYSSYARTSIRASYTF 960
 DB 923 RKTUVNFPEDDEALGTAFCVQMPAHGLFPWCGILLDRILEVOSDYSSYARTSIRASYTF 982
 QY 961 NNGFKAGRMNRKLFVVLKCHSLFLDQVNSLOTCVCTNIIKILLQAYRHAVALDLP 1020
 DB 983 NNGFKAGRMNRKLFVVLKCHSLFLDQVNSLOTCVCTNIIKILLQAYRHAVALDLP 1042
 QY 1021 FHQOVKNPFLFRLVSDTASLCYSILKAKNAGMSIGAKGAGPLPSSAVQLCHQATLL 1080
 DB 1043 FHQOVKNPFLFRLVSDTASLCYSILKAKNAGMSIGAKGAGPLPSSAVQLCHQATLL 1102
 QY 1081 KLTRHEVTVVPLIGSLRTAQOTLSRKLPGTTTLTALEAANPALPSPDFTIIL 1132
 DB 1103 KLTRHEVTVVPLIGSLRTAQOTLSRKLPGTTTLTALEAANPALPSPDFTIIL 1154

RESULT 24
 AAM47008
 ID AAM47008 standard; protein; 1189 AA.
 XX
 AC AAM47008;
 XX
 DT 13-AUG-1998 (first entry)
 XX
 DE Glutathione-S-transferase and hTERT fusion protein 8.
 XX
 KM Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
 KW cell proliferation; cancer; ageing; ribonucleoprotein.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 22..23
 FT /note="enterokinase cleavage site"
 XX
 GN GB2317891-A.
 XX
 PD 08-APR-1998.
 XX
 PE 01-OCT-1997; 97GB-00020890.
 XX
 PR 01-OCT-1996; 96US-00724643.
 PR 18-APR-1997; 97US-00844419.
 PR 25-APR-1997; 97US-00846017.
 PR 06-MAY-1997; 97US-00851843.
 PR 09-MAY-1997; 97US-00854050.
 PR 14-AUG-1997; 97US-00911312.
 PR 14-AUG-1997; 97US-00912951.
 PR 14-AUG-1997; 97US-00915503.
 XX
 PA (GERO-) GERON CORP.
 PA (UYTE-) UNIV TECHNOLOGY CORP.
 XX
 PI Czech TR, Langner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
 PI Andrews WH;
 XX
 DR WPI; 1998-171633/16.
 XX
 PT Pure and recombinant human telomerase Reverse Transcriptase and its
 PT variants - are useful in the diagnosis, prognosis and treatment of cell
 PT proliferation conditions especially cancer and ageing.
 XX
 PS Example 6; Page 234-235; 387pp; English.
 XX
 CC The present sequence represents a fusion protein from an example of the
 CC present invention which describes human telomerase reverse transcriptase
 CC (hTERT). The present invention also describes the following methods: (A)
 CC determining whether a test compound is a modulator of hTERT, by detecting
 CC the change in hTERT recombinant protein or polynucleotide, on
 CC administration of the compound; (B) preparation of recombinant telomerase
 CC by contacting a protein preparation of hTERT with a telomerase RNA
 CC component; (C) detection of the hTERT RNA or protein in a sample by
 CC binding a relevant probe to the sample and detecting the complex formed
 CC or in the case of RNA detection, amplifying the product and correlating
 CC the presence of complex or amplification product with presence of hTERT in
 CC the sample; and (D) increasing the proliferation of a vertebrate cell by
 CC increasing hTERT expression; and (E) the use of an agent that causes an
 CC increase in cell vertebrate cell proliferation to create a medicament
 CC that inhibits ageing. A protein preparation of hTERT and the
 CC polynucleotide encoding hTERT can be used in the manufacture of
 CC medicaments for inhibiting the effect of ageing or cancer. Inhibitors of
 CC telomerase activity can be used to treat conditions that are associated
 CC with high telomerase activity. A protein preparation of hTERT can also be
 CC used in the new methods
 XX
 SQ Sequence 1189 AA;

Query Match 99.8%; Score 5952; DB 2; Length 1189;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLRSYREVLPLATFVRRLSGQGRVLRGDPAAFPALVNCVLCVW 60
 DB 58 MPAPRCRAVRSLLRSYREVLPLATFVRRLSGQGRVLRGDPAAFPALVNCVLCVW 117

QY 61 DAAPPAPAPSPFQVSCIKELVAFLVLRQRCGAKNVLAFFALLDARGGPEAFTTSVR 120
 DB 118 DAAPPAPAPSPFQVSCIKELVAFLVLRQRCGAKNVLAFFALLDARGGPEAFTTSVR 177

QY 121 SYLPNTVTDLRSSGAMGLLRVGDVYLHLARCALFLVLPSCAYQVCGPEPLYQLA 180
 DB 178 SYLPNTVTDLRSSGAMGLLRVGDVYLHLARCALFLVLPSCAYQVCGPEPLYQLA 237

QY 181 ATQARPPEPHASGRRRLGCEBAMNHSVREAGVPLGPAPGARRRGSSASRSLPLRPRPR 240
 DB 238 ATQARPPEPHASGRRRLGCEBAMNHSVREAGVPLGPAPGARRRGSSASRSLPLRPRPR 297

QY 241 GAAPPEPRTVVGQGSMAHPGRTGSPSDRGFCVSPAPAEATSLFGALSGTRHSPSVG 300
 DB 298 GAAPPEPRTVVGQGSMAHPGRTGSPSDRGFCVSPAPAEATSLFGALSGTRHSPSVG 357

QY 301 RQHAGPSTSRPPRMDTFCPPVYAEKTKFLYSQGDKEQLRSPFLSSLRPELTGARL 360
 DB 358 RQHAGPSTSRPPRMDTFCPPVYAEKTKFLYSQGDKEQLRSPFLSSLRPELTGARL 417

QY 361 VETIFLGSRPMDGTPRRRLRPLRQRYQWMLPFLLELLGNHAGCPYGVLLKTHCPLEAAVT 420
 DB 418 VETIFLGSRPMDGTPRRRLRPLRQRYQWMLPFLLELLGNHAGCPYGVLLKTHCPLEAAVT 477

QY 421 PAAGVAREKPGSVAPAEEDDPRIYQVLLRQHSPPQVYGFVACLRPLVPGMGWS 480
 DB 478 PAAGVAREKPGSVAPAEEDDPRIYQVLLRQHSPPQVYGFVACLRPLVPGMGWS 537

QY 481 RHNERERFLRNTKFFISLQKAKLSLOELTWKSVRCAMLRSPGVGCVPAAEHRLREI 540
 DB 538 RHNERERFLRNTKFFISLQKAKLSLOELTWKSVRCAMLRSPGVGCVPAAEHRLREI 597

QY 541 LAFLWMLSVYVELLRSEFFYTETTPQKNRLEFFRPSWKLQSIGRQHKRYQLE 600
 DB 598 LAFLWMLSVYVELLRSEFFYTETTPQKNRLEFFRPSWKLQSIGRQHKRYQLE 657

QY 601 LSAEVRQHEAPALITSLRFLPKPDGLRPIVMNDVYVGARTFERREARSLTSRYVA 660
 DB 658 LSAEVRQHEAPALITSLRFLPKPDGLRPIVMNDVYVGARTFERREARSLTSRYVA 717

QY 661 LFSVLNYSRRRFGLLGASVGLDLDIHRAMRTFVLVRADQPEPPELVFKVVDVTAQYDTI 720
 DB 718 LFSVLNYSRRRFGLLGASVGLDLDIHRAMRTFVLVRADQPEPPELVFKVVDVTAQYDTI 777

QY 721 PQRRLTEVLAISLTKQNTQVRRYAVVQKAAGHVAKAFKSHSTLTDIOPVYRQVATL 780
 DB 778 PQRRLTEVLAISLTKQNTQVRRYAVVQKAAGHVAKAFKSHSTLTDIOPVYRQVATL 837

QY 781 QETSPLRDVAVIEQSSSLNEASGLFVPLRFMCHNAVIRGKSYVQCGGIGSLISTL 840
 DB 838 QETSPLRDVAVIEQSSSLNEASGLFVPLRFMCHNAVIRGKSYVQCGGIGSLISTL 897

QY 841 LGSLLCYGDMENKLFAGIRRDGGLLRVDDFLVTHLTAKTFLRLVNGVEYGCVVNL 900
 DB 898 LGSLLCYGDMENKLFAGIRRDGGLLRVDDFLVTHLTAKTFLRLVNGVEYGCVVNL 957

QY 901 RKTVMFPVEDELGGTAFAVQMPAHGLFPWCGLLTRTLEVOSSDYVSARFISIRASVFP 960
 DB 958 RKTVMFPVEDELGGTAFAVQMPAHGLFPWCGLLTRTLEVOSSDYVSARFISIRASVFP 1017

QY 961 NRQFKAGRNRRKLFGLVRLKCHSLFLDIQVNSLQVTCNIIYKILLQAYRHACYQLQLP 1020
 DB 1018 NRQFKAGRNRRKLFGLVRLKCHSLFLDIQVNSLQVTCNIIYKILLQAYRHACYQLQLP 1077

QY 1021 FHOQWKNPTFFLRVISTDASLQCYSLIKKANAGMSLGAKGAGPLPSEAVQWMLCHQAFLL 1080

DB 1078 FHOQWKNPTFFLRVISTDASLQCYSLIKKANAGMSLGAKGAGPLPSEAVQWMLCHQAFLL 1137

QY 1081 KLTRRATVYVPLLSGLRPAQQLSRKLPGTTLTLEAANALPSDFKTIID 1132

DB 1138 KLTRRATVYVPLLSGLRPAQQLSRKLPGTTLTLEAANALPSDFKTIID 1189

RESULT 25
 AAM47000
 ID AAM47000 standard; protein; 1285 AA.

AC AAM47000;
 DT 13-AUG-1998 (first entry)
 DE HIS tagged thioredoxin moiety and full length hTERT fusion protein.
 DE Human, telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
 KM cell proliferation; cancer; ageing; ribonucleoprotein.
 OS Synthetic.
 OS Homo sapiens.
 FH Key
 FT Misc-difference 119..120
 FT /note="nucleotide cleavage site"
 FT Region 120..1285
 FT /label="hTERT
 FT /note="full length human telomerase reverse
 FT transcriptase"
 XX

PN GB2317891-A.
 PD 08-APR-1998.
 XX
 PD 01-OCT-1997; 97GB-00020890.
 PF
 XX
 PR 01-OCT-1996; 96US-00724643.
 PR 18-APR-1997; 97US-00844419.
 PR 25-APR-1997; 97US-00846017.
 PR 06-MAY-1997; 97US-00851843.
 PR 09-MAY-1997; 97US-00854050.
 PR 14-AUG-1997; 97US-00911312.
 PR 14-AUG-1997; 97US-00912951.
 PR 14-AUG-1997; 97US-00915503.
 XX
 PA (GERO-) GERON CORP.
 PA (UYTE-) UNIV TECHNOLOGY CORP.
 XX
 PI Cecch TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
 PI Andrews WH;
 XX
 DR WPI, 1998-171633/16.
 XX
 PT Pure and recombinant human Telomerase Reverse Transcriptase and its
 PT variants - are useful in the diagnosis, prognosis and treatment of cell
 PT proliferation conditions especially cancer and ageing.
 XX
 PS Example 6; Page 223; 387pp; English.

CC The present sequence represents a fusion protein from an example of the
 CC present invention which describes human telomerase reverse transcriptase
 CC (hTERT). The present invention also describes the following methods: (A)
 CC determining whether a test compound is a modulator of hTERT, by detecting
 CC the change in hTERT recombinant protein or polynucleotide, on
 CC administration of the compound; (B) preparation of recombinant telomerase
 CC by contacting a protein preparation of hTERT with a telomerase RNA
 CC component; (C) detection of the hTERT RNA or protein in a sample by
 CC binding a relevant probe to the sample and detecting the complex formed
 CC or in the case of RNA detection, amplifying the product and correlating
 CC the presence of complex or amplification product with presence of hTERT in
 CC the sample; and (D) increasing the proliferation of a vertebrate cell by

CC increasing hTERT expression; and (E) the use of an agent that causes an
 CC increase in cell vertebrate cell proliferation to create a medicament
 CC that inhibits ageing. A protein preparation of hTERT and the
 CC polynucleotide encoding hTERT can be used in the manufacture of
 CC medicaments for inhibiting the effect of ageing or cancer. Inhibitors of
 CC telomerase activity can be used to treat conditions that are associated
 CC with high telomerase activity. A protein preparation of hTERT can also be
 CC used in the new methods

XX Sequence 1285 AA;

Query Match 99.7%; Score 5946; DB 2; Length 1285;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1129; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRAPPCRVRLSLSHSEVPLATFVRRLGPGQGRVVGDPAPAFALVAQCVCVPM 60
 DB 154 MRAPPCRVRLSLSHSEVPLATFVRRLGPGQGRVVGDPAPAFALVAQCVCVPM 213
 QY 61 DARPPAPSPFQVSCLEKELVARVLQRLCERGAKNVLAFGFALDGAAGPPEATTSSVR 120
 DB 214 DARPPAPSPFQVSCLEKELVARVLQRLCERGAKNVLAFGFALDGAAGPPEATTSSVR 273
 QY 121 SYLPNTVDALRGSGAGMLLRVGDVYLHLLACALFVLAPEGCAVQGGPPLYQGA 180
 DB 274 SYLPNTVDALRGSGAGMLLRVGDVYLHLLACALFVLAPEGCAVQGGPPLYQGA 333.
 QY 181 ATQARPPHASPGRRLGGERAMNHSVREAGVPLGAPARRRGSASRSLPLPKRRR 240
 DB 334 ATQARPPHASPGRRLGGERAMNHSVREAGVPLGAPARRRGSASRSLPLPKRRR 393
 QY 241 GAAPBERTPVQGSWAHPRTGSPDRGFCVSPAPPAEATSLGALSGTRSHSEV 300
 DB 394 GAAPBERTPVQGSWAHPRTGSPDRGFCVSPAPPAEATSLGALSGTRSHSEV 453
 QY 301 ROHHAGPSTSPRPMDTCCPPVYAETKHFYSSGDEKQLRPSFLSLSLRPSLTGARL 360
 DB 454 ROHHAGPSTSPRPMDTCCPPVYAETKHFYSSGDEKQLRPSFLSLSLRPSLTGARL 513
 QY 361 VETIFLGSRRMWPGRRLPLRLPORYQWRPLFLELGNHACPYVILLKTHCPRAAVT 420
 DB 514 VETIFLGSRRMWPGRRLPLRLPORYQWRPLFLELGNHACPYVILLKTHCPRAAVT 573
 QY 421 PAAGVAREKPGQSVAAPEEDTDPRLVQLLRHSSPMQYGFRACTLRRLVPPGLMS 480
 DB 574 PAAGVAREKPGQSVAAPEEDTDPRLVQLLRHSSPMQYGFRACTLRRLVPPGLMS 633
 QY 481 RHNERFLNTKKFISLGHAKLSIQELTWKMSVDCAMLRSPGVGCVPAAEHRLREI 540
 DB 634 RHNERFLNTKKFISLGHAKLSIQELTWKMSVDCAMLRSPGVGCVPAAEHRLREI 693
 QY 541 LAKFLHMLMSYVVELLSFFVYETETTPQKRLFFYRPSWMSKLSIGIQLHKKVQURE 600
 DB 694 LAKFLHMLMSYVVELLSFFVYETETTPQKRLFFYRPSWMSKLSIGIQLHKKVQURE 753
 QY 601 LSEAEVROHREARPALITSLRLRFIPKQGLRPIYMDYVVGARTPRREKAERLTSRYKA 660
 DB 754 LSEAEVROHREARPALITSLRLRFIPKQGLRPIYMDYVVGARTPRREKAERLTSRYKA 813
 QY 661 LFSVLYNERBARPPGLIGASVIGLDDIHRAMRTFVLRAQDPPPELYVYKDVGTAVYTI 720
 DB 814 LFSVLYNERBARPPGLIGASVIGLDDIHRAMRTFVLRAQDPPPELYVYKDVGTAVYTI 873
 QY 721 PDLRLLEVASTIKPONTYCVRRYAVVQKAAHGHVKAFAKSVSLTLDIQLPMRFVAVHL 780
 DB 874 PDLRLLEVASTIKPONTYCVRRYAVVQKAAHGHVKAFAKSVSLTLDIQLPMRFVAVHL 933
 QY 781 QETSPLRDAVLEOSSSLNEASSGLFDFVLRFCMCHAVIRKSYVQCGIPQGSILSTL 840
 DB 934 QETSPLRDAVLEOSSSLNEASSGLFDFVLRFCMCHAVIRKSYVQCGIPQGSILSTL 993
 QY 841 LGSICGDMENKLFAGIRRDGILLRLVDDFLVTHTLAKTFLATLRGVPEYGCYVNL 900

DB 994 LGSICGDMENKLFAGIRRDGILLRLVDDFLVTHTLAKTFLATLRGVPEYGCYVNL 1053
 QY 901 RKTIVNPPVEDEALGGTAVQMPAHGLFPWCGILLDTFLFVQSDYSSYARISASVTF 960
 DB 1054 RKTIVNPPVEDEALGGTAVQMPAHGLFPWCGILLDTFLFVQSDYSSYARISASVTF 1113
 QY 961 NRGFKAGRMNRKTLFVLRKCHSLFLDLQVNSLQVCTNIYKILLQVRFHACVQLP 1020
 DB 1114 NRGFKAGRMNRKTLFVLRKCHSLFLDLQVNSLQVCTNIYKILLQVRFHACVQLP 1173
 QY 1021 FHOQVKNPFFFLRVISDPAISCYSTLKAKMGMSLGAAGAGPLPSEAVQMLCHQAFLL 1080
 DB 1174 FHOQVKNPFFFLRVISDPAISCYSTLKAKMGMSLGAAGAGPLPSEAVQMLCHQAFLL 1233
 QY 1081 KLTRHRVTVPPLLSLRTAQTLRSKLPQTTLTALEAANPALPSDFKTIID 1132
 DB 1234 KLTRHRVTVPPLLSLRTAQTLRSKLPQTTLTALEAANPALPSDFKTIID 1285

RESULT 26
 AAW71376
 ID AAW71376 standard; protein; 1132 AA.
 XX

AC AAW71376;

DT 04-DEC-1998 (first entry)

DE Human telomerase catalytic subunit referred to as hEST2.

KW Catalytic subunit; human; telomerase; telomere maintenance; diagnosis; treatment; cancer.

XX Homo sapiens.

XX WO9837181-A2.

PN 27-AUG-1998.

PD 20-FEB-1998; 98WO-US003404.

XX 20-FEB-1997; 97US-0038750P.

XX 20-MAY-1997; 97US-0047151P.

PR 01-AUG-1997; 97US-0054549P.

PR 14-AUG-1997; 97US-0055762P.

PR 30-OCT-1997; 97US-0064322P.

XX (WHEED) WHITEHEAD INST BIOMEDICAL RES.

XX Counter CM, Meyerson M, Weinberg RA;

XX WPI: 1998-495367/42.

XX N-PSDB: AAV60320.

XX New isolated human telomerase catalytic sub-unit gene - used to develop

XX products for increasing or reducing the life span of cells such as cancer

XX cells or transformed cells.

XX Claim 5; Fig 6; 96pp; English.

XX The present sequence represents the catalytic subunit of a human

XX telomerase holoenzyme. Disruption of the telomerase gene alters telomere

XX maintenance. The DNA is essential for telomerase activity, and the

XX protein is physically associated with telomerase and a constituent of

XX active telomerase complex. The products can be used for increasing or

XX reducing the lifespan of cells such as cancer cells or transformed cells.

XX They can also be used in the diagnosis and treatment of malignancies. In

XX addition, cells with a longer lifespan can be transplanted into or

XX grafted onto an individual (e.g. as skin grafts), as systems for delivery

XX of therapeutic proteins, such as hormones and enzymes), to whom they

XX provide therapeutic benefit

XX Sequence 1132 AA;

Query Match 99.7%; Score 5945; DB 2; Length 1132;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1129; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSILRSHYREVLPATFVRRLGPGQWRVYVGDDPAAPFALVACLVCPW 60
 DB 1 MPAPRCRAVRSILRSHYREVLPATFVRRLGPGQWRVYVGDDPAAPFALVACLVCPW 60
 QY 61 DAPPPAPSPFROVSCIKELVARVLOLRCGAKNVLAEPALDDAGGPPPEAFTTSR 120
 DB 61 DAPPPAPSPFROVSCIKELVARVLOLRCGAKNVLAEPALDDAGGPPPEAFTTSR 120
 QY 121 SYLPTVTDLARGSGAWGLLRVGGDVVHLARCALFVLVAPSGAYVCGEPPLYQLGA 180
 DB 121 SYLPTVTDLARGSGAWGLLRVGGDVVHLARCALFVLVAPSGAYVCGEPPLYQLGA 180
 QY 181 ATQARPPPHASGRRRLGGERAMNHSVREXGVPLGAPARARRGGSASRSLPLRRPRR 240
 DB 181 ATQARPPPHASGRRRLGGERAMNHSVREXGVPLGAPARARRGGSASRSLPLRRPRR 240
 QY 241 GAAPPEPRTVGGGSMWHPGRTGSPDRGFCVSPAPAPAEATSLGALSGTRHSPSYG 300
 DB 241 GAAPPEPRTVGGGSMWHPGRTGSPDRGFCVSPAPAPAEATSLGALSGTRHSPSYG 300
 QY 301 ROHHAGPSTSRPPRPMWDTCPPVYATKHFLLYSGGDKQOLRPSLLSLRPSLTGARRL 360
 DB 301 ROHHAGPSTSRPPRPMWDTCPPVYATKHFLLYSGGDKQOLRPSLLSLRPSLTGARRL 360
 QY 361 VETIFLGSRPMWGTPLRLPQRYWQMRPLFLELLGNACQCPYVLLKTHQPLRAAYT 420
 DB 361 VETIFLGSRPMWGTPLRLPQRYWQMRPLFLELLGNACQCPYVLLKTHQPLRAAYT 420
 QY 421 PAAGVCAREKPGQSVAAPEEDTDPRLLVOLLROHSSPMWYGVFACTRLVPPGLMGS 480
 DB 421 PAAGVCAREKPGQSVAAPEEDTDPRLLVOLLROHSSPMWYGVFACTRLVPPGLMGS 480
 QY 481 RHNERRLRTKTKFTSLGKIAKLSLOELTWKMSVRCAMLRBSPGVCPPAAHRLREI 540
 DB 481 RHNERRLRTKTKFTSLGKIAKLSLOELTWKMSVRCAMLRBSPGVCPPAAHRLREI 540
 QY 541 LAKEFLHMLSVYVVELRSFFVYETETFOKNRLFFRPSVWSLQSIGIRQHLKRYOLRE 600
 DB 541 LAKEFLHMLSVYVVELRSFFVYETETFOKNRLFFRPSVWSLQSIGIRQHLKRYOLRE 600
 QY 601 LSAEAVRQHEARPAALITSLRFLPKPDGLRPIVNMDDYVGAATFERREKRAELTSRYVA 660
 DB 601 LSAEAVRQHEARPAALITSLRFLPKPDGLRPIVNMDDYVGAATFERREKRAELTSRYVA 660
 QY 661 LFEVLNVERARRPGLLGASVGLGDDIHRARTFVLRLVRAODPPELYEVVDTGAYDTI 720
 DB 661 LFEVLNVERARRPGLLGASVGLGDDIHRARTFVLRLVRAODPPELYEVVDTGAYDTI 720
 QY 721 POORLFEVIAIITKPONTYCVRRYAVVQKAHGVRAKFSHVSTLTDIOPYWRQFVAHL 780
 DB 721 POORLFEVIAIITKPONTYCVRRYAVVQKAHGVRAKFSHVSTLTDIOPYWRQFVAHL 780
 QY 781 OETSPRLDAVIVIOSSSLNASSGLFVFLRPMCHAVRIRGKSYVOCQSIGPGLSTLSTL 840
 DB 781 OETSPRLDAVIVIOSSSLNASSGLFVFLRPMCHAVRIRGKSYVOCQSIGPGLSTLSTL 840
 QY 841 LQSLCYGDMENKLFAGIRRDGLLLRLVDPLVTLPHLTAKTLLRLVNGVEPGCVNL 900
 DB 841 LQSLCYGDMENKLFAGIRRDGLLLRLVDPLVTLPHLTAKTLLRLVNGVEPGCVNL 900
 QY 901 RKTIVVAFVDEALGTAFAVQMPAHGLFPWCGLLDLRLTEVSDVSSVARTSTRASLTFF 960
 DB 901 RKTIVVAFVDEALGTAFAVQMPAHGLFPWCGLLDLRLTEVSDVSSVARTSTRASLTFF 960
 QY 961 NRGFKARNNRRKLFGLYLRKCSLFLDLQVNSIQCTVNIYKILLQAVRFACVLOLP 1020
 DB 961 NRGFKARNNRRKLFGLYLRKCSLFLDLQVNSIQCTVNIYKILLQAVRFACVLOLP 1020
 QY 1021 FHQGVKNPTFFFLRVISDTASLCSILKAKNAGSLGAKGAGPLPSEAVQMTCHQAFLL 1080

DB 1021 FHQGVKNPTFFFLRVISDTASLCSILKAKNAGSLGAKGAGPLPSEAVQMTCHQAFLL 1080
 QY 1081 KLTRRRVTVVPLGSLRTAQOLSRKPLGTTLLTLEAANALPSDFETIID 1132
 DB 1081 KLTRRRVTVVPLGSLRTAQOLSRKPLGTTLLTLEAANALPSDFETIID 1132

RESULT 27

AA00627
 ID AA00627 standard; protein, 1132 AA.

XX AA00627;

DT 26-JUL-1999 (first entry)

DE Human telomerase protein sequence.

KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilms' tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.

OS Homo sapiens.

PN W09901560-A1.

PD 14-JAN-1999.

PP 01-JUL-1998; 98WO-US013835.

PR 01-JUL-1997; 97US-0051410P.

PR 21-JUL-1997; 97US-0053018P.

PR 21-JUL-1997; 97US-0053329P.

PR 04-AUG-1997; 97US-0054642P.

PR 09-SEP-1997; 97US-0058287P.

PA (CAMB-) CANBIA BIOSYSTEMS LLC.

PI Kilian A, Bowtell D;

DR WPI: 1999-106060/09.

PT N-PSDB; AAX18254.

PS New isolated vertebrate telomerase genes - used to develop products for

PT treating cancers or for organ regeneration, nerve cell or brain cell

PT growth following injury or bone marrow transplantation.

XX Claim 19; Fig 1; 134pp; English.

CC This sequence is the human telomerase of the invention. Primers that
 CC amplify the telomerase coding sequence can be used in a method for
 CC diagnosing cancer in a patient. The telomerase can be used for detection,
 CC diagnosis and drug screening. Inhibitors of telomerase activity can be
 CC used to treat cancers such as melanomas, other skin cancers,
 CC neuroblastomas, breast carcinomas, colon carcinomas, leukemias,
 CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
 CC growths. Enhancers of telomerase may be used to stimulate stem cell
 CC proliferation and differentiation (expansion of haematopoietic stem cells
 CC could be administered in the bone marrow transplant context). As well,
 CC many tissues have stem cells. Proliferation of these cells may be useful
 CC in wound healing, hair growth, treatment of disease such as Wilms' s
 CC tumour, organ regeneration or differentiation after injury or diseases,
 CC nerve cell or brain cell growth following injury

XX Sequence 1132 AA;

Query Match 99.7%; Score 5945; DB 2; Length 1132;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1129; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSILRSHYREVLPATFVRRLGPGQWRVYVGDDPAAPFALVACLVCPW 60
 |||

```

Db      1 MPRAFCRAVRSILRSHYREVLPPLATFVARLPGQGRVLVQSGDPAAPRALVAQCLVCVPM 60
Qy      61 DARPFAAPSFRVOSCLKEIVARVLORLCERGAKNVLAFGFLLDGAAGPEAFTTSVR 120
Db      61 DARPFAAPSFRVOSCLKEIVARVLORLCERGAKNVLAFGFLLDGAAGPEAFTTSVR 120
Qy      121 SYLPNTVTDALRGSGAMGILLRRVGGDVLVHLLASCALFVLVAFSCAYQVCGPPLYOLGA 180
Db      121 SYLPNTVTDALRGSGAMGILLRRVGGDVLVHLLASCALFVLVAFSCAYQVCGPPLYOLGA 180
Qy      181 ATOQAPPPHLAGSPRRRLGGERAMNHSYRPAQVPLGLPAGARRRGSGASRLPLPKRRR 240
Db      181 ATOQAPPPHLAGSPRRRLGGERAMNHSYRPAQVPLGLPAGARRRGSGASRLPLPKRRR 240
Qy      241 GAAPSEERTPVQGSVAHGRTRGSDRGFCVSPAPPAEATSLGALSGTRHSHPEVG 300
Db      241 GAAPSEERTPVQGSVAHGRTRGSDRGFCVSPAPPAEATSLGALSGTRHSHPEVG 300
Qy      301 ROHAGPSTSRPPRPWDTPCPPVYAEKTHPLYSQDKEQLRPSFLSLSLRSLTGARL 360
Db      301 ROHAGPSTSRPPRPWDTPCPPVYAEKTHPLYSQDKEQLRPSFLSLSLRSLTGARL 360
Qy      361 VETIFLGSRPMMGPTRRLPRLPORYWQMRPLFELIGNHACQPYGVLLKTHCPRLAAVT 420
Db      361 VETIFLGSRPMMGPTRRLPRLPORYWQMRPLFELIGNHACQPYGVLLKTHCPRLAAVT 420
Qy      421 PAAGVAREKBPQGSVAAPBEEDTDPRRLVOLLROHSSPWQYGFVRAQLRLVPPGLMGS 480
Db      421 PAAGVAREKBPQGSVAAPBEEDTDPRRLVOLLROHSSPWQYGFVRAQLRLVPPGLMGS 480
Qy      481 RHNERRFLRNTKFFLSLGHAKLSLOELTWKMSVDCAMLRSPGVGVPAEHLRREI 540
Db      481 RHNERRFLRNTKFFLSLGHAKLSLOELTWKMSVDCAMLRSPGVGVPAEHLRREI 540
Qy      541 LAKFLHMLMSYVVELLRSFYVETTFQKNRLFYRPSVMSKQSIGIRHOLKXVQURE 600
Db      541 LAKFLHMLMSYVVELLRSFYVETTFQKNRLFYRPSVMSKQSIGIRHOLKXVQURE 600
Qy      601 LSEAEVRQREARPAALITSLRFLPIKPGDLRPIVMDYVVGARTREKREKARLTSRYKA 660
Db      601 LSEAEVRQREARPAALITSLRFLPIKPGDLRPIVMDYVVGARTREKREKARLTSRYKA 660
Qy      661 LFSVLNVERARRPGLLGASVLDLDDIHRAMRTFVLRYAQAODPPPLVVKVDVGAAYTI 720
Db      661 LFSVLNVERARRPGLLGASVLDLDDIHRAMRTFVLRYAQAODPPPLVVKVDVGAAYTI 720
Qy      721 PODRLTEVIASIIKPNNTYCVARRVAVQXAHGVRKAFKSHVSTLTLOPYMRQFVAHL 780
Db      721 PODRLTEVIASIIKPNNTYCVARRVAVQXAHGVRKAFKSHVSTLTLOPYMRQFVAHL 780
Qy      781 QETSPLRDVAVIQOSSSLNEASSGLFDVFLRFMCHAAVRIRKGSIVQCOGILPQGSILSTL 840
Db      781 QETSPLRDVAVIQOSSSLNEASSGLFDVFLRFMCHAAVRIRKGSIVQCOGILPQGSILSTL 840
Qy      841 LCSLCYGDMENTLFAQIRRDGLLRLVDFLLVTEHLTHAKTFLRTIVRGVEYGCVVNL 900
Db      841 LCSLCYGDMENTLFAQIRRDGLLRLVDFLLVTEHLTHAKTFLRTIVRGVEYGCVVNL 900
Qy      901 KRTVVNFPVEDALGTAIVQMPAHGLFPWCGLLDTITLLEVQSYSSYARSTIASLTF 960
Db      901 KRTVVNFPVEDALGTAIVQMPAHGLFPWCGLLDTITLLEVQSYSSYARSTIASLTF 960
Qy      961 NNGFVAGRMRRKLFGLVRLKCHSLFLDIQVNSLQTVCTNLYKILLDQAYRFAVCVQLP 1020
Db      961 NNGFVAGRMRRKLFGLVRLKCHSLFLDIQVNSLQTVCTNLYKILLDQAYRFAVCVQLP 1020
Qy      1021 FHQOVWKNPTFLRLVISTDASLCYSILKAKAKAGSLGAKGAAGPLPSBAVOMLCHQAFLL 1080
Db      1021 FHQOVWKNPTFLRLVISTDASLCYSILKAKAKAGSLGAKGAAGPLPSBAVOMLCHQAFLL 1080
Qy      1081 KLTRRVTYVPLLGSLRTAQOTLSRKLPTLTALAEAAANPALPBDFTIIL 1132
Db      1081 KLTRRVTYVPLLGSLRTAQOTLSRKLPTLTALAEAAANPALPBDFTIIL 1132

```

```

RESULT 28
AA00638
ID AA00638 standard; protein; 1132 AA.
XX
AC AA00638;
XX
DT 26-JUL-1999 (first entry)
XX
DE Truncated telomerase protein sequence.
XX
KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW smooth muscle cell hyperplasia; stem cell proliferation; Wilms' tumour;
KW stem cell differentiation; organ regeneration; organ differentiation.
XX
OS Homo sapiens.
OS Synthetic.
PN WC0901560-A1.
PD 14-JAN-1999.
PE 01-JUL-1998; 98WO-US013835.
PR 01-JUL-1997; 97US-0051410P.
PR 21-JUL-1997; 97US-0053018P.
PR 21-JUL-1997; 97US-0053329P.
PR 04-AUG-1997; 97US-0054642P.
PR 09-SEP-1997; 97US-0058287P.
XX
PA (CAMP-) CAMBIA BIOSYSTEMS LLC.
XX
PI Killian A, Bowtell D;
XX
DR WPI; 1999-106060/09.
DR N-PSDB; AAX18266.
XX
PT New isolated vertebrate telomerase genes - used to develop products for
PT treating cancers or for organ regeneration; nerve cell or brain cell
PT growth following injury or bone marrow transplantation.
XX
PS Claim 4; Fig 11f-1; 134pp; English.
XX
SS
CC This sequence is a truncated human telomerase of the invention. Primers
CC that amplify the telomerase coding sequence can be used in a method for
CC diagnosing cancer in a patient. The telomerase can be used for detection,
CC diagnosis and drug screening. Inhibitors of telomerase activity can be
CC used to treat cancers such as melanomas, other skin cancers,
CC neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC growths. Enhancers of telomerase may be used to stimulate stem cell
CC proliferation and differentiation (expansion of haematopoietic stem cells
CC could be administered in the bone marrow transplant context). As well,
CC many tissues have stem cells. Proliferation of these cells may be useful
CC in wound healing, hair growth, treatment of disease such as Wilms'
CC tumour, organ regeneration or differentiation after injury or diseases,
CC nerve cell or brain cell growth following injury
XX
SQ Sequence 1132 AA;
XX
Query Match 99.7%; Score 5945; DB 2; Length 1132;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1129; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 121 SYLPNTATLARGSGAWGLLRVGGDVVHLLARCALFVLPASGAYOCGPYQLGA 180
DB 121 SYLPNTATLARGSGAWGLLRVGGDVVHLLARCALFVLPASGAYOCGPYQLGA 180
QY 181 ATGAPPPHAGSPRRRLGCEAMNHSYREAGVPLGAPGARRRGSSASRLPPRR 240
DB 181 ATGAPPPHAGSPRRRLGCEAMNHSYREAGVPLGAPGARRRGSSASRLPPRR 240
QY 241 GAAPPEPRTVGGGSMHPERTGSPRGCVVSPAPAEANSLGALSGTHSPG 300
DB 241 GAAPPEPRTVGGGSMHPERTGSPRGCVVSPAPAEANSLGALSGTHSPG 300
QY 301 ROHHAGPSTSPRPDPCCPVYATKHFLLSSGDKQJLRPSFLSLRPSLTGARL 360
DB 301 ROHHAGPSTSPRPDPCCPVYATKHFLLSSGDKQJLRPSFLSLRPSLTGARL 360
QY 361 VETIFLGSRPMMGTTPRLPRLQRYWQAPFLLELGNHACQPYGLKTHCPPLAAT 420
DB 361 VETIFLGSRPMMGTTPRLPRLQRYWQAPFLLELGNHACQPYGLKTHCPPLAAT 420
QY 421 PAAGVCAKREKPGQSVAAPEEDDPRLVOLLROHSSPMQVGFVACLRPLVPGJMS 480
DB 421 PAAGVCAKREKPGQSVAAPEEDDPRLVOLLROHSSPMQVGFVACLRPLVPGJMS 480
QY 481 RHNERREFLRNTKKFISLGKHAKLSELTLWKSVDCAMLRSPGVGCVAASHRLREET 540
DB 481 RHNERREFLRNTKKFISLGKHAKLSELTLWKSVDCAMLRSPGVGCVAASHRLREET 540
QY 541 LAKEFLHMLSVVVELLRSEFYVETETEOKNRLPEVRPSWKLQSLGRHCHKVQLE 600
DB 541 LAKEFLHMLSVVVELLRSEFYVETETEOKNRLPEVRPSWKLQSLGRHCHKVQLE 600
QY 601 LSEAEVQHREARPALTSRLRFPKPDGLRPIVNMVYVAGARTFRREKAEELTGRVXA 660
DB 601 LSEAEVQHREARPALTSRLRFPKPDGLRPIVNMVYVAGARTFRREKAEELTGRVXA 660
QY 661 LFSVLNTERARRPCLGASVGLDDDIRAMRTFVLRRADPPPELYFVNDVTGAYDTI 720
DB 661 LFSVLNTERARRPCLGASVGLDDDIRAMRTFVLRRADPPPELYFVNDVTGAYDTI 720
QY 721 POBLTEVIAIIRKPORTYCVRRAYAVQKAAHGVKRAKFSHSTLTLDOPVWROFVAH 780
DB 721 POBLTEVIAIIRKPORTYCVRRAYAVQKAAHGVKRAKFSHSTLTLDOPVWROFVAH 780
QY 781 QETSPLRDAAVIEOSSSLNASSGLFVPLRPMCHAVIRIGKSVYOCQIPGGSILSTL 840
DB 781 QETSPLRDAAVIEOSSSLNASSGLFVPLRPMCHAVIRIGKSVYOCQIPGGSILSTL 840
QY 841 LCSIACVDMENKLPAGIRRDGLLRIVDDPLVTPHILTHAKTELRLTRVCPVGVVNL 900
DB 841 LCSIACVDMENKLPAGIRRDGLLRIVDDPLVTPHILTHAKTELRLTRVCPVGVVNL 900
QY 901 RKTIVNFEVEDEALGTAFAVQMPAHGLFPMCGLLDTRILEVSDVSSVARTISRASTLF 960
DB 901 RKTIVNFEVEDEALGTAFAVQMPAHGLFPMCGLLDTRILEVSDVSSVARTISRASTLF 960
QY 961 NRGKARARNRRKLPGLVLRKCHSLFTDLQVNSIQVYCNINIKYLLILQARHFACTQCP 1020
DB 961 NRGKARARNRRKLPGLVLRKCHSLFTDLQVNSIQVYCNINIKYLLILQARHFACTQCP 1020
QY 1021 FHQGWANPFPFLRVISDTASLCYSILKAKNAGSLGAKAAGPLPSEAVQWMLCHQAFLL 1080
DB 1021 FHQGWANPFPFLRVISDTASLCYSILKAKNAGSLGAKAAGPLPSEAVQWMLCHQAFLL 1080
QY 1081 KLTTHRTVTVPLUGSLRTAQTOLSRKLPGLTTLTLEAANPALPSDKTILLD 1132
DB 1081 KLTTHRTVTVPLUGSLRTAQTOLSRKLPGLTTLTLEAANPALPSDKTILLD 1132

```

```

XX AA28401;
AC 22-SEP-1999 (first entry)
XX
XX Human EST2 protein sequence.
DE
XX EST2: Proliferative capacity; cellular proliferation; decubitus ulcer;
XX telomerase-activating therapeutic agent; cell life-span extension;
XX venous disease; venous stasis ulcer; excessive pressure; arterial ulcer;
XX tissue regeneration enhancer; atherosclerosis; therapy.
XX
XX Homo sapiens.
OS
XX WO9935243-A2.
XX
XX 15-JUL-1999.
XX
XX 12-JAN-1999; 99WO-US000682.
XX
XX 13-JAN-1998; 98US-0071220P.
XX 12-JAN-1998; 98US-0071455P.
XX 21-APR-1998; 98US-00063657.
XX
XX (COLD-) COLD SPRING HARBOR LAB.
XX
XX Hannon GJ, Wang J, Beach DH;
XX
XX WPI: 1999-444196/37.
XX
XX N-P8DB; AAX89424.
XX
XX Increasing proliferative capacity of cells useful for promoting wound
XX healing.
XX
XX Claim 3: Page 65-70; 73pp; English.
XX
XX This sequence is the human EST2 protein, and can be used in the method of
XX the invention. The method is for increasing the proliferative capacity of
XX cells, and comprises contacting the cell with a telomerase-activating
XX therapeutic agent (TAA). The method can be used for extending the life-
XX span of cells, e.g. by increasing the number of mitotic divisions. The
XX can be used for e.g. the extension of skin or other epithelial cell
XX cultures or grafts, the expansion of mesenchymal cell cultures or grafts,
XX and the expansion of chondrocyte or osteocyte cultures or grafts. They
XX can be applied to e.g. neuronal, haematopoietic, epithelial, pancreatic,
XX hepatic, chondrocytic and osteocytic stem and progenitor cells in
XX vivo, in vitro or ex vivo protocols. The methods can be used for
XX promoting the healing of wounds resulting from e.g. surgery, burns,
XX inflammation or irritation or ulcers resulting from e.g. venous disease
XX (venous stasis ulcers), excessive pressure (decubitus ulcers) or arterial
XX ulcers. They can also be used to enhance tissue regeneration processes,
XX e.g. of the skin, hair and/or fingernails. They can also be used for
XX treating age-related conditions, e.g. atrophy of the skin through loss of
XX extracellular matrix homeostasis in dermal fibroblasts, age-related
XX macular degeneration caused by accumulation of lipofuscin and
XX downregulation of a neuronal survival factor in retinal pigmented
XX epithelial (RPE) cells, and atherosclerosis caused by loss of
XX proliferative capacity and overexpression of hypertensive and thrombotic
XX factors in endothelial cells. Expanded populations of normal or
XX genetically engineered rejuvenated cells could be used for autologous or
XX allogeneic cell and gene therapy. They can also be used for prolonging
XX the lifespan of a culture of normal cells or tissue being used to secrete
XX therapeutic or other commercially significant proteins and products
XX
XX Sequence 1132 AA;

```

```

QY Query Match 99.7%; Score 5945; DB 2; Length 1132;
DB Best Local Similarity 99.7%; Pred. No. 0;
Matches 1129; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 MPBAPRCVAVSLLSHYREVLPATFVRRLGPGQMRIVGSDPAFAFALVAQCLVCPW 60
DB 1 MPBAPRCVAVSLLSHYREVLPATFVRRLGPGQMRIVGSDPAFAFALVAQCLVCPW 60

```

QY 61 DAPPPAAASFRQVSLKELVAVVQRLCERGAQVLAAPGMLLGAAGGPEAFTTSVR 120
DB 61 DAPPPAAASFRQVSLKELVAVVQRLCERGAQVLAAPGMLLGAAGGPEAFTTSVR 120
QY 121 SYLENTVTDALSGSGMGLLRVGDVVLHLLACALFVLAAPSCAYOVCGPPLYQGA 180
DB 121 SYLENTVTDALSGSGMGLLRVGDVVLHLLACALFVLAAPSCAYOVCGPPLYQGA 180
QY 181 ATQARPPPASGRRRLGGERAMNHSVREAGVPLGPAFGARRGGSASRSLPLKRRR 240
DB 181 ATQARPPPASGRRRLGGERAMNHSVREAGVPLGPAFGARRGGSASRSLPLKRRR 240
QY 241 GAAPERPPTVGGGSAHAGRTGSDRGFCVSPAPARBEATSEGLASGRHSHPVG 300
DB 241 GAAPERPPTVGGGSAHAGRTGSDRGFCVSPAPARBEATSEGLASGRHSHPVG 300
QY 301 ROHAGPSTSRPRPMDTPCPVYATKHFYSSGDKEQLRPSFLSLRPSLTGARL 360
DB 301 ROHAGPSTSRPRPMDTPCPVYATKHFYSSGDKEQLRPSFLSLRPSLTGARL 360
QY 361 VETIFLGSRPWMPGTRRLPRLPORVMWRPLFELIGHACCPYGLLKHCPRLAVT 420
DB 361 VETIFLGSRPWMPGTRRLPRLPORVMWRPLFELIGHACCPYGLLKHCPRLAVT 420
QY 421 PAAGVCAREKPOGSAAPBEEDTDRRLVOLRHSPPVOYGFYACLRRLVPPGLWS 480
DB 421 PAAGVCAREKPOGSAAPBEEDTDRRLVOLRHSPPVOYGFYACLRRLVPPGLWS 480
QY 481 RHNERFELNKKFISLGNALSLQELTKMSVDCAMLRSPGVCPAERHLEBEI 540
DB 481 RHNERFELNKKFISLGNALSLQELTKMSVDCAMLRSPGVCPAERHLEBEI 540
QY 541 LAKEFHMELSVVVELLRFYVTEFTTPOKNRLFYRPSVMSKOSIGIRHLEKVR 600
DB 541 LAKEFHMELSVVVELLRFYVTEFTTPOKNRLFYRPSVMSKOSIGIRHLEKVR 600
QY 601 LBAEVRQREARPALTSRLRFPKPDGLRPIVMDYVAGARTRRKARLTSRYKA 660
DB 601 LBAEVRQREARPALTSRLRFPKPDGLRPIVMDYVAGARTRRKARLTSRYKA 660
QY 661 LBSVLYNEBARBPGLLGAIVLGLDIDHRAWRFFVLRVAODPPPELVKQDVTA 720
DB 661 LBSVLYNEBARBPGLLGAIVLGLDIDHRAWRFFVLRVAODPPPELVKQDVTA 720
QY 721 PODRLTEVIASIIKQNTYCVRYAVVOKAAHGRKAFKSHVSTLTLQPYMRQFVA 780
DB 721 PODRLTEVIASIIKQNTYCVRYAVVOKAAHGRKAFKSHVSTLTLQPYMRQFVA 780
QY 781 QETSPLRDAVVT EOGSSINLASSGLFDVYLRPMCHAVIRKSKYVOCQGI 840
DB 781 QETSPLRDAVVT EOGSSINLASSGLFDVYLRPMCHAVIRKSKYVOCQGI 840
QY 841 LQSLCYGDMENKLFAGIRRDGLLRVDFLLVTEPHLTHAKTFLTLVGVPEYCV 900
DB 841 LQSLCYGDMENKLFAGIRRDGLLRVDFLLVTEPHLTHAKTFLTLVGVPEYCV 900
QY 901 RKTVMFPEDEALGTAIVOMPAHGLPFWCGLLDITLVEQSYSSYATSTRASTF 960
DB 901 RKTVMFPEDEALGTAIVOMPAHGLPFWCGLLDITLVEQSYSSYATSTRASTF 960
QY 961 NNGFAGRMARAKLFGVLRKCHSLFLDLQVNSLQVCTNICYKILLDAYFFHAC 1020
DB 961 NNGFAGRMARAKLFGVLRKCHSLFLDLQVNSLQVCTNICYKILLDAYFFHAC 1020
QY 1021 FHQOVWKNFTFLRVLVISTASLCYSILKAKNAGSLGKGAAGPJPSSAVOML 1080
DB 1021 FHQOVWKNFTFLRVLVISTASLCYSILKAKNAGSLGKGAAGPJPSSAVOML 1080
QY 1081 KLTBRHVTVP LGLSRTAQTOLSRKPGTTLTALAAANPALPSPDFTI 1132
DB 1081 KLTBRHVTVP LGLSRTAQTOLSRKPGTTLTALAAANPALPSPDFTI 1132

RESULT 30
AA96566
ID AA96566 standard; protein; 1132 AA.
XX
AC AA96566;
XX
DT 12-SEP-2000 (first entry)
XX
DE hEST2, a human telomerase catalytic subunit homologue.
XX
XX hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span;
XX retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;
XX proliferation; immortal; tumour therapy; macular degeneration;
XX activator. INK4.
XX
OS Homo sapiens.
XX
EN W0200031238-A2.
XX
PD 02-JUN-2000.
XX
PE 24-NOV-1999; 99NO-US027907.
XX
PR 25-NOV-1998; 98US-010991P.
XX
PR 17-FEB-1999; 99US-0120549P.
XX
PA (GENE-) GENETICA INC.
XX
FI Hannon GJ, Beach DH;
XX
DR WPI; 2000-400055/34.
XX
DR N-PSDB; AAA29388.
XX
PT New method for increasing the proliferative capacity of cell lines
PT comprises administering agents reversibly activating telomerase activity
PT and reversibly inactivating Rb/INK4 and/or p53 pathways useful in
PT treating age related diseases.
XX
PS
XX
XX Claim 14; Page 116-119; 123pp; English.
XX
XX This protein, designated hEST2, is a human telomerase catalytic subunit
XX homologue of yeast EST2p and Euplores p123. hEST2 is a member of the
XX reverse transcriptase family of enzymes. The invention concerns methods
XX and reagents for extending the life-span, e.g. the number of mitotic
XX divisions, of a cell. The method relies on activation of a telomerase
XX activity and inhibition of one or both of a retinoblastoma (Rb)/INK4
XX pathway or a p53 pathway. Phosphorylation of Rb by cyclin-dependent
XX kinases, cdk4 and cdk6, releases the cells into the division cycle.
XX Binding of INK4 family members, e.g. the tumour suppressor p16INK4,
XX inhibits kinase activity and results in growth arrest. Rb inactivators
XX can selectively and reversibly inactivate an Rb/INK4 pathway, especially
XX an Rb/p16INK4 pathway. The oncoprotein MDM2 is a cellular inhibitor of
XX Rb/EST2 function and the p53 tumour suppressor and can also be used in the
XX methods. Other molecules which can be used include cdk4 or cdk6 mutants.
XX In particular, a cdk4 mutant is one which differs from at one or more of
XX residues K23, R24, H95 and/or D97. Additional constructs include a
XX papilloma virus E7 protein, or other viral oncoprotein which bypasses Rb
XX and/or p53. Antisense constructs of the Rb and p16INK4 genes may also be
XX used. The methods are useful for increasing the proliferative capacity of
XX cells. The cells are subsequently of use in pharmaceutical and cosmetic
XX preparations used to treat conditions related to (premature) ageing, e.g.
XX macular degeneration and arteriosclerosis. The cells can also be used to
XX replace tumour cell lines in vitro and for studies on biochemical and
XX physiological aspects of growth and differentiation. Long lived
XX (immortal) cells could also be of use in the production of normal or
XX genetically engineered biotechnology products
XX

SO Sequence 1132 AA;
Query Match 99.7%; Score 5945; DB 3; Length 1132;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1129; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	MPBARCRAVRSLLRSHYREVLPLATFVPRLLPGCGMVLVORGDPAAARALVAOCLVCPM	60
Ds	1	MPBARCRAVRSLLRSHYREVLPLATFVPRLLPGCGMVLVORGDPAAARALVAOCLVCPM	60
QY	61	DABPPAAPSFRQVSCIKETLVARVLORICERGANVLAFGALUDGARGPPEAFTTSVR	120
Ds	61	DABPPAAPSFRQVSCIKETLVARVLORICERGANVLAFGALUDGARGPPEAFTTSVR	120
QY	121	SYLNTYTDALRSGGANGLLRRVGDVLYHLLRCALFVLVASSCAVYVCGPRLYOLGA	180
Ds	121	SYLNTYTDALRSGGANGLLRRVGDVLYHLLRCALFVLVASSCAVYVCGPRLYOLGA	180
QY	181	ATQARPEPHASGPRRLGCEPAMNHSVEAGVPLGLPAPGARRRGSASRLPLPKRPRR	240
Ds	181	ATQARPEPHASGPRRLGCEPAMNHSVEAGVPLGLPAPGARRRGSASRLPLPKRPRR	240
QY	241	GAAPEPEPTVYGGSGMAHPGRTGSPDRGFCVSPAPPAEPAITSLEGALSTRHSHPVG	300
Ds	241	GAAPEPEPTVYGGSGMAHPGRTGSPDRGFCVSPAPPAEPAITSLEGALSTRHSHPVG	300
QY	301	ROHAGPSTSRPPRPMDTCCPPYAETKEHLYSGGXECOLRPSFLLSLSPSTGARRL	360
Ds	301	ROHAGPSTSRPPRPMDTCCPPYAETKEHLYSGGXECOLRPSFLLSLSPSTGARRL	360
QY	361	VEITFLGSRPMPGTPRRLPRLPORWQMRBLFELIGNHAOCCEYVLLKXHCPLRAAVT	420
Ds	361	VEITFLGSRPMPGTPRRLPRLPORWQMRBLFELIGNHAOCCEYVLLKXHCPLRAAVT	420
QY	421	PAAGVCAREKQGSVAABEEEDTPRRLYOLLROHSSPWQYGVGRACLRLLVPPGJMS	480
Ds	421	PAAGVCAREKQGSVAABEEEDTPRRLYOLLROHSSPWQYGVGRACLRLLVPPGJMS	480
QY	481	RHNERRFLRNTKFTISLQKHAKLSTOEITWQMSVRDCAMLRSPGVGCVPAAEHRLREEI	540
Ds	481	RHNERRFLRNTKFTISLQKHAKLSTOEITWQMSVRDCAMLRSPGVGCVPAAEHRLREEI	540
QY	541	LAKELHMLMSYVVELLRSPFYVTETTTQKNRLLFPYRPSVMSKQISICIRQHLKRVQJRE	600
Ds	541	LAKELHMLMSYVVELLRSPFYVTETTTQKNRLLFPYRPSVMSKQISICIRQHLKRVQJRE	600
QY	601	LSEAEVRQHRARAPLTLSTRLEFIPKPGGLPIYMDVVGAATFRREKRAERLTSRYKA	660
Ds	601	LSEAEVRQHRARAPLTLSTRLEFIPKPGGLPIYMDVVGAATFRREKRAERLTSRYKA	660
QY	661	LFSVLYNVERARPGJLGSVJGLDDIHRAMRTFVLRVRAODPPELYFVKVDVTGAYDTI	720
Ds	661	LFSVLYNVERARPGJLGSVJGLDDIHRAMRTFVLRVRAODPPELYFVKVDVTGAYDTI	720
QY	721	PODLUTEVIASIIKPKQNTYCVRRAYAVQKAAHGVRKAFKSHVSTLMDLQYMQQFAHL	780
Ds	721	PODLUTEVIASIIKPKQNTYCVRRAYAVQKAAHGVRKAFKSHVSTLMDLQYMQQFAHL	780
QY	781	QETSPELRVAVYIEOSSJLNEASSGLFDFELRFMCHHARIRIKSGSYVCGQIGPOCSILSTL	840
Ds	781	QETSPELRVAVYIEOSSJLNEASSGLFDFELRFMCHHARIRIKSGSYVCGQIGPOCSILSTL	840
QY	841	LCSLCYGEMENKLPAGIRRDGLLRLVDDFLVLTPLHTAATFLRLTVRGVPEYGCYVNL	900
Ds	841	LCSLCYGEMENKLPAGIRRDGLLRLVDDFLVLTPLHTAATFLRLTVRGVPEYGCYVNL	900
QY	901	RKTYVNFVEDEBALGGTAFVQMPAHGFLPWCGLLDDTTEVQSPYSYATRSRASYTF	960
Ds	901	RKTYVNFVEDEBALGGTAFVQMPAHGFLPWCGLLDDTTEVQSPYSYATRSRASYTF	960
QY	961	NRGFAGNMRKTLFGLVRLKCHSLFDLQVNSLQTVCTNITYKILLQAYFHAACVLQLP	1020
Ds	961	NRGFAGNMRKTLFGLVRLKCHSLFDLQVNSLQTVCTNITYKILLQAYFHAACVLQLP	1020
QY	1021	FHQQWKPQPTFLARYISDTASLCYSIIKAAQAGMSLAKGAAGPLPESAVOYMLCHQAFIL	1080
Ds	1021	FHQQWKPQPTFLARYISDTASLCYSIIKAAQAGMSLAKGAAGPLPESAVOYMLCHQAFIL	1080

```

Oy 108 KLTNRHTVYVLLGSLRTAQTQSLSRKLPSTTLVLAEAANPALPSDEKTLID 1132
Db 1081 KLTNRHTVYVLLGSLRTAQTQSLSRKLPSTTLVLAEAANPALPSDEKTLID 1132

RESULT 31
ID ADC47061 standard; protein; 1132 AA.
XX
AC ADC47061;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human TERT amino acid sequence #SEQ ID 2.
XX
KW Human; TERT; telomerase; antibody; reverse transcriptase; tumour;
KM autoimmune disease; liver cancer.
XX
OS Homo sapiens.
XX
FN MO2003054545-A1.
XX
PD 03-JUL-2003.
XX
PF 19-DEC-2002; 2002MO-JP013310.
XX
PT 21-DEC-2001; 2001JP-00390050.
XX
PR (MITS-) MITSUBISHI KAGAKU MEDICAL INC.
PA (MURA) MURAKAMI S.
PA (KANE/) KANEKO S.
XX
PI Murakami S, Kaneko S, Masutomi K;
XX
DR WPI: 2003-569289/53.
XX
DR N-PSDB; ADC47060.
XX
PT Detecting anti-telomerase antibody for detecting tumors and autoimmune
PT disease.
XX
XX
XX Example Examples; Page 36-41; 45pp; Japanese.
XX
PS The invention relates to a method for detecting an anti-telomerase
CC antibody. The method of the invention comprises reacting telomerase
CC producing protein and a fragment or complex of template RNA with anti-
CC telomerase antibody in a sample, and analysing the product. The
CC telomerase producing protein is preferably telomerase reverse
CC transcriptase, and the analysis method is preferably western blot. The
CC method can be used to detect for tumours and autoimmune disease. The
CC method can also be used for detecting liver cancer. The current sequence
CC represents the human TERT amino acid sequence.
XX
XX
SQ Sequence 1132 AA:
Oy Query Match 99.7%; Score 5945; DB 7; Length 1132;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1129; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Oy 1 MPRAPRCAVAVSLIRSHYREVLPATFVRRLGPGGMRIVQRGDPAPAFALVAOCIVCPW 60
Db 1 MPRAPRCAVAVSLIRSHYREVLPATFVRRLGPGGMRIVQRGDPAPAFALVAOCIVCPW 60
Oy 61 DARPPAPAPSRQVSCLEKELVARVLRQRCERGANVLAFGFALDAGARGPPEAFTTSVR 120
Db 61 DARPPAPAPSRQVSCLEKELVARVLRQRCERGANVLAFGFALDAGARGPPEAFTTSVR 120
Oy 121 SYLNTVTDALRSGAGWGLLRVGGDDVLVHLLARCALEVLVAPSCAYQVCGPPLYQIGA 180
Db 121 SYLNTVTDALRSGAGWGLLRVGGDDVLVHLLARCALEVLVAPSCAYQVCGPPLYQIGA 180
Oy 181 ATOARPPPHAGSPRRRLGCEERAMHSHVREAGVPLGPAPGARRRGSGASRSLPLKRPBR 240
Db 181 ATOARPPPHAGSPRRRLGCEERAMHSHVREAGVPLGPAPGARRRGSGASRSLPLKRPBR 240

```

QY 241 GAAPERTPVGGSAHAPGRTGSDRGFCVVASPARAEATSLGALSGTRHSPSVG 300
 DB 241 GAAPERTPVGGSAHAPGRTGSDRGFCVVASPARAEATSLGALSGTRHSPSVG 300
 QY 301 ROHHAGPSTSPRPWDTPCPVVAETGFLYSSGDKQLRPSLSSLRPSLTGARL 360
 DB 301 ROHHAGPSTSPRPWDTPCPVVAETGFLYSSGDKQLRPSLSSLRPSLTGARL 360
 QY 361 VETIFLGSPPMGPFRRLPRLPORYMQRPLFLSLGNHACPGVLLKTHCPRAVY 420
 DB 361 VETIFLGSPPMGPFRRLPRLPORYMQRPLFLSLGNHACPGVLLKTHCPRAVY 420
 QY 421 PAAGVCAKPKPOGSVAAPEDTDPRRLVOLLRHSSPMQVGYFVACLRRLVPPGLMGS 480
 DB 421 PAAGVCAKPKPOGSVAAPEDTDPRRLVOLLRHSSPMQVGYFVACLRRLVPPGLMGS 480
 QY 481 RHNERFLNTRKPTSLGKHAQSLQELTWKMSVDCAMLRSPGVCPAAERLRREI 540
 DB 481 RHNERFLNTRKPTSLGKHAQSLQELTWKMSVDCAMLRSPGVCPAAERLRREI 540
 QY 541 LAKFLHMLSVYVVELLRSPFYVETTFQKRLFFYRPSVSKLQSIGRHLKRVQRE 600
 DB 541 LAKFLHMLSVYVVELLRSPFYVETTFQKRLFFYRPSVSKLQSIGRHLKRVQRE 600
 QY 601 LSEAEVROHREARPAULTSLRLEFIKPPGLRPIVMQDVVGAFTRRKRAERLTSRYKA 660
 DB 601 LSEAEVROHREARPAULTSLRLEFIKPPGLRPIVMQDVVGAFTRRKRAERLTSRYKA 660
 QY 661 LFSVLYNEARRPGLLGASVLDLIDHRAMTFVLRVADPPPELVKXDVTAAYPTI 720
 DB 661 LFSVLYNEARRPGLLGASVLDLIDHRAMTFVLRVADPPPELVKXDVTAAYPTI 720
 QY 721 PODRLTEVASTIKQNTYCVRRYAVVQKAAHGVKRAFKSHVSTLDLPYMRQFVAHL 780
 DB 721 PODRLTEVASTIKQNTYCVRRYAVVQKAAHGVKRAFKSHVSTLDLPYMRQFVAHL 780
 QY 781 QETSPRLADVIEQSSSLNEASSGLFDFVLRMCHAVIRKGSYVOCQIPQGSILSTL 840
 DB 781 QETSPRLADVIEQSSSLNEASSGLFDFVLRMCHAVIRKGSYVOCQIPQGSILSTL 840
 QY 841 LCSLCYGDENKLFAGIRDDGLLRLVDFLLVTPHLLTHAKFTLTVRGVPEYGVNLT 900
 DB 841 LCSLCYGDENKLFAGIRDDGLLRLVDFLLVTPHLLTHAKFTLTVRGVPEYGVNLT 900
 QY 901 RKTIVNPEPEDBALGTAFAVQMPAHGLFPWCGLLDPTLLEQSSYSYATSTIRASVTF 960
 DB 901 RKTIVNPEPEDBALGTAFAVQMPAHGLFPWCGLLDPTLLEQSSYSYATSTIRASVTF 960
 QY 961 NRGFYAGRMRRKTLFGVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYEFHACVQLP 1020
 DB 961 NRGFYAGRMRRKTLFGVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYEFHACVQLP 1020
 QY 1021 FHQOVWKNPTFLRVIISDTASLCYSLIKAKXAGSLGAKGAAGPLPSAVVWLCHQAFLL 1080
 DB 1021 FHQOVWKNPTFLRVIISDTASLCYSLIKAKXAGSLGAKGAAGPLPSAVVWLCHQAFLL 1080
 QY 1081 KLTRHRTVYVPLGSLRTAQTLQSLKRLGTTLLTALEAANPALPSDFITLD 1132
 DB 1081 KLTRHRTVYVPLGSLRTAQTLQSLKRLGTTLLTALEAANPALPSDFITLD 1132
 RESULT 32
 ADE40482
 ID ADE40482 standard; protein; 1132 AA.
 AC ADE40482;
 DT 29-JAN-2004 (first entry)
 XX Human telomerase reverse transcriptase (hTERT).
 DE Immortal porcine cell; telomerase reverse transcriptase; epithelial cell;
 XX
 KW

KW uterine endometrial glandular tissue; virus quantification;
 KW virus production; porcine reproductive and respiratory syndrome virus;
 KW PRRSV; toxicity evaluation; human; hTERT; enzyme.
 OS Homo sapiens.
 XX
 XX W02003077853-A2.
 XX
 XX 25-SEP-2003.
 XX
 XX 11-MAR-2003; 2003MO-US007526.
 XX
 XX 11-MAR-2002; 2002US-0363129P.
 XX
 XX (MINTU) UNIV MINNESOTA.
 XX
 XX Farris JA, Foster DN, O'Grady SM;
 XX
 XX WPI: 2003-779075/73.
 XX
 XX N-PSDB; ADE40481.
 XX
 XX New immortal porcine cell comprising a polynucleotide encoding an
 XX exogenous telomerase reverse transcriptase polypeptide, useful for
 XX measuring the amount of virus in a sample or for evaluating toxicity of a
 XX compound.
 XX
 XX Claim 4; SEQ ID NO 2; 42pp; English.
 PS
 XX
 XX The invention relates to immortal porcine cells comprising a
 XX polynucleotide encoding an exogenous telomerase reverse transcriptase
 XX (TERT). The invention also encompasses the method of making immortal
 XX porcine cells, and the use of the immortal porcine cells for measuring
 XX the amount of virus in a sample, producing a virus, and evaluating the
 XX toxicity of a compound. The cells of the invention may be diploid or
 XX aneuploid, and may be an epithelial cell obtained from uterine
 XX endometrial glandular tissue. The exogenous telomerase reverse
 XX transcriptase expressed by the cells of the invention is preferably human
 XX telomerase reverse transcriptase (ADE40482). The immortal porcine cells
 XX are useful for measuring an amount of a virus in a sample, producing a
 XX virus (especially porcine reproductive and respiratory syndrome virus
 XX (PRRSV)), or for evaluating toxicity of a compound. The present sequence
 XX represents human telomerase reverse transcriptase (hTERT), which is
 XX claimed for use in the immortal cells of the invention.
 SQ Sequence 1132 AA;
 Query Match 99.7%; Score 5945; DB 7; Length 1132;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1129; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MPAPRCRAVRSILRSHYREVLPATFVRLPQGRRLVQRODPAFRALVAQCLVCFM 50
 DB 1 MPAPRCRAVRSILRSHYREVLPATFVRLPQGRRLVQRODPAFRALVAQCLVCFM 50
 QY 61 DARPAPASPFQVSCLEKELVARVYLQRCERGAQVLAFGFALLDQARGCPPEARTTSVR 120
 DB 61 DARPAPASPFQVSCLEKELVARVYLQRCERGAQVLAFGFALLDQARGCPPEARTTSVR 120
 QY 121 SYLPNTVTALRGSGAMGILLRRVGDVYVHLLARCAFLVVAPOCAVOVGPPIYOLGA 180
 DB 121 SYLPNTVTALRGSGAMGILLRRVGDVYVHLLARCAFLVVAPOCAVOVGPPIYOLGA 180
 QY 121 SYLPNTVTALRGSGAMGILLRRVGDVYVHLLARCAFLVVAPOCAVOVGPPIYOLGA 180
 DB 121 SYLPNTVTALRGSGAMGILLRRVGDVYVHLLARCAFLVVAPOCAVOVGPPIYOLGA 180
 QY 181 ATQARPAPASGRRRLGGERAMNHSVRBAGVPLGLPAGARRGSGASRSJLPKRPBR 240
 DB 181 ATQARPAPASGRRRLGGERAMNHSVRBAGVPLGLPAGARRGSGASRSJLPKRPBR 240
 QY 241 GAAPERTPVGGSAHAPGRTGSDRGFCVVASPARAEATSLGALSGTRHSPSVG 300
 DB 241 GAAPERTPVGGSAHAPGRTGSDRGFCVVASPARAEATSLGALSGTRHSPSVG 300
 QY 301 ROHHAGPSTSPRPWDTPCPVVAETGFLYSSGDKQLRPSLSSLRPSLTGARL 360
 DB 301 ROHHAGPSTSPRPWDTPCPVVAETGFLYSSGDKQLRPSLSSLRPSLTGARL 360

Qy	361	VEITFISGRPMWPGPRRLPRLOQYQWQMRPLFELLGNHQOCXGVLTKHCHCPLRAVY	420
Dp	361	VEITFISGRPMWPGPRRLPRLOQYQWQMRPLFELLGNHQOCXGVLTKHCHCPLRAVY	420
Qy	421	PAAGYCARKEPQGSVAABEEDTDPRJLVOLRHQSPMOYGFVACIRLVRPGLMG	480
Dp	421	PAAGYCARKEPQGSVAABEEDTDPRJLVOLRHQSPMOYGFVACIRLVRPGLMG	480
Qy	481	RHNERPRLNTKKFISLGKHAKLSTQELTWKMSVDCMWRBSPGVCCVPAEHRLEETI	540
Dp	481	RHNERPRLNTKKFISLGKHAKLSTQELTWKMSVDCMWRBSPGVCCVPAEHRLEETI	540
Qy	541	LAKPLHMLMSYVVVVELLSFFVVBETTEQOKRLFEYRPSWMSKIOSIGIROHLKXVOIRE	600
Dp	541	LAKPLHMLMSYVVVVELLSFFVVBETTEQOKRLFEYRPSWMSKIOSIGIROHLKXVOIRE	600
Qy	601	LSEAEVRCHREARPALTLSTRJRFIPKPDGRLPIVMMDVVGARTPRREKREARLTSRYKA	660
Dp	601	LSEAEVRCHREARPALTLSTRJRFIPKPDGRLPIVMMDVVGARTPRREKREARLTSRYKA	660
Qy	661	LFSVINTYRRARPGILGASVUGLDIIRHAMRTFVLKVAODPBPPLFYVKVDVTGAYTTI	720
Dp	661	LFSVINTYRRARPGILGASVUGLDIIRHAMRTFVLKVAODPBPPLFYVKVDVTGAYTTI	720
Qy	721	PODLRLTEVIASIKPKONTYCVRRYVAVQKAAHGHKRXKFKSHVSUTLLOPRMRFVAHL	780
Dp	721	PODLRLTEVIASIKPKONTYCVRRYVAVQKAAHGHKRXKFKSHVSUTLLOPRMRFVAHL	780
Qy	781	QETSELPDRAVYIEOSSSLNEASGGLFEDYFLRPMCHAVIRGKSYVQCCGIPQGSILSTL	840
Dp	781	QETSELPDRAVYIEOSSSLNEASGGLFEDYFLRPMCHAVIRGKSYVQCCGIPQGSILSTL	840
Qy	841	LCSJCYGCMENKLPFGIRRDGILLRLVDDFLLVPHLTHAKTFLRTLYRGVPEYGCYVNL	900
Dp	841	LCSJCYGCMENKLPFGIRRDGILLRLVDDFLLVPHLTHAKTFLRTLYRGVPEYGCYVNL	900
Qy	901	RKTYVNFPEVDEBAGGTAFFVOMPAHGLRPMCGILLDTRELOSYSYASRTISASTYF	960
Dp	901	RKTYVNFPEVDEBAGGTAFFVOMPAHGLRPMCGILLDTRELOSYSYASRTISASTYF	960
Qy	961	NRGFGAGNMRKLPFGLRLKXSHFLDLOVNSLDQVCNTNYKILLLOAYEFHACVLDLP	1020
Dp	961	NRGFGAGNMRKLPFGLRLKXSHFLDLOVNSLDQVCNTNYKILLLOAYEFHACVLDLP	1020
Qy	1021	FHQQYWKMPTEFLRVIYSTASICYSILKAKNAGMSLGAKGAAGPLPSPAQVOMLCHQAFLL	1080
Dp	1021	FHQQYWKMPTEFLRVIYSTASICYSILKAKNAGMSLGAKGAAGPLPSPAQVOMLCHQAFLL	1080
Qy	1081	KLTRHRVYVYVLLGSLRTAQOTLSKLDGTTLLTAAEANPMLPBDFTIILD 1132	
Dp	1081	KLTRHRVYVYVLLGSLRTAQOTLSKLDGTTLLTAAEANPMLPBDFTIILD 1132	

RESULT	33
AAW56101	
ID	AAW56101 standard; protein; 1405 AA.
XX	
XX	AAW56101;
XX	
DT	13-AUG-1998 (first entry)
XX	
DE	Enhanced green fluorescent protein and hTRT fusion protein.
XX	
KW	Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;
KW	cell proliferation; cancer; ageing; ribonucleoprotein.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
FT	Key
FT	Location/Qualifiers
FT	1..250
FT	/note="enhanced green fluorescent protein fragment"

FT	Region	276..1405	/note= "hTERT protein fragment"
FT	XX	GB2317891-A.	
XX	XX	08-APR-1998.	
XX	XX	01-OCT-1997;	97GB-00020890.
XX	XX	01-OCT-1996;	96US-00724643.
XX	XX	18-APR-1997;	97US-00844419.
XX	XX	25-APR-1997;	97US-00846017.
XX	XX	06-MAY-1997;	97US-00851843.
XX	XX	09-MAY-1997;	97US-00854050.
XX	XX	14-AUG-1997;	97US-00911312.
XX	XX	14-AUG-1997;	97US-00912951.
XX	XX	14-AUG-1997;	97US-00915503.
XX	XX	(GERO-) GERON CORP.	
XX	XX	(UYTE-) UNIV TECHNOLOGY CORP.	
XX	XX	Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB, Andrews WH;	
XX	XX	WPI, 1998-171633/16.	
XX	XX	Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing.	
XX	XX	Example 15, Page 269-270; 387pp; English.	
XX	XX	The present sequence represents a fusion protein from an example of the present invention which describes human telomerase reverse transcriptase (hTERT). The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTERT, by detecting the change in hTERT recombinant protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein preparation of hTERT with a telomerase RNA component; (C) detection of the hTERT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or amplification product with presence of hTERT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTERT expression; and (E) the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTERT and the polynucleotide encoding hTERT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions that are associated with high telomerase activity. A protein preparation of hTERT can also be used in the new methods	
XX	XX	Sequence 1405 AA:	
XX	XX	Query Match	99.4%; Score 5929; DB 2; Length 1405;
XX	XX	Best Local Similarity	99.8%; Pred. No. 0;
XX	XX	Matches 1130; Conservative	0; Mismatches 0; Indels 2; Gaps 2;
XX	XX	1 MPRAPRCAVRSLSLRSHYREVLPPLATEFRRIRPGQWRLVORGDEPAFRALVAQCLVCFW	60
XX	XX	276 MPRAPRCAVRSLSLRSHYREVLPPLATEFRRIRPGQWRLVORGDEPAFRALVAQCLVCFW	335
XX	XX	61 DARPAPPAASFQVSCILKELVARTLCGLERGANVLAFAFALLDGAAGGPEAFPTTSVR	120
XX	XX	336 DARPAPPAASFQVSCILKELVARTLCGLERGANVLAFAFALLDGAAGGPEAFPTTSVR	395
XX	XX	121 SYLENTVTDLRSGGAWGLLRRYGDVVLVHLLARCALFVLVAPSCAVQVCGPPLYLQGA	180
XX	XX	396 SYLENTVTDLRSGGAWGLLRRYGDVVLVHLLARCALFVLVAPSCAVQVCGPPLYLQGA	455
XX	XX	181 ATQARPPHAGSPRRIRIGCEBAMNHSVREAGVPLGLPAPGARRRGGASRLPLPKPRR	240

Db 456 ATQASPPHASPRRRLGGERAMNHSVREAGVPLGLPAPGARRRGGSASRSLLPJKRBR 515
 QY 241 GAPEPERTPVQGSMAHPRTGSPDRGFCVSPAPAEATSTEGALSGTRSHSPVG 300
 Db 516 GAPEPERTPVQGSMAHPRTGSPDRGFCVSPAPAEATSTEGALSGTRSHSPVG 575
 QY 301 ROHHAQPESTSPRPMDTCCPPVYAEKHFVSSGDYEQLRPSLLSLPSLTGAARL 360
 Db 576 ROHHAQPESTSPRPMDTCCPPVYAEKHFVSSGDYEQLRPSLLSLPSLTGAARL 634
 QY 361 VETIFLGSPPMWPGRPRRLPRLPORVWOMRPLFELLNHNOCPYGLVLLKHCPLRAAVT 420
 Db 635 VETIFLGSPPMWPGRPRRLPRLPORVWOMRPLFELLNHNOCPYGLVLLKHCPLRAAVT 694
 QY 421 PAAGVAREKPGQSVAAPEEDTDPRRLVOLLROHSSPMOYGYFVACLRRLVPPGLMGS 480
 Db 695 PAAGVAREKPGQSVAAPEEDTDPRRLVOLLROHSSPMOYGYFVACLRRLVPPGLMGS 754
 QY 481 RHNERRFLNTRKFFSLGHAHLSQELTWKMSVDCAMLRSPGVGPPAAHRLREI 540
 Db 755 RHNERRFLNTRKFFSLGHAHLSQELTWKMSVDCAMLRSPGVGPPAAHRLREI 814
 QY 541 LAKFLHMLMSVYVELLSFFVYETTFQKNRLFYRPSVMSKQSIGIRHOLKRVOLRE 600
 Db 815 LAKFLHMLMSVYVELLSFFVYETTFQKNRLFYRPSVMSKQSIGIRHOLKRVOLRE 874
 QY 601 LSEAEVROHREARPAALTSRLRPIKPDGLPIVMDYVVGARTFRKRAERLTSRYKA 660
 Db 875 LSEAEVROHREARPAALTSRLRPIKPDGLPIVMDYVVGARTFRKRAERLTSRYKA 934
 QY 661 LPSVNLNERARPPGLGASVLGLDDIHRAMRPFVLRVAOPPEPLTVKTDVGAVDYI 720
 Db 935 LPSVNLNERARPPGLGASVLGLDDIHRAMRPFVLRVAOPPEPLTVKTDVGAVDYI 994
 QY 721 PODRLTEVIASIIKQNTVCVRYAVVQKAAGHVRKAFKSHVSTLIDLPYMRQFVAHL 780
 Db 995 PODRLTEVIASIIKQNTVCVRYAVVQKAAGHVRKAFKSHVSTLIDLPYMRQFVAHL 1054
 QY 781 QSTSPRDAVVVEOSSSLNEASSGLFDFELRPMCHAVRIGSKSVQCGIIPQSIISLT 840
 Db 1055 QSTSPRDAVVVEOSSSLNEASSGLFDFELRPMCHAVRIGSKSVQCGIIPQSIISLT 1114
 QY 841 LLSLQCGDMENKLFAGIRRDGLLRVLVDPLLPHLTHAKFTLTVRAGVEXGVNVL 900
 Db 1115 LLSLQCGDMENKLFAGIRRDGLLRVLVDPLLPHLTHAKFTLTVRAGVEXGVNVL 1174
 QY 901 RKTVMFPIVEDALGTAFFVQVPAHGLPFWCGLLIDRTLEVOSSYSSYARTSIRASTF 960
 Db 1175 RKTVMFPIVEDALGTAFFVQVPAHGLPFWCGLLIDRTLEVOSSYSSYARTSIRASTF 1234
 QY 961 NRGFKAGRMRRKLFGLVSLKCHSFLDLQVNSLQTVCTNIYKILLQAYRFAHCVLQLP 1020
 Db 1235 NRGFKAGRMRRKLFGLVSLKCHSFLDLQVNSLQTVCTNIYKILLQAYRFAHCVLQLP 1294
 QY 1021 FHQGVAKNFTFPLRVISDTASLCYSILKAKNAGSLGAKGAAGLPSEAVOMLCHQAFLL 1080
 Db 1295 FHQGVAKNFTFPLRVISDTASLCYSILKAKNAGSLGAKGAAGLPSEAVOMLCHQAFLL 1354
 QY 1081 KLTRHRTVYVPLLGSLRTAQOTLSRKLPGTTLTALEAANPALPSDFPTIID 1132
 Db 1355 KLTRHRTVYVPLLGSLRTAQOTLSRKLPGTTLTALEAANPALPSDFPTIID 1405
 RESULT 34
 ID AA00647
 AA00647 standard; protein; 1166 AA.
 XX AC AA00647;
 XX 26-JUL-1999 (first entry)
 XX Telomerase (ver. 2) protein sequence.
 XX

KM Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KM neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KM smooth muscle cell hyperplasia; stem cell proliferation; Wilms' tumor;
 KM stem cell differentiation; organ regeneration; organ differentiation.
 OS Homo sapiens.
 OS Synthetic.
 PN WO9901560-A1.
 XX 14-JAN-1999.
 PD 01-JUL-1998; 98MO-US013635.
 PF 01-JUL-1998; 98MO-US013635.
 XX 01-JUL-1997; 97US-0051410P.
 PR 21-JUL-1997; 97US-0053018P.
 PR 21-JUL-1997; 97US-0053329P.
 PR 04-AUG-1997; 97US-0054642P.
 PR 09-SEP-1997; 97US-0058287P.
 XX (CAMP-) CAMBIA BIOSYSTEMS LLC.
 PA Killian A, Bowtell D;
 PI WPI; 1999-106060/09.
 DR N-PDB; AAX18275.
 DR
 XX New isolated vertebrate telomerase genes - used to develop products for
 PT treating cancers or for organ regeneration, nerve cell or brain cell
 PT growth following injury or bone marrow transplantation.
 PS Claim 4; Fig 11z-ac; 134pp; English.
 XX
 CC This sequence is a truncated human telomerase of the invention. Primers
 CC that amplify the telomerase coding sequence can be used in a method for
 CC diagnosing cancer in a patient. The telomerase can be used for detection,
 CC diagnosis and drug screening. Inhibitors of telomerase activity can be
 CC used to treat cancers such as melanomas, other skin cancers,
 CC neuroblastomas, breast carcinomas, colon carcinomas, leukemias,
 CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
 CC growths. Enhancers of telomerase may be used to stimulate stem cell
 CC proliferation and differentiation (expansion of haematopoietic stem cells
 CC could be administered in the bone marrow transplant context). As well,
 CC many tissues have stem cells. Proliferation of these cells may be useful
 CC in wound healing, hair growth, treatment of disease such as Wilms'
 CC tumour, organ regeneration or differentiation after injury or diseases,
 CC nerve cell or brain cell growth following injury
 XX
 SQ Sequence 1166 AA;
 Query Match 99.2%; Score 5918; DB 2; Length 1166;
 Best Local Similarity 96.8%; Pred. No. 0;
 Matches 1129; Conservative 1; Mismatches 2; Indels 34; Gaps 1;
 QY 1 MPAPRCRAVRSLLRSHREVLPLATFVRRLPGQGRLLVQRDDPAFRLLVACIVCVPM 60
 Db 1 MPAPRCRAVRSLLRSHREVLPLATFVRRLPGQGRLLVQRDDPAFRLLVACIVCVPM 60
 QY 61 DARPAPAAASFROY-----SCLKEIVARVLQ 86
 Db 61 DARPAPAAASFROYGLPGVAVLGLRAAGNQRAHSAAGSGRPPRSCLKEIVARVLQ 120
 QY 87 RLCERGAKNVLAFGPALLDGAAGCPPEAFTTSYSTLENTVTDAIRGSGAMGLLRVVD 146
 Db 121 RLCERGAKNVLAFGPALLDGAAGCPPEAFTTSYSTLENTVTDAIRGSGAMGLLRVVD 180
 QY 147 DVIYHLARCALFVLVAPSCAYOVGPPLYOIGAATQAPRPHASGPPRLGGERAMNHS 206
 Db 181 DVIYHLARCALFVLVAPSCAYOVGPPLYOIGAATQAPRPHASGPPRLGGERAMNHS 240
 QY 207 VREAGVPLGLPAPGARRGGSASRSLLPDKRRRGAAPERTPVQGSMAHPGRTGPS 266
 Db 241 VREAGVPLGLPAPGARRGGSASRSLLPDKRRRGAAPERTPVQGSMAHPGRTGPS 300


```

QY 267 DRGFCVSPARPAEATSEALSGTRHSHPSVGRHNAQPSSTASPPRMDTCCPVYA 326
DB 301 DRGFCVSPARPAEATSEALSGTRHSHPSVGRHNAQPSSTASPPRMDTCCPVYA 360
QY 327 ETKHFLYSSGDKQLRPSFLSSLRPSLTGARLVEITFLGSPRPMGPTRRRLPRIPQY 386
DB 361 ETKHFLYSSGDKQLRPSFLSSLRPSLTGARLVEITFLGSPRPMGPTRRRLPRIPQY 420
QY 387 WQNRPLFELLGNHQAQCPYVLLKTHCPRLAAVTPAAGVCAKPKQGSVAAPBEDTDR 446
DB 421 WQNRPLFELLGNHQAQCPYVLLKTHCPRLAAVTPAAGVCAKPKQGSVAAPBEDTDR 480
QY 447 RLVOQLLRQSHSPWQVYGFVACLRRLVPEGLMGRHNERFLNNTKFFISLGHAALSIQ 506
DB 481 RLVOQLLRQSHSPWQVYGFVACLRRLVPEGLMGRHNERFLNNTKFFISLGHAALSIQ 540
QY 507 ELTWKMSVDRCAWLRSPGVGCVPAAEHRLEBEILAKFLHMLMSYVVELLRGFFVTEP 566
DB 541 ELTWKMSVDRCAWLRSPGVGCVPAAEHRLEBEILAKFLHMLMSYVVELLRGFFVTEP 600
QY 567 TFOQNRLEFFRPSVWSKLSIGIRQLKRVQLRELSEAEVYQHRERAPALLTSRLRPIK 626
DB 601 TFOQNRLEFFRPSVWSKLSIGIRQLKRVQLRELSEAEVYQHRERAPALLTSRLRPIK 660
QY 627 PDGLRPIVNDYVYGARTFRERKRAERLTSRVKALPSVLYERARAPGLIGAVLGLDDI 686
DB 661 PDGLRPIVNDYVYGARTFRERKRAERLTSRVKALPSVLYERARAPGLIGAVLGLDDI 720
QY 687 HRAWRITFVLRADPEPPELVFKVDYTAGYDTIPQDRILEVTASIIKPNITYCVARYAV 746
DB 721 HRAWRITFVLRADPEPPELVFKVDYTAGYDTIPQDRILEVTASIIKPNITYCVARYAV 780
QY 747 VQRAAHGVKAKAFKSHVSTLTDQPYMKQFVAHQETSPERDAVVEQSSSLNEASSGIF 806
DB 781 VQRAAHGVKAKAFKSHVSTLTDQPYMKQFVAHQETSPERDAVVEQSSSLNEASSGIF 840
QY 807 DVEFLRFCHHAVIRGKSYVQCOGIPQGSILSTLCSLCYGDENKTLFAGIRRDGLLRL 866
DB 841 DVEFLRFCHHAVIRGKSYVQCOGIPQGSILSTLCSLCYGDENKTLFAGIRRDGLLRL 900
QY 867 VDOPFLVTPPLTHAKTFLRTLNVGVPYGCVVNLKRTVNFPEVEDALGSTAFVQMPAHG 926
DB 901 VDOPFLVTPPLTHAKTFLRTLNVGVPYGCVVNLKRTVNFPEVEDALGSTAFVQMPAHG 960
QY 927 LRFMGGLDTRTLEVOSSYSYARTSIRASVTENFGFKGRMWRKTLFGVLRKCHSIF 986
DB 961 LRFMGGLDTRTLEVOSSYSYARTSIRASVTENFGFKGRMWRKTLFGVLRKCHSIF 1020
QY 987 LDIQVNSLQVCTNIIKILLQAYRPAACVLOLPHQOQWKNPTFLRVISDTASLCYSI 1046
DB 1021 LDIQVNSLQVCTNIIKILLQAYRPAACVLOLPHQOQWKNPTFLRVISDTASLCYSI 1080
QY 1047 LKAKNMGMSGAGAGAGPLSEAVOWMLCHQAFLLKTLRHVYVYVPLLSGRTQOTLSRK 1106
DB 1081 LKAKNMGMSGAGAGAGPLSEAVOWMLCHQAFLLKTLRHVYVYVPLLSGRTQOTLSRK 1140
QY 1107 LPGTTTLTALBAANPALPSDFKTIID 1132
DB 1141 LPGTTTLTALBAANPALPSDFKTIID 1166

```

RESULT 35
ID AAM47007 standard; protein; 1199 AA.

XX AAM47007;
XX
DT 13-AUG-1998 (first entry)
XX
DE Glutathione-S-transferase and hTERT fusion protein 7.
XX
KW Human; telomerase reverse transcriptase; hTERT; TRF; diagnosis; prognosis;

```

KW cell proliferation; cancer; ageing; ribonucleoprotein.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT Misc-difference 32..33
FT /note= "enterokinase cleavage site"
XX
XX GB2317891-A.
XX
XX 08-APR-1998.
XX
XX 01-OCT-1997; 97GB-00020890.
XX
XX 01-OCT-1996; 96US-00724643.
XX
XX 18-APR-1997; 97US-00844419.
XX
XX 25-APR-1997; 97US-00846017.
XX
XX 06-MAY-1997; 97US-00851843.
XX
XX 09-MAY-1997; 97US-00854050.
XX
XX 14-AUG-1997; 97US-00911312.
XX
XX 14-AUG-1997; 97US-00912951.
XX
XX 14-AUG-1997; 97US-00915503.
XX
XX (GERO-) GERON CORP.
XX
XX (UYTE-) UNIV TECHNOLOGY CORP.
XX
XX Cech TR, Lignner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
XX Andrews WH;
XX WPI; 1998-171633/16.
XX
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
XX variants - are useful in the diagnosis, prognosis and treatment of cell
XX proliferation conditions especially cancer and ageing.
XX
XX Example 6; Page 233; 387pp; English.
XX
XX The present sequence represents a fusion protein from an example of the
XX present invention which describes human telomerase reverse transcriptase
XX (hTERT). The present invention also describes the following methods: (A)
XX determining whether a test compound is a modulator of hTERT, by detecting
XX the change in hTERT recombinant protein or polynucleotide, on
XX administration of the compound; (B) preparation of recombinant telomerase
XX by contacting a protein preparation of hTERT with a telomerase RNA
XX component; (C) detection of the hTERT RNA or protein in a sample by
XX binding a relevant probe to the sample and detecting the complex formed
XX or in the case of RNA detection, amplifying the product and correlating
XX the presence of complex or amplification product with presence of hTERT in
XX the sample; and (D) increasing the proliferation of a vertebrate cell by
XX increasing hTERT expression; and (E) the use of an agent that causes an
XX increase in cell vertebrate cell proliferation to create a medicament
XX that inhibits ageing. A protein preparation of hTERT and the
XX polynucleotide encoding hTERT can be used in the manufacture of
XX medicaments for inhibiting the effect of ageing or cancer. Inhibitors of
XX telomerase activity can be used to treat conditions that are associated
XX with high telomerase activity. A protein preparation of hTERT can also be
XX used in the new methods
XX
XX Sequence 1199 AA:

```

Query Match 99.0%; Score 5902.5; DB 2; Length 1199;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1127; Conservative 1; Mismatches 2; Indels 3; Gaps 3;

```

QY 1 MPAPRCAGVRSILRSHREVLPATFVRRLGPOGMRLVQGDPAAFALVAQCLVCPM 60
DB 69 MPAPRCAGVRSILRSHREVLPATFVRRLGPOGMRLVQGDPAAFALVAQCLVCPM 128
QY 61 DARPPAPSPROYSCLELVARVQLRCERKAKNTLAFGALLDAGRGPPPAFTTSV 119
DB 129 DARPPAPSPROYSCLELVARVQLRCERKAKNTLAFGALLDAGRGPPPAFTTSV 188

```

QY 120 RSYLPTVTALRGSGAWGLLRVGVDDVYLHLLARCALFVLVAESCAVYVCGPELYOLG 179
 DB 189 RSYLPTVTALRGSGAWGLLRVGVDDVYLHLLARCALFVLVAESCAVYVCGPELYOLG 248
 QY 190 AATQARPPPHASGPPRRRLGCEPAMNHSVREAGVPLGLAPGARRRSGASSLPPLPKPR 239
 DB 249 AATQARPPPHASGPPRRRLGCEPAMNHSVREAGVPLGLAPGARRRSGASSLPPLPKPR 308
 QY 240 RGAAPPEPRTPVQSGSMAPGRTGSDRGFCVSPAPABEATSLEGALSGTRSHPSV 299
 DB 309 RGAAPPEPRTPVQSGSMAPGRTGSDRGFCVSPAPABEATSLEGALSGTRSHPSV 368
 QY 300 GRQHGAGPSTSRPPRPMPTPCPPYAEFKHFLYSSGSGKEQLRPSFLLSLRPLTGARR 359
 DB 369 GRQHGAGPSTSRPPRPMPTPCPPYAEFKHFLYSSGSGKEQLRPSFLLSLRPLTGARR 428
 QY 360 LVETTFILGSRPMMPCGTPRRLPLRPLRQYOMRPLFELLGNHAOCYGVLLTHCPRLAAV 419
 DB 429 LVETTFILGSRPMMPCGTPRRLPLRPLRQYOMRPLFELLGNHAOCYGVLLTHCPRLAAV 488
 QY 420 TPAAGVCAAEKPOGSAABEEDTDPRRLVOLLRQHSBPQYGVVRACLRLVPPGLWG 479
 DB 489 TPAAGVCAAEKPOGSAABEEDTDPRRLVOLLRQHSBPQYGVVRACLRLVPPGLWG 547
 QY 480 SHNERRPLRNTKPFSLGKHAKLSLOELTWKMSVRDCAMLRSPGVCVPAAEHRLREE 539
 DB 548 SHNERRPLRNTKPFSLGKHAKLSLOELTWKMSVRDCAMLRSPGVCVPAAEHRLREE 607
 QY 540 ILAKFLHMLMSYVVELLRSPFYVETETFOKNRLFYRPSVWSKLSIGIRQHLKRVOLR 599
 DB 608 ILAKFLHMLMSYVVELLRSPFYVETETFOKNRLFYRPSVWSKLSIGIRQHLKRVOLR 667
 QY 600 ELSEAEVRQHRARAPLLTLRLRFLPKPGLRPIYMMYVVGARFFRREKXAERLTSLVK 659
 DB 668 ELSEAEVRQHRARAPLLTLRLRFLPKPGLRPIYMMYVVGARFFRREKXAERLTSLVK 727
 QY 660 ALFSLVNTERRARPGILGASVGLDDIRHAWRTFVLRYAODPPELTFVAVDYTGADY 719
 DB 728 ALFSLVNTERRARPGILGASVGLDDIRHAWRTFVLRYAODPPELTFVAVDYTGADY 787
 QY 720 IQODRLTEVTLASITIKPONTYCVRYAVVQKAAHGVRAKFSHVSTLTDLOPYMKQFVAH 779
 DB 788 IQODRLTEVTLASITIKPONTYCVRYAVVQKAAHGVRAKFSHVSTLTDLOPYMKQFVAH 847
 QY 780 LOETSPLRDAVYIEGSSSLNEASGFLPFTLRFCMHAVRIRGKSYVCCQIGIPOSTLIST 839
 DB 848 LOETSPLRDAVYIEGSSSLNEASGFLPFTLRFCMHAVRIRGKSYVCCQIGIPOSTLIST 907
 QY 840 LLOSLCYGMENKLPAGIRRDGLLRVDDPLVTPHILTHAKTFLRLVKGVPYRGCVN 899
 DB 908 LLOSLCYGMENKLPAGIRRDGLLRVDDPLVTPHILTHAKTFLRLVKGVPYRGCVN 967
 QY 900 LKRTVVPFVEDEALGDTAFVQMPAHGLFPMCGLLDRLTLEVOGDSYVARTSIRASVT 959
 DB 968 LKRTVVPFVEDEALGDTAFVQMPAHGLFPMCGLLDRLTLEVOGDSYVARTSIRASVT 1027
 QY 960 FNRGFVAGNMRRKLFGLRLKCHSLFLDLQVNSLQVCTNLYKILLQVAFHACVQL 1019
 DB 1028 FNRGFVAGNMRRKLFGLRLKCHSLFLDLQVNSLQVCTNLYKILLQVAFHACVQL 1087
 QY 1020 PHQOQVWKPTFFLRVISTLASLCSILKAKNAGSISAKGAGLSEBAVQMLCHQAF 1079
 DB 1088 PHQOQVWKPTFFLRVISTLASLCSILKAKNAGSISAKGAGLSEBAVQMLCHQAF 1147
 QY 1080 LKLTTRHVVYVPLGLSLRTAQTOLSRKLPGLTTLTLEAANPALSDPKTILD 1132
 DB 1148 LKLTTRHVVYVPLGLSLRTAQTOLSRKLPGLTTLTLEAANPALSDPKTILD 1199

RESULT 36
 AAY00641
 ID AAY00641 standard; protein; 1120 AA.
 XX

AC AAY00641;
 XX
 DT 26-JUL-1999 (first entry)
 XX
 DE Telomerase protein sequence lacking motif A.
 XX
 KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilms' tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FN W09901560-A1.
 XX
 PD 14-JAN-1999.
 XX
 PF 01-JUL-1998; 98MO-US013835.
 XX
 PR 01-JUL-1997; 97US-0051410P.
 PR 21-JUL-1997; 97US-0053018P.
 PR 21-JUL-1997; 97US-0053329P.
 PR 04-AUG-1997; 97US-0054642P.
 PR 09-SEP-1997; 97US-0058287P.
 XX
 PA (CAMP-) CAMBIA BIOSYSTEMS LLC.
 XX
 PI Killian A, Bowtell D,
 XX
 DR WPI; 1999-106060/09.
 DR N-PSDB; AAX18269.
 XX
 PT New isolated vertebrate telomerase genes - used to develop products for
 PT treating cancers or for organ regeneration, nerve cell or brain cell
 PT growth following injury or bone marrow transplantation.
 XX
 PS Claim 4; Fig 11n-o; 134bp; English.
 XX
 CC This sequence is a truncated human telomerase of the invention. Primers
 CC that amplify the telomerase coding sequence can be used in a method for
 CC diagnosing cancer in a patient. The telomerase can be used for detection,
 CC diagnosis and drug screening. Inhibitors of telomerase activity can be
 CC used to treat cancers such as melanomas, other skin cancers,
 CC neuroblastomas, breast carcinomas, colon carcinomas, leukemias,
 CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
 CC growths. Enhancers of telomerase may be used to stimulate stem cell
 CC proliferation and differentiation (expansion of haematopoietic stem cells
 CC could be administered in the bone marrow transplant context). As well,
 CC many tissues have stem cells. Proliferation of these cells may be useful
 CC in wound healing, hair growth, treatment of disease such as Wilms'
 CC tumour, organ regeneration or differentiation after injury or diseases,
 CC nerve cell or brain cell growth following injury
 CC
 SO Sequence 1120 AA;
 Query Match 98.5%; Score 5873; DB 2; Length 1120;
 Best Local Similarity 98.8%; Pred. No. 0;
 Matches 1118; Conservative 1; Mismatches 1; Indels 12; Gaps 1;
 QY 1 MPARPCRAVRSLLRSHYREVLPATFVRIRLIGQGRLVQRGPPAFRALVQCLCVPM 60
 DB 1 MPARPCRAVRSLLRSHYREVLPATFVRIRLIGQGRLVQRGPPAFRALVQCLCVPM 60
 QY 61 DARPPAPSPFVQSGCLKEIVARVLOQLCEGAKNYLAFGALLDAGRGGPEAFTTSVR 120
 DB 61 DARPPAPSPFVQSGCLKEIVARVLOQLCEGAKNYLAFGALLDAGRGGPEAFTTSVR 120
 QY 121 SYLPTVTALRGSGAWGLLRVGVDDVYLHLLARCALFVLVAESCAVYVCGPELYOLGA 180
 DB 121 SYLPTVTALRGSGAWGLLRVGVDDVYLHLLARCALFVLVAESCAVYVCGPELYOLGA 180
 QY 181 AATQARPPPHASGPPRRRLGCEPAMNHSVREAGVPLGLAPGARRRSGASSLPPLPKPR 240

```

Db      181 ATGARRPPHAGSPRRRLGGERAMNHSVREAGVPLGLAPAPARRRGASASLPLPRPRR 240
Qy      241 GAAPERTPTVGGGSAHMPGRTGPRGRCVVSAPAPAEATSLGALSCTHSHPSVG 300
Db      241 GAAPERTPTVGGGSAHMPGRTGPRGRCVVSAPAPAEATSLGALSCTHSHPSVG 300
Qy      301 ROHAGPSTSRPRPMDTCPPIYAEKFKIVSSGGKEQLRPSFLSSRPSLTGARRL 360
Db      301 ROHAGPSTSRPRPMDTCPPIYAEKFKIVSSGGKEQLRPSFLSSRPSLTGARRL 360
Qy      361 VETIFLGSRPMPGTPRRLPLRQYWMRPLFELLGNACCPYGLKTHCPRAAYT 420
Db      361 VETIFLGSRPMPGTPRRLPLRQYWMRPLFELLGNACCPYGLKTHCPRAAYT 420
Qy      421 PAAGVCAKREKQGVAAPEEDDPRLVOLLROHSSPMQVGFVAACLRILVPGMG 480
Db      421 PAAGVCAKREKQGVAAPEEDDPRLVOLLROHSSPMQVGFVAACLRILVPGMG 480
Qy      481 RHNERRFLRNTKFKISLGKAKLSLOELTWKMSVRCDCAMLRSPGVCPAAHRLREI 540
Db      481 RHNERRFLRNTKFKISLGKAKLSLOELTWKMSVRCDCAMLRSPGVCPAAHRLREI 540
Qy      541 LAFLEHLMVYVVELLSFFYTETTFQKNRLFPPRPSVSKLQSIGRQHLKRYQLR 600
Db      541 LAFLEHLMVYVVELLSFFYTETTFQKNRLFPPRPSVSKLQSIGRQHLKRYQLR 600
Qy      601 LSEAEVQHRERAPALLTSRLRFIPKPDGLPIVNDYVVGARTPREKAEELTGRVA 660
Db      601 LSEAEVQHRERAPALLTSRLRFIPKPDGLPIVNDYVVGARTPREKAEELTGRVA 660
Qy      661 LFSVLNTERARRPGLGASVGLDDIHRANRFLVRAADPEPELYPVKVDYTAGYDT 720
Db      661 LFSVLNTERARRPGLGASVGLDDIHRANRFLVRAADPEPELYPVKVDYTAGYDT 720
Qy      721 PODRLTEVIASIIKPNITCVBRVAVVQKAHGHVRAKFSHSTLTDLOPMYRCFVAH 780
Db      721 PODRLTEVIASIIKPNITCVBRVAVVQKAHGHVRAKFSHSTLTDLOPMYRCFVAH 780
Qy      781 QETSPLDVAVIGQSSSLNEASGLPDVFLRFMCHNAVRIRGKSYVQCGIIPQGSILSTL 840
Db      781 QETSPLDVAVIGQSSSLNEASGLPDVFLRFMCHNAVRIRGKSYVQCGIIPQGSILSTL 840
Qy      841 LGLCLGDMENKLFAGIRBDGLLRLVDDDLVTPHHTAKTLRLTLVNGVPEYGVNL 900
Db      841 LGLCLGDMENKLFAGIRBDGLLRLVDDDLVTPHHTAKTLRLTLVNGVPEYGVNL 900
Qy      901 RKTIVNFPVDEALGTAFAVQMPAHGLFPGCGLLDRLEVOSSDYASVARSIRASYTF 960
Db      889 RKTIVNFPVDEALGTAFAVQMPAHGLFPGCGLLDRLEVOSSDYASVARSIRASYTF 948
Qy      961 NRGFKAGRNRRKLFVYLRLKCHSLFLDLQVNSLQVTCNIVYILLQAYRFACVLOLP 1020
Db      949 NRGFKAGRNRRKLFVYLRLKCHSLFLDLQVNSLQVTCNIVYILLQAYRFACVLOLP 1008
Qy      1021 FHOQWKNPTFFRIVISDTASLCYSILKAKNAGMSIGAKAAGPLSEAVOMLCHQAFLL 1080
Db      1009 FHOQWKNPTFFRIVISDTASLCYSILKAKNAGMSIGAKAAGPLSEAVOMLCHQAFLL 1068
Qy      1081 KLTRHRTVYVLLGSLRTAQTQSLRKLPGTTTLTALEAANPALPSDFKILL 1132
Db      1069 KLTRHRTVYVLLGSLRTAQTQSLRKLPGTTTLTALEAANPALPSDFKILL 1120

```

```

RESULT 37
AA100650
ID AA100650 standard; protein; 1120 AA.
XX
AC AA100650;
XX
DT 26-JUL-1999 (first entry)
XX
DE Telomerase (ver. 2) protein sequence lacking motif A.

```

```

XX      Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW      neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW      smooth muscle cell hyperplasia; stem cell proliferation; Wilms' tumour;
KW      stem cell differentiation; organ regeneration; organ differentiation.
OS      Homo sapiens.
OS      Synthetic.
XX      WO9901560-A1.
XX      14-JAN-1999.
XX      01-JUL-1998; 98WO-US013835.
XX      01-JUL-1997; 97US-0054410P.
XX      21-JUL-1997; 97US-0053018P.
XX      21-JUL-1997; 97US-0053329P.
XX      04-AUG-1997; 97US-0054642P.
XX      09-SEP-1997; 97US-0058287P.
XX      (CAMEB) CAMBIA BIOSYSTEMS LLC.
XX      Kilian A, Bowtell D;
XX      WPI; 1999-106060/09.
XX      DR N-PSDB; AAX18278.
XX      PT New isolated vertebrate telomerase genes - used to develop products for
XX      treating cancers or for organ regeneration, nerve cell or brain cell
XX      growth following injury or bone marrow transplantation.
XX      Claim 4; Fig 11ah-aj; 134pb; English.
XX
CC      This sequence is a truncated human telomerase of the invention. Primers
CC      that amplify the telomerase coding sequence can be used in a method for
CC      diagnosing cancer in a patient. The telomerase can be used for detection,
CC      diagnosis and drug screening. Inhibitors of telomerase activity can be
CC      used to treat cancers such as melanomas, other skin cancers,
CC      neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC      lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC      growths. Enhancers of telomerase may be used to stimulate stem cell
CC      proliferation and differentiation (expansion of hematopoietic stem cells
CC      could be administered in the bone marrow transplant context). As well,
CC      many tissues have stem cells. Proliferation of these cells may be useful
CC      in wound healing, hair growth, treatment of disease such as Wilms'
CC      tumour, organ regeneration or differentiation after injury or diseases,
CC      nerve cell or brain cell growth following injury. Note: The N-terminus of
CC      this sequence can be replaced by the sequences shown in AA100656-100658
CC
XX      Sequence 1120 AA:

```

```

Query Match      98.3%; Score 5864; DB 2; Length 1120;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 117; Conservative 1; Mismatches 2; Indels 12; Gaps 1;

```

```

Qy      1 MPRARCAVAVSLRSHREVLPATFVRRLGPGGMVLVQGGDPAAPFALVACLVCPW 60
Db      1 MPRARCAVAVSLRSHREVLPATFVRRLGPGGMVLVQGGDPAAPFALVACLVCPW 60
Qy      61 DARPPAPSPROYSCLELVARVLORLCERGANVLAFGFALDGAAGGPPFAFTTSVR 120
Db      61 DARPPAPSPROYSCLELVARVLORLCERGANVLAFGFALDGAAGGPPFAFTTSVR 120
Qy      121 SYLPNTVTDALRGSGAWCLLRVGGDVLVHLRLCALFVVAASCAYOVGCPPLVQLGA 180
Db      121 SYLPNTVTDALRGSGAWCLLRVGGDVLVHLRLCALFVVAASCAYOVGCPPLVQLGA 180
Qy      181 ATQARPPHAGSPRRRLGGERAMNHSVREAGVPLGLAPAPARRRGASASRLPLPKRPR 240
Db      181 ATQARPPHAGSPRRRLGGERAMNHSVREAGVPLGLAPAPARRRGASASRLPLPKRPR 240
Qy      241 GAAPERTPTVGGGSAHMPGRTGPRGRCVVSAPAPAEATSLGALSCTHSHPSVG 300

```

```

Db      241 GAAPPERPFPVQGGSHARHGRTRGSDGFCVVSAPRAAEHTSLSEGLSTGRSHPEVG 300
Qy      301 RQHHAGPSTSPPPRWDTPCPVYAETKHLVSSGDYEQLRPSLILSLRPSLTGAARL 360
Db      301 RQHHAGPSTSPPPRWDTPCPVYAETKHLVSSGDYEQLRPSLILSLRPSLTGAARL 360
Qy      361 VETIFLGSPPMWPCTPRRLPRLPORVQWQMRPLFELLGNHOCPEVGLKTHCPRAVLT 420
Db      361 VETIFLGSPPMWPCTPRRLPRLPORVQWQMRPLFELLGNHOCPEVGLKTHCPRAVLT 420
Qy      421 PAAGVAREKPOGSAVAPEEDTDPRLVQLRQSSPMOYGVFVACLRRLVPPGLWGS 480
Db      421 PAAGVAREKPOGSAVAPEEDTDPRLVQLRQSSPMOYGVFVACLRRLVPPGLWGS 480
Qy      481 RHNERFLNTRKFLISLGHAKLSLOELTWKMSVDCAMLRSPGVGVPAEHLRREI 540
Db      481 RHNERFLNTRKFLISLGHAKLSLOELTWKMSVDCAMLRSPGVGVPAEHLRREI 540
Qy      541 LAKEFLHMLSVYVELLRSFYVETTFQKRLFPYRPSVMSKLOSIGIRQHLKVCURE 600
Db      541 LAKEFLHMLSVYVELLRSFYVETTFQKRLFPYRPSVMSKLOSIGIRQHLKVCURE 600
Qy      601 LSEAEVQRHREARPALITSLRFLPKPGCLPIVNMVYVGAFTREKREARLTSRYKA 660
Db      601 LSEAEVQRHREARPALITSLRFLPKPGCLPIVNMVYVGAFTREKREARLTSRYKA 660
Qy      661 LRSVLYEARPPGLGASVGLDIDIRAMRTFVLVRADPPPELVKVDYGTAYDTI 720
Db      661 LRSVLYEARPPGLGASVGLDIDIRAMRTFVLVRADPPPELVKVDYGTAYDTI 720
Qy      721 PODRLTEVIASIIKPNVYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLOPYMROFVAHL 780
Db      721 --DLRLTEVIASIIKPNVYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLOPYMROFVAHL 780
Qy      781 QETSPLRDVAVIEQSSLINEASSGLFDVLRPMCHAVIRKSKYVVOCGIPQGSILSTL 840
Db      781 QETSPLRDVAVIEQSSLINEASSGLFDVLRPMCHAVIRKSKYVVOCGIPQGSILSTL 840
Qy      841 LSLCYGDMENKLFAGIRRDGLLRVDDFLLVTHLTHAKFLRTLVRGVPEYGCYVNL 900
Db      841 LSLCYGDMENKLFAGIRRDGLLRVDDFLLVTHLTHAKFLRTLVRGVPEYGCYVNL 900
Qy      901 RKTVNVFPEDEALGATAVQVPAHGLPWCGLLDTRLEQSYSSYARSTASTF 960
Db      901 RKTVNVFPEDEALGATAVQVPAHGLPWCGLLDTRLEQSYSSYARSTASTF 960
Qy      961 NRGFKAGRMRRRLFGVLRKCHSLFLDQVNSLQTVCTNIYKILLQAYRFAVCVLQDP 1020
Db      961 NRGFKAGRMRRRLFGVLRKCHSLFLDQVNSLQTVCTNIYKILLQAYRFAVCVLQDP 1020
Qy      949 NRGFKAGRMRRRLFGVLRKCHSLFLDQVNSLQTVCTNIYKILLQAYRFAVCVLQDP 1008
Db      1021 FHOQVKNPFLFRLVISTDASLCYSTLKAKNAGMSIGAKGAPLPSEAVQWLCQAATLL 1080
Qy      1021 FHOQVKNPFLFRLVISTDASLCYSTLKAKNAGMSIGAKGAPLPSEAVQWLCQAATLL 1080
Db      1009 FHOQVKNPFLFRLVISTDASLCYSTLKAKNAGMSIGAKGAPLPSEAVQWLCQAATLL 1068
Qy      1081 KLTRHNVTVVPLIGSLRTAQTOLSRKLPETTLTALAANPALPSPDFKTIID 1132
Db      1069 KLTRHNVTVVPLIGSLRTAQTOLSRKLPETTLTALAANPALPSPDFKTIID 1120

```

```

OS      Synthetic.
XX      Homo sapiens.
PN      GB2317891-A.
XX      08-Apr-1998.
PD      01-OCT-1997; 97GB-00020890.
XX      01-OCT-1996; 96US-00724643.
PR      18-APR-1997; 97US-00844419.
PR      25-APR-1997; 97US-00846017.
PR      06-MAY-1997; 97US-00851843.
PR      09-MAY-1997; 97US-00854050.
PR      14-AUG-1997; 97US-00911312.
PR      14-AUG-1997; 97US-00912951.
PR      14-AUG-1997; 97US-00915503.
XX      (GERO-) GERON CORP.
PA      (UYTE-) UNIV TECHNOLOGY CORP.
XX      Cech TR, Langer J, Nakamura T, Chapman KB, Morin GB, Harley CB;
PI      Andrews WH;
XX      WPI; 1998-171633/16.
XX      Pure and recombinant human Telomerase Reverse Transcriptase and its
PT      variants - are useful in the diagnosis, prognosis and treatment of cell
PT      proliferation conditions especially cancer and ageing.
XX      Example 6; Page 231-232; 387pp; English.
PS      The present sequence represents a fusion protein from an example of the
XX      present invention which describes human telomerase reverse transcriptase
XX      (hTERT). The present invention also describes the following methods: (A)
XX      determining whether a test compound is a modulator of hTERT, by detecting
XX      the change in hTERT recombinant protein or polynucleotide, on
XX      administration of the compound; (B) preparation of recombinant telomerase
XX      by contacting a protein preparation of hTERT with a telomerase RNA
XX      component; (C) detection of the hTERT RNA or protein in a sample by
XX      binding a relevant probe to the sample and detecting the complex formed
XX      or in the case of RNA detection, amplifying the product and correlating
XX      the presence of complex or amplification product with presence of hTERT in
XX      the sample; and (D) increasing the proliferation of a vertebrate cell by
XX      increasing hTERT expression; and (E) the use of an agent that causes an
XX      increase in cell vertebrate cell proliferation to create a medicament
XX      that inhibits ageing. A protein preparation of hTERT and the
XX      polynucleotide encoding hTERT can be used in the manufacture of
XX      medicaments for inhibiting the effect of ageing or cancer. Inhibitors of
XX      telomerase activity can be used to treat conditions that are associated
XX      with high telomerase activity. A protein preparation of hTERT can also be
XX      used in the new methods
SQ      Sequence 1150 AA;
Qy      Query Match 95.8%; Score 5712; DB 2; Length 1150;
Db      Best Local Similarity 97.6%; Pred. No. 0;
Db      Matches 110; Conservative 7; Mismatches 6; Indels 14; Gaps 13;
Qy      1 MPRAPRCAVRSLRSHYREVPLATFVRRLGQGWRLVQGGPAPFALVQCVPM 60
Db      1 MPRAPRCAVRSLRSHYREVPLATFVRRLGQGWRLVQGGPAPFALVQCVPM 60
Qy      61 DARPAPAPSFROVSCIKELVAVRLQRCERGAQVLAFCFALLDARGGPEAFTTSVR 120
Db      61 DARPAPAPSFROVSCIKELVAVRLQRCERGAQVLAFCFALLDARGGPEAFTTSVR 120
Qy      121 SYLPNTVTDLRSGGAWGLLRVGDVVLHLLARCALFVLVAPSCAYOVCGPPLVQLGA 180
Db      121 SYLPNTVTDLRSGGAWGLLRVGDVVLHLLARCALFVLVAPSCAYOVCGPPLVQLGA 180
Qy      181 ATGARPPHAGRRRLICERAMNHSYRAGVPLGAPGARRGGSASRSPLPRPRR 240

```

```

Db      181 ATGARPPEPHASGPRRLGGERAMNHSVREAGVPLGLPAPGARRRGGSASRLPLPKRRR 240
Qy      241 GAAPERTPTVGGGSAWHPGRTGSPDRGCVVSPAPAEATSLGALSSTHSPSVG 300
Db      241 GAAPERTPTVGGGSAWHPGRTGSPDRGCVVSPAPAEATSLGALSSTHSPSVG 300
Qy      301 ROHHAGSPSTSRPRPMDTCPPIYATKTHPLVSSGGKEOLRPSFLSSRLSGARRL 360
Db      301 ROHHAGSPSTSRPRPMDTCPPIYATKTHPLVSSGGKEOLRPSFLSSRLSGARRL 360
Qy      361 VETIFLGSRPWPMPGTPRRRLPRLPQRYWQMRPLFELLGNHAGCPYGLTKHCPLEAAVT 420
Db      361 VETIFLGSRPWPMPGTPRRRLPRLPQRYWQMRPLFELLGNHAGCPYGLTKHCPLEAAVT 419
Qy      421 PARGVCAREKPGQSVAAPEEEDDPRLVOLLROHSSPMQVGFVAPACLRVAPGL-WG 479
Db      420 PARGVCAREKPGQSVAAPEEEDDPRLVOLLROHSSPMQVGFVAPACLRVAPGLEVG 479
Qy      480 SRHNERFLLNTKKFISLGNHAKLSLOELTWKMSVRDCAWLRSPGVGCPAAEHLRRE 539
Db      480 SRHNERFLLNTKKFISLGNHAKLSLOELTWKMSVRDCAWLRSPGVGCPAAEHLRRE 539
Qy      540 ILAKFLHMLSVYVVELLSFFYTETTFQCNRLFYRBSVSKLSIGRQHLKRYOLR 599
Db      540 ILAKFLHMLSVYVVELLSFFW-TETTFQCNRLFYRKSWSKLSIGRQHLKRYOLR 598
Qy      600 ELASAEVROHREARPAALLTSRLRFPKPDGLRP-VN-MDYVGARTPRRREKARELTSTRY 658
Db      599 ELASAEVROHREARPAALLTSRLRFPKPDGLRP-VNMDM-VGARTPRRREKARELTSTRY 657
Qy      659 KALFVINYRPARRPGLLGASVGLDDIHPAMRTFVLRAQDPPELYFVKVDVGAAYD 718
Db      658 KALFVINYRPARRPGLLGASVGLDDIHPAMRTFVLRAQDPPELYFVKVDVGAAYD 717
Qy      719 TIPODLTEVIASIIKPONTYCVRRYAVVOKAHGHRKAFKSHVSTLIDLPYMRQFVA 778
Db      718 TIPODLTEVIASIIKPONTYCVRRYAVVOKAHGHRKAFKSHVSTLIDLPYMRQFVA 777
Qy      779 HLOETSLRDVAVYVIEQSSSL-NEASGSLPDVFLRFMCHAAVIRKSYVOCQGIPOGSI 837
Db      778 HLOETSLRDVAVYVIEQSSSL-NEASGSLPDVFLRFMCHAAVIRKSYVOCQGIPOGSI 835
Qy      838 STLLCSICYGDMENKLPAGIRBGDLRLVDDDLVTPHILTAKTPIRTIYRQVPEYGV 897
Db      836 STLLCSICYGDMENKLPAGIRBGDLRLVDDDLVTPHILTAKTPIRTIYRQVPEYGV 894
Qy      898 VNRKTYVNFVEDEALGTAFAVQMPAHGLFPM-CGLLDTRILEVQSDYSYARTSIRA 956
Db      895 VNRKTYVNFVEDEALGTAFAVQMPAHGLFPM-CGLLDTRILEVQSDYSYARTSIRA 952
Qy      957 SVTPNRCFKAGR-NMRKTLFGLRLKCHSLFDLQVNSLOTCVTNITYKIILLQAYFHC 1015
Db      953 SVTPNRCFKAGR-NMRKTLFGLRLKCHSLFDLQVNSLOTCVTNITYKIILLQAYFHC 1012
Qy      1016 VLOLPFQOQWKNPTFLRVIISDPAISLCYSLKAKNAGMSLGAKGAGPLPSBAVOMLCH 1075
Db      1013 VLOLPFQOQWKNPTFLRVIISDPAISLCYSLKAKNAGMSLGAKGAGPLPSBAVOMLCH 1072
Qy      1076 QAFLLKLTTRRVTYVPLLSGLRTAQOLSRKLPQTTVTALEAANPALPSDFKTIID 1132
Db      1073 QAFLLKLTTRRVTYVPLLSGLRTAQOLSRKLPQTTVTALEAANPAL-SDFKTIID 1128

```

```

RESULT 39
AAy00640
ID AAy00640 standard; protein; 1053 AA.
XX
AC AAy00640;
XX
DT 26-JUL-1999 (first entry)
XX
DE Altered C-terminus telomerase protein sequence.
XX

```

```

KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW stem cell differentiation; organ regeneration; organ differentiation.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9901560-A1.
XX
PD 14-JAN-1999.
XX
PF 01-JUL-1998; 98WO-US013835.
XX
PR 01-JUL-1997; 97US-0051410P.
PR 21-JUL-1997; 97US-0053018P.
PR 21-JUL-1997; 97US-0053329P.
PR 04-AUG-1997; 97US-0054642P.
PR 09-SEP-1997; 97US-0058287P.
XX
PA (CMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI Kilian A, Bowtell D;
XX
DR WPI; 1999-106060/09.
DR N-PSDB; AAX18268.
XX
PT New isolated vertebrate telomerase genes - used to develop products for
PT treating cancers or for organ regeneration, nerve cell or brain cell
PT growth following injury or bone marrow transplantation.
XX
PS Claim 4; Fig 111-m; 134pp; English.
XX
CC This sequence is a truncated human telomerase of the invention. Primers
CC that amplify the telomerase coding sequence can be used in a method for
CC diagnosing cancer in a patient. The telomerase can be used for detection,
CC diagnosis and drug screening. Inhibitors of telomerase activity can be
CC used to treat cancers such as melanomas, other skin cancers,
CC neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC growths. Enhancers of telomerase may be used to stimulate stem cell
CC proliferation and differentiation (expansion of hematopoietic stem cells
CC could be administered in the bone marrow transplant context). As well,
CC many tissues have stem cells. Proliferation of these cells may be useful.
CC in wound healing, hair growth, treatment of disease such as Wilm's
CC tumour, organ regeneration or differentiation after injury or diseases,
CC nerve cell or brain cell growth following injury. Note: The C-terminus of
CC this sequence can be replaced by the sequence shown in AAy00654
XX
SQ Sequence 1053 AA;

```

```

Query Match 93.0%; Score 5546; DB 2; Length 1053;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1050; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 MRRAPRCRAVSLLSHRHYEVLPATFFRRIGPOCMRLVYOGDPAFAFALVAQCIVCPW 60
Db      1 MRRAPRCRAVSLLSHRHYEVLPATFFRRIGPOCMRLVYOGDPAFAFALVAQCIVCPW 60
Qy      61 DARPPAPSPFQVSCLELVARVLORLCERGAKNVLAFGFALLDGAAGGPEAFTTSVR 120
Db      61 DARPPAPSPFQVSCLELVARVLORLCERGAKNVLAFGFALLDGAAGGPEAFTTSVR 120
Qy      121 STLPNTVTDALRGSAWGLLRRVGDVVLVHLARCAFLVVAHSCAYQVGGPPIYQGA 180
Db      121 STLPNTVTDALRGSAWGLLRRVGDVVLVHLARCAFLVVAHSCAYQVGGPPIYQGA 180
Qy      181 ATQARPPPHASGPRRLGGERAMNHSVREAGVPLGLPAPGARRRGGSASRLPLPKRRR 240
Db      181 ATQARPPPHASGPRRLGGERAMNHSVREAGVPLGLPAPGARRRGGSASRLPLPKRRR 240
Qy      241 GAAPERTPTVGGGSAWHPGRTGSPDRGCVVSPAPAEATSLGALSSTHSPSVG 300

```

```

Db      241 GAAPERTPVGGSNAHPGRTGSDRGFCVSSAPAEATSLGALSGTRHSPVG 300
Qy      301 ROHAGPPTSRPPRWDTPCPPVYAETGFLYSSGDKQOLRPSFLSLSLRSLTGARL 360
Db      301 ROHAGPPTSRPPRWDTPCPPVYAETGFLYSSGDKQOLRPSFLSLSLRSLTGARL 360
Qy      361 VETIFLGSPPMGPTRRLPLPQRYWQMRPLFELLGNHACPYGVLKTHCPRAAVT 420
Db      361 VETIFLGSPPMGPTRRLPLPQRYWQMRPLFELLGNHACPYGVLKTHCPRAAVT 420
Qy      421 PAAGVAREKPGGSVAAPREEDTDRRLVQLRQSSPMQYGFRACLRRLVPPGLMS 480
Db      421 PAAGVAREKPGGSVAAPREEDTDRRLVQLRQSSPMQYGFRACLRRLVPPGLMS 480
Qy      481 RHNERFLNTKFKISLGHAKLSLOBLTKMSVDCAMLRSPGVCVPAEHRLEBEI 540
Db      481 RHNERFLNTKFKISLGHAKLSLOBLTKMSVDCAMLRSPGVCVPAEHRLEBEI 540
Qy      541 LAKFLHMLSVYVVELLRFYVETETTPQKRLFFYRPSWSKLSIGIRQHLKRVQRE 600
Db      541 LAKFLHMLSVYVVELLRFYVETETTPQKRLFFYRPSWSKLSIGIRQHLKRVQRE 600
Qy      601 LSEAEVROHREARPPALITRLRFPKPDGLRPIVNMDDYVGARTFRREKRAERLTSRYKA 660
Db      601 LSEAEVROHREARPPALITRLRFPKPDGLRPIVNMDDYVGARTFRREKRAERLTSRYKA 660
Qy      661 LRSVLNVEBARPPGLIGASVLDLDIRAMRTFVLKPAQDPPEPLFYKVDVTGADYTI 720
Db      661 LRSVLNVEBARPPGLIGASVLDLDIRAMRTFVLKPAQDPPEPLFYKVDVTGADYTI 720
Qy      721 POORLEVASIIKPNQTCVARYAVVOKAAGHVKAFKSHVSTLTLQPMROFVAHL 780
Db      721 POORLEVASIIKPNQTCVARYAVVOKAAGHVKAFKSHVSTLTLQPMROFVAHL 780
Qy      781 QETSPLRDAVLEQSSSLNEASSGLFDVFLRFMCHAVIRKSGSYVQCGIIPQGSILSTL 840
Db      781 QETSPLRDAVLEQSSSLNEASSGLFDVFLRFMCHAVIRKSGSYVQCGIIPQGSILSTL 840
Qy      841 LQSLCYGDMENKLPFARIRDLGLLRVDFLLVTPHLTHAKFLMLTLVRAQPEYICVNL 900
Db      841 LQSLCYGDMENKLPFARIRDLGLLRVDFLLVTPHLTHAKFLMLTLVRAQPEYICVNL 900
Qy      901 RKTAVNFPVEDDALGCTAFVQMPAHGLFPMGILLDTRTLEVOQSYSSARTSIRASYTF 960
Db      901 RKTAVNFPVEDDALGCTAFVQMPAHGLFPMGILLDTRTLEVOQSYSSARTSIRASYTF 960
Qy      961 NRGFKAGRNRRKLPFVLRKCHSLFLDQVNSLQTVCTNIXKILLQAYRHACVQLP 1020
Db      961 NRGFKAGRNRRKLPFVLRKCHSLFLDQVNSLQTVCTNIXKILLQAYRHACVQLP 1020
Qy      1021 FHQGVKNPFFLRVISTDASLCYSILKAKNA 1052
Db      1021 FHQGVKNPFFLRVISTDASLCYSILKAKNA 1052

```

RESULT 40

```

AA00649
ID AA00649 standard; protein; 1093 AA.
XX
AC AA00649;
XX
DT 26-JUL-1999 (first entry)
XX
DE Altered C-terminus telomerase (ver. 2) protein sequence.
XX
KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW stem cell differentiation; organ regeneration; organ differentiation.
XX
OS Homo sapiens.
XX
SY Synthetic.
XX

```

```

PN      W09901560-A1.
XX      14-JAN-1999.
XX      01-JUL-1998; 98WC-US013835.
XX      01-JUL-1997; 97US-0051410P.
XX      21-JUL-1997; 97US-0053018P.
XX      21-JUL-1997; 97US-005329P.
XX      04-AUG-1997; 97US-0054642P.
XX      09-SEP-1997; 97US-0058287P.
XX      (CMB-) CAMBIA BIOSYSTEMS LLC.
XX      Kilian A, Bowtell D;
XX      MPI; 1999-106060/09.
XX      DR N-PSDB; AAX18277.
XX      PT New isolated vertebrate telomerase genes - used to develop products for
XX      treating cancers or for organ regeneration, nerve cell or brain cell
XX      growth following injury or bone marrow transplantation.
XX      Claim 4; Fig 11af-ag; 134p; English.
XX
CC      This sequence is a truncated human telomerase of the invention. Primers
CC      that amplify the telomerase coding sequence can be used in a method for
CC      diagnosing cancer in a patient. The telomerase can be used for detection,
CC      diagnosis and drug screening. Inhibitors of telomerase activity can be
CC      used to treat cancers such as melanomas, other skin cancers,
CC      neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC      lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC      growths. Enhancers of telomerase may be used to stimulate stem cell
CC      proliferation and differentiation (expansion of haematopoietic stem cells
CC      could be administered in the bone marrow transplant context). As well,
CC      many tissues have stem cells. Proliferation of these cells may be useful
CC      in wound healing, hair growth, treatment of disease such as Wilm's
CC      tumour, organ regeneration or differentiation after injury or diseases,
CC      nerve cell or brain cell growth following injury. Note: The N-terminus of
CC      this sequence can be replaced by the sequences shown in AA00654
CC      and the C-terminus can be replaced by the sequence shown in AA00654
XX
SQ      Sequence 1093 AA;
XX
Query Match 92.4%; Score 5507; DB 2; Length 1093;
Best Local Similarity 96.1%; Pred. No. 0;
Matches 1049; Conservative 1; Mismatches 2; Indels 40; Gaps 1;

```

Db 361 VETIFLGRPMWPGTFRPLRLPQRYWQMRPLLELLGNHACPPYGLTKHCPLRAAVT 420
QY 421 PAAGVCAREKRPQGSVAAPREEDTDPRRLVOLLRQSSPMQVGFVACLRILVPRGLMGS 480
Db 421 PAAGVCAREKRPQGSVAAPREEDTDPRRLVOLLRQSSPMQVGFVACLRILVPRGLMGS 480
QY 481 RHNERRFLRNTKKFISLQKAKLSLOE----- 507
Db 481 RHNERRFLRNTKKFISLQKAKLSLOELTWKMSVRCAMLRRSPGVGCPAAEHLREBI 540
QY 508 -----LTWKMSVRCAMLRRSPGVGCPAAEHLREBI 560
Db 541 LAFLHLTWKMSVRCAMLRRSPGVGCPAAEHLREBI 600
QY 561 FYVTETTFQKRLFEYRPSVMSKLOSIGIRQHLKRVOLRELSAEVROHREARPALITSR 620
Db 601 FYVTETTFQKRLFEYRPSVMSKLOSIGIRQHLKRVOLRELSAEVROHREARPALITSR 660
QY 621 LRPIPKPDGLRPIVNDYVVGARTFRERKRAERLTSRKALFSVLNERARPRGLGASY 680
Db 661 LRPIPKPDGLRPIVNDYVVGARTFRERKRAERLTSRKALFSVLNERARPRGLGASY 720
QY 681 LGJDDIHRARFTFLRARADPPPELYFVKVDYTGAVDTIPODRLTEVLASIIKQNTYC 740
Db 721 LGJDDIHRARFTFLRARADPPPELYFVKVDYTGAVDTIPODRLTEVLASIIKQNTYC 780
QY 741 VRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHLQETSPLDAVIEQSSLINE 800
Db 781 VRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHLQETSPLDAVIEQSSLINE 840
QY 801 ASSGLFVFLRPMCHAVRIRGKSYYVOCQIPOGSIISTLLCSLCYGDMMENKLPAGIRRD 860
Db 841 ASSGLFVFLRPMCHAVRIRGKSYYVOCQIPOGSIISTLLCSLCYGDMMENKLPAGIRRD 900
QY 861 GLILRLVDDFLVPHLTHAKTFLRTLVRGVPEYGCYVNIKTVNFPVEDEALGTAFFV 920
Db 901 GLILRLVDDFLVPHLTHAKTFLRTLVRGVPEYGCYVNIKTVNFPVEDEALGTAFFV 960
QY 921 QMPAHGILFPMCGILDLTRILEVQSDYSSYARTSIRASVTFRNGFKAGRNRRKLPGLRL 980
Db 961 QMPAHGILFPMCGILDLTRILEVQSDYSSYARTSIRASVTFRNGFKAGRNRRKLPGLRL 1020
QY 981 KCHSLFELDQVNSIQVCTNIYKILIQAYRFAVCYLQLPFHQVWKNPFFELRVISDTA 1040
Db 1021 KCHSLFELDQVNSIQVCTNIYKILIQAYRFAVCYLQLPFHQVWKNPFFELRVISDTA 1080
QY 1041 SLCYSIILKAKNA 1052
Db 1081 SLCYSIILKAKNA 1092

Search completed: December 20, 2004, 15:58:35
Job time : 112 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 20, 2004, 15:55:46 ; Search time 42 Seconds
(without alignments)
1787.428 Million cell updates/sec

Title: US-08-974-584c-118
Sequence: 5963
Sequence: 1 MPRAPRCRAVRSILRSHYRE.....TALEAANPALPSDFKTLID 1132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 120 summaries

Database : Issued Parents AA: *
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep: *
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep: *
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep: *
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep: *
5: /cgn2_6/prodata/1/iaa/6C_COMB.pep: *
6: /cgn2_6/prodata/1/iaa/backfill1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5963	100.0	1132	3	US-08-974-549A-344 Sequence 344, App
2	5963	100.0	1132	4	US-09-402-181B-344 Sequence 344, App
3	5963	100.0	1132	4	US-09-721-456B-344 Sequence 344, App
4	5963	100.0	1407	3	US-08-974-549A-628 Sequence 628, App
5	5963	100.0	1407	4	US-08-912-951-334 Sequence 334, App
6	5963	100.0	1407	4	US-09-402-181B-628 Sequence 628, App
7	5963	100.0	1407	4	US-09-721-456B-628 Sequence 628, App
8	5963	99.8	1132	3	US-08-851-843A-225 Sequence 225, App
9	5963	99.8	1132	3	US-08-974-549A-225 Sequence 225, App
10	5963	99.8	1132	3	US-08-854-050-225 Sequence 225, App
11	5963	99.8	1132	3	US-09-430-323-225 Sequence 225, App
12	5963	99.8	1132	3	US-09-128-354-225 Sequence 225, App
13	5963	99.8	1132	4	US-09-675-321-225 Sequence 2, Appli
14	5963	99.8	1132	4	US-09-052-919-225 Sequence 2, Appli
15	5963	99.8	1132	4	US-08-912-951-225 Sequence 2, Appli
16	5963	99.8	1132	4	US-09-402-181B-225 Sequence 2, Appli
17	5963	99.8	1132	4	US-09-721-456B-225 Sequence 2, Appli
18	5963	99.8	1132	4	US-09-553-052-225 Sequence 2, Appli
19	5963	99.8	1132	4	US-09-042-460-322 Sequence 3, Appli
20	5963	99.8	1132	4	US-08-974-549A-611 Sequence 611, App
21	5963	99.8	1132	4	US-08-912-951-323 Sequence 323, App
22	5963	99.8	1132	4	US-09-402-181B-611 Sequence 611, App
23	5963	99.8	1132	4	US-09-721-456B-611 Sequence 611, App
24	5963	99.8	1132	4	US-08-974-549A-613 Sequence 613, App
25	5963	99.8	1132	4	US-08-912-951-325 Sequence 325, App
26	5963	99.8	1132	4	US-08-402-181B-613 Sequence 613, App
27	5963	99.8	1132	4	US-09-721-456B-613 Sequence 613, App

28	5952	99.8	1200	3	US-08-974-549A-612 Sequence 612, App
29	5952	99.8	1200	4	US-08-912-951-324 Sequence 324, App
30	5952	99.8	1200	4	US-09-402-181B-612 Sequence 612, App
31	5952	99.8	1200	4	US-09-721-456B-612 Sequence 612, App
32	5952	99.8	1285	3	US-08-974-549A-600 Sequence 600, App
33	5952	99.8	1285	4	US-08-912-951-114 Sequence 314, App
34	5952	99.8	1285	4	US-09-402-181B-600 Sequence 600, App
35	5952	99.8	1285	4	US-09-721-456B-600 Sequence 600, App
36	4046	67.9	807	3	US-08-974-549A-5 Sequence 5, Appli
37	4046	67.9	807	4	US-08-912-951-5 Sequence 5, Appli
38	4046	67.9	807	4	US-09-402-181B-5 Sequence 5, Appli
39	4046	67.9	807	4	US-09-721-456B-5 Sequence 5, Appli
40	3810.5	63.9	1003	3	US-08-851-843A-217 Sequence 217, App
41	3810.5	63.9	1003	3	US-08-974-549A-336 Sequence 336, App
42	3810.5	63.9	1003	3	US-08-854-050-217 Sequence 217, App
43	3810.5	63.9	1003	3	US-09-430-323-217 Sequence 217, App
44	3810.5	63.9	1003	4	US-09-402-181B-336 Sequence 336, App
45	3810.5	63.9	1003	4	US-09-721-456B-336 Sequence 336, App
46	3496	58.6	1122	4	US-09-042-460-2 Sequence 2, Appli
47	3125	52.4	622	4	US-09-582-924B-12 Sequence 12, Appli
48	2178	36.5	438	4	US-09-582-924B-10 Sequence 10, Appli
49	2163.5	36.3	437	4	US-09-582-924B-2 Sequence 2, Appli
50	2079	34.9	564	3	US-08-851-843A-101 Sequence 101, App
51	2079	34.9	564	3	US-08-854-050-101 Sequence 101, App
52	2079	34.9	564	3	US-09-430-323-101 Sequence 101, App
53	2079	34.9	564	3	US-08-974-549A-267 Sequence 267, App
54	2079	34.9	564	4	US-09-402-181B-267 Sequence 267, App
55	2079	34.9	564	4	US-09-721-456B-267 Sequence 267, App
56	1666.5	27.9	364	4	US-09-417-485D-40 Sequence 40, Appli
57	1565	26.2	538	3	US-08-974-549A-602 Sequence 602, App
58	1565	26.2	538	4	US-08-912-951-316 Sequence 316, App
59	1565	26.2	538	4	US-09-402-181B-602 Sequence 602, App
60	1565	26.2	538	4	US-09-721-456B-602 Sequence 602, App
61	1506	25.3	514	3	US-08-974-549A-605 Sequence 605, App
62	1506	25.3	514	4	US-08-912-951-119 Sequence 319, App
63	1506	25.3	514	4	US-09-402-181B-605 Sequence 605, App
64	1506	25.3	514	4	US-09-721-456B-605 Sequence 605, App
65	1454	24.4	517	3	US-08-974-549A-606 Sequence 606, App
66	1454	24.4	517	4	US-08-912-951-320 Sequence 320, App
67	1454	24.4	517	4	US-09-402-181B-606 Sequence 606, App
68	1454	24.4	517	4	US-09-721-456B-606 Sequence 606, App
69	1447	24.3	530	3	US-08-974-549A-603 Sequence 603, App
70	1447	24.3	530	4	US-08-912-951-317 Sequence 317, App
71	1447	24.3	530	4	US-09-402-181B-603 Sequence 603, App
72	1447	24.3	530	4	US-09-721-456B-603 Sequence 603, App
73	1438	24.1	283	4	US-09-424-226-6 Sequence 6, Appli
74	1386	23.2	515	3	US-08-974-549A-604 Sequence 604, App
75	1386	23.2	515	4	US-08-912-951-318 Sequence 318, App
76	1386	23.2	515	4	US-09-402-181B-604 Sequence 604, App
77	1386	23.2	515	4	US-09-721-456B-604 Sequence 604, App
78	1243.5	20.9	364	4	US-09-417-485D-41 Sequence 41, Appli
79	1090	18.3	253	3	US-08-974-549A-10 Sequence 10, Appli
80	1090	18.3	253	4	US-08-912-951-10 Sequence 10, Appli
81	1090	18.3	253	4	US-09-402-181B-10 Sequence 10, Appli
82	1090	18.3	253	4	US-09-721-456B-10 Sequence 10, Appli
83	929	15.6	222	3	US-08-851-843A-202 Sequence 202, App
84	929	15.6	222	3	US-08-974-549A-321 Sequence 321, App
85	929	15.6	222	3	US-08-854-050-302 Sequence 202, App
86	929	15.6	222	3	US-08-854-050-302 Sequence 202, App
87	929	15.6	222	4	US-09-402-181B-321 Sequence 321, App
88	929	15.6	222	4	US-09-721-456B-321 Sequence 321, App
89	905.5	15.2	330	3	US-08-851-843A-203 Sequence 203, App
90	905.5	15.2	330	3	US-08-974-549A-322 Sequence 322, App
91	905.5	15.2	330	3	US-08-854-050-203 Sequence 203, App
92	905.5	15.2	330	3	US-09-430-323-203 Sequence 203, App
93	905.5	15.2	330	4	US-09-402-181B-322 Sequence 322, App
94	905.5	15.2	330	4	US-09-721-456B-322 Sequence 322, App
95	728	12.2	381	4	US-09-417-485D-47 Sequence 47, Appli
96	646	10.8	129	3	US-08-851-843A-67 Sequence 67, Appli
97	646	10.8	129	3	US-08-974-549A-13 Sequence 13, Appli
98	646	10.8	129	3	US-08-854-050-67 Sequence 67, Appli
99	646	10.8	129	3	US-09-430-323-67 Sequence 67, Appli
100	646	10.8	129	4	US-08-912-951-13 Sequence 13, Appli

101 646 10 8 129 4 US-09-402-181B-13
 102 646 10 8 129 4 US-09-721-455-13
 103 588 9 9 988 3 US-08-851-843A-69
 104 588 9 9 988 3 US-08-974-549A-112
 105 588 9 9 988 3 US-08-854-050-69
 106 588 9 9 988 3 US-09-430-323-69
 107 588 9 9 988 4 US-08-912-951-112
 108 588 9 9 988 4 US-09-402-181B-112
 109 588 9 9 988 4 US-09-721-455-112
 110 440.5 7 4 897 3 US-08-974-549A-189
 111 440.5 7 4 897 4 US-09-402-181B-189
 112 440.5 7 4 897 4 US-09-721-455-189
 113 440.5 7 4 1007 3 US-08-851-843A-86
 114 440.5 7 4 1007 3 US-08-974-549A-187
 115 440.5 7 4 1007 3 US-08-854-050-86
 116 440.5 7 4 1007 3 US-09-430-323-86
 117 440.5 7 4 1007 4 US-09-402-181B-187
 118 440.5 7 4 1007 4 US-09-721-455-187
 119 440.5 7 4 1031 3 US-08-851-843A-2
 120 440.5 7 4 1031 3 US-08-974-549A-110

ALIGNMENTS

Sequence 13, Appl
 Sequence 13, Appl
 Sequence 69, Appl
 Sequence 112, Appl
 Sequence 69, Appl
 Sequence 69, Appl
 Sequence 112, Appl
 Sequence 112, Appl
 Sequence 112, Appl
 Sequence 189, Appl
 Sequence 189, Appl
 Sequence 189, Appl
 Sequence 86, Appl
 Sequence 86, Appl
 Sequence 86, Appl
 Sequence 86, Appl
 Sequence 187, Appl
 Sequence 187, Appl
 Sequence 2, Appl
 Sequence 110, Appl

RESULT 1
 US-08-974-549A-344
 ; Sequence 344, Application US/08974549A
 ; Patent No. 6166178
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; APPLICANT: Lingner, Joachim
 ; APPLICANT: Nakamura, Toru
 ; APPLICANT: Chapman, Karen B.
 ; APPLICANT: Morin, Gregg B.
 ; APPLICANT: Harley, Calvin B.
 ; APPLICANT: Andrews, William H.
 ; TITLE OF INVENTION: Human telomerase Catalytic Subunit
 ; NUMBER OF SEQUENCES: 727
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/974,549A
 ; FILING DATE: 19-NOV-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/724,643
 ; FILING DATE: 01-OCT-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/844,419
 ; FILING DATE: 18-APR-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/846,017
 ; FILING DATE: 25-APR-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/851,843
 ; FILING DATE: 06-MAY-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/854,050
 ; FILING DATE: 09-MAY-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/911,312
 ; FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/17618
 FILING DATE: 01-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 344:
 LENGTH: 1132 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-974-549A-344

Query Match 100.0%; Score 5963; DB 3; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSILRSHYREVLPLATFVRLPGQWRVLRQDPAAFRLVQCLVCFW 60
 DB 1 MPAPRCRAVRSILRSHYREVLPLATFVRLPGQWRVLRQDPAAFRLVQCLVCFW 60
 QY 61 DARPAPAPSPROVSLCKELVARVLRORLCERGAQVLAAGFLLDGAAGPPEAFTTSR 120
 DB 61 DARPAPAPSPROVSLCKELVARVLRORLCERGAQVLAAGFLLDGAAGPPEAFTTSR 120
 QY 121 SYLVNTVDALRSGAGWGLLRVGGDVLVHLIARCALFVLAFCAYQVCGPPLYQGA 180
 DB 121 SYLVNTVDALRSGAGWGLLRVGGDVLVHLIARCALFVLAFCAYQVCGPPLYQGA 180
 QY 181 ATOARPPHAGSGRRRLGCEBAMNHSVRAGVPLGPAAGARRGASARSLLPLRPPR 240
 DB 181 ATOARPPHAGSGRRRLGCEBAMNHSVRAGVPLGPAAGARRGASARSLLPLRPPR 240
 QY 241 GAAPERTPVGGGSAHAGTRGPDRCFCVSPAPAEATSLGALSGTRHSPVVG 300
 DB 241 GAAPERTPVGGGSAHAGTRGPDRCFCVSPAPAEATSLGALSGTRHSPVVG 300
 QY 301 ROHHAAPSTSPRRPMDTPCPVYAETGHLFYSQDKQLRPSLLSLRPSLTGARRL 360
 DB 301 ROHHAAPSTSPRRPMDTPCPVYAETGHLFYSQDKQLRPSLLSLRPSLTGARRL 360
 QY 361 VETIFGSRPMWGTGTRRLPLPORYWQRPFLFELIGHAQCPIYVLLKTHCPRAAVT 420
 DB 361 VETIFGSRPMWGTGTRRLPLPORYWQRPFLFELIGHAQCPIYVLLKTHCPRAAVT 420
 QY 421 PAAGVCAAREKPOGSAVAPEEDTDPRLVOLLROHSSPVQVGYFACIRLVPGLMGS 480
 DB 421 PAAGVCAAREKPOGSAVAPEEDTDPRLVOLLROHSSPVQVGYFACIRLVPGLMGS 480
 QY 481 RHNERPFLNRTKKTSLSGAKLSLOELTWKMSVDCALRRSPGVGCVPAEHLREBI 540
 DB 481 RHNERPFLNRTKKTSLSGAKLSLOELTWKMSVDCALRRSPGVGCVPAEHLREBI 540
 QY 541 LAKFLHMLSVYVELLRSPFYVETTFQKNLFFYRPSVMSKLSIGIRQLKRVQIRE 600
 DB 541 LAKFLHMLSVYVELLRSPFYVETTFQKNLFFYRPSVMSKLSIGIRQLKRVQIRE 600
 QY 601 LSTAEVROREARPALITRLRFIRKPDGLRIYAMDYVVGARTRRERARLRSRYVA 660
 DB 601 LSTAEVROREARPALITRLRFIRKPDGLRIYAMDYVVGARTRRERARLRSRYVA 660

```

Db 601 LSEAEVROHREARPAALLTSRLRPIPKPDGLRPIVNDYVVGARTFRREKRAEELTSRYKA 660
Qy 661 LFSVLNVERARRRQGLGASVYLGLDDHRAWRITVLRARODPEPELYFVKVDTAGYDTI 720
Db 661 LFSVLNVERARRRQGLGASVYLGLDDHRAWRITVLRARODPEPELYFVKVDTAGYDTI 720
Qy 721 PQRLTEVIASIIKPPNTYCVRRYAVVQKAHSHVKAHFKSHVSTLTLDIOPYWRQFVAAL 780
Db 721 PQRLTEVIASIIKPPNTYCVRRYAVVQKAHSHVKAHFKSHVSTLTLDIOPYWRQFVAAL 780
Qy 781 QETSPLADAVIIOSSSLNASSGGLFVFLRFMCHHVRIRGSGYVOCGIPQGSILSTL 840
Db 781 QETSPLADAVIIOSSSLNASSGGLFVFLRFMCHHVRIRGSGYVOCGIPQGSILSTL 840
Qy 841 LGSILCGDMENKLFAGIRRDGLLRVDLVLVTPHLTHAKTFLRLVGVPEYGCVANL 900
Db 841 LGSILCGDMENKLFAGIRRDGLLRVDLVLVTPHLTHAKTFLRLVGVPEYGCVANL 900
Qy 901 RKTVAHPVDEALGGAFAVQMPAHGIFPMCGILLDTRTIEVQSDYSYARTISIRASVTF 960
Db 901 RKTVAHPVDEALGGAFAVQMPAHGIFPMCGILLDTRTIEVQSDYSYARTISIRASVTF 960
Qy 961 NRGFKAGRMNRKLFVYLRLKCHSLFLDLQVNSLQVCTNIYKILLLOAFHFACVLOLP 1020
Db 961 NRGFKAGRMNRKLFVYLRLKCHSLFLDLQVNSLQVCTNIYKILLLOAFHFACVLOLP 1020
Qy 1021 FHQVQKNPFPELRVISTDASLCYSIIKANAGMSLGAKGAPLPSEAVOMLCHOAFIL 1080
Db 1021 FHQVQKNPFPELRVISTDASLCYSIIKANAGMSLGAKGAPLPSEAVOMLCHOAFIL 1080
Qy 1081 KLTRHRTYVPLIGSLRTAQTOLSRKLPJTTLTALLEANPALPSPFKTIL 1132
Db 1081 KLTRHRTYVPLIGSLRTAQTOLSRKLPJTTLTALLEANPALPSPFKTIL 1132

```

```

RESULT 2
US-09-402-181B-344
; Sequence 344, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Linger, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843

```

```

; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Auenhue, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 344:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 344:
US-09-402-181B-344

Query Match 100.0%; Score 5963; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MPBARCAVAVSLIRSHREVLPATFVRLGPOGWRVORGDPAAPRALVAOCIVCPM 60
1 MPBARCAVAVSLIRSHREVLPATFVRLGPOGWRVORGDPAAPRALVAOCIVCPM 60
61 DARPPPAAPSPROYCLNELVAVYLQRLCERGANVLAFGALLDAGRGPEAFTSVR 120
61 DARPPPAAPSPROYCLNELVAVYLQRLCERGANVLAFGALLDAGRGPEAFTSVR 120
121 SYLPNTVDALRGSAWLLLRVGDVYLHLLARCALFVLVAPSCAQQVGGPPLVQGA 180
121 SYLPNTVDALRGSAWLLLRVGDVYLHLLARCALFVLVAPSCAQQVGGPPLVQGA 180
121 SYLPNTVDALRGSAWLLLRVGDVYLHLLARCALFVLVAPSCAQQVGGPPLVQGA 180
181 ATQARPPEHAGSPRRRLCERAMNHSVYEAQVPLGLPAPGARRGSGASRSLPLPKRPR 240
181 ATQARPPEHAGSPRRRLCERAMNHSVYEAQVPLGLPAPGARRGSGASRSLPLPKRPR 240
241 GAAPPERTPVQGGWAMHPTRGSDRGFCVSPAPAEATSLSEGLSGTRSHPSVG 300
241 GAAPPERTPVQGGWAMHPTRGSDRGFCVSPAPAEATSLSEGLSGTRSHPSVG 300
241 GAAPPERTPVQGGWAMHPTRGSDRGFCVSPAPAEATSLSEGLSGTRSHPSVG 300
301 ROHAGPSTSPRPWPOTPCBPVYAEKHFVYSGDKEQLRPSFLSLSPSLTGARL 360
301 ROHAGPSTSPRPWPOTPCBPVYAEKHFVYSGDKEQLRPSFLSLSPSLTGARL 360
301 ROHAGPSTSPRPWPOTPCBPVYAEKHFVYSGDKEQLRPSFLSLSPSLTGARL 360
361 VETIFLGRPMWPGTFRRLPRLPORVWQMRPLFELLGNHAQCPYGVLLKTHCPRAAVT 420
361 VETIFLGRPMWPGTFRRLPRLPORVWQMRPLFELLGNHAQCPYGVLLKTHCPRAAVT 420
361 VETIFLGRPMWPGTFRRLPRLPORVWQMRPLFELLGNHAQCPYGVLLKTHCPRAAVT 420
421 PAAGVCAEKQGSVAAPAEEDTDPRRLVOLLROHSSWQYGFYFACLRRLVPPGLGMS 480
421 PAAGVCAEKQGSVAAPAEEDTDPRRLVOLLROHSSWQYGFYFACLRRLVPPGLGMS 480
421 PAAGVCAEKQGSVAAPAEEDTDPRRLVOLLROHSSWQYGFYFACLRRLVPPGLGMS 480
481 RHNERRFLRNTKFLSLGKHAFLSLQELTWKSVYDCAMLRSPGVGCPAAEHLREI 540
481 RHNERRFLRNTKFLSLGKHAFLSLQELTWKSVYDCAMLRSPGVGCPAAEHLREI 540
481 RHNERRFLRNTKFLSLGKHAFLSLQELTWKSVYDCAMLRSPGVGCPAAEHLREI 540
541 LAKFLHMLMSYVVELLASFVYVETTFQKRLFFYRSVWSKQSIIRQHLKRVQURE 600
541 LAKFLHMLMSYVVELLASFVYVETTFQKRLFFYRSVWSKQSIIRQHLKRVQURE 600
541 LAKFLHMLMSYVVELLASFVYVETTFQKRLFFYRSVWSKQSIIRQHLKRVQURE 600
601 LSEAEVROHREARPAALLTSRLRPIPKPDGLRPIVNDYVVGARTFRREKRAEELTSRYKA 660
601 LSEAEVROHREARPAALLTSRLRPIPKPDGLRPIVNDYVVGARTFRREKRAEELTSRYKA 660

```

Db 601 LSEAEVQREARFALLTSRLRIFIKPQGLRPIVNMVYVVGARTREKREARLTSRYKA 660
 Qy 661 LFSVLYNEARRRPGLIGASVGLGDDIHRAMTFVLRVADPPPELVKVDVYGAQYTI 720
 Db 661 LFSVLYNEARRRPGLIGASVGLGDDIHRAMTFVLRVADPPPELVKVDVYGAQYTI 720
 Qy 721 PODRLTEVIASITIKPONTYCVRRYAVVOGAHGVHAKAFKSHVSTLTLQPYMRQFVAHL 780
 Db 721 PODRLTEVIASITIKPONTYCVRRYAVVOGAHGVHAKAFKSHVSTLTLQPYMRQFVAHL 780
 Qy 781 QESPLRDAVVLBOSSSLNEASSGLFDVFLRMCHAVRIRKSVYVQCGIPQGSILSTL 840
 Db 781 QESPLRDAVVLBOSSSLNEASSGLFDVFLRMCHAVRIRKSVYVQCGIPQGSILSTL 840
 Qy 841 LCSLCYGMENKLPAGIRRDGLLRVDDFLVTEHLTHAKTFRLTLVGVPEYGVVNL 900
 Db 841 LCSLCYGMENKLPAGIRRDGLLRVDDFLVTEHLTHAKTFRLTLVGVPEYGVVNL 900
 Qy 901 RTVVNFPEDALGOTAFVOMPAHGLPWCGLLIDTRLEVQSGSYASTSTRASVTF 960
 Db 901 RTVVNFPEDALGOTAFVOMPAHGLPWCGLLIDTRLEVQSGSYASTSTRASVTF 960
 Qy 961 NGEFKAGRMRRKLFEGVLRKCHSLFLDQVNSLQTVCTNIYKILLQAFEFHACVLQLP 1020
 Db 961 NGEFKAGRMRRKLFEGVLRKCHSLFLDQVNSLQTVCTNIYKILLQAFEFHACVLQLP 1020
 Qy 1021 FHQVWKNPFTFLRYISDTASLCYSILKAKAKGMSLGAAGPPLPSAVOMLCHQATLL 1080
 Db 1021 FHQVWKNPFTFLRYISDTASLCYSILKAKAKGMSLGAAGPPLPSAVOMLCHQATLL 1080
 Qy 1081 KLTRHRTVYVPLGSLRTAQTOLSRKLPOTTLTALAAANPALPSPDFITIID 1132
 Db 1081 KLTRHRTVYVPLGSLRTAQTOLSRKLPOTTLTALAAANPALPSPDFITIID 1132

RESULT 3
 US-09-721-456-344
 ; Sequence 344, Application US/09721456
 ; Patent No. 6617110
 ; GENERAL INFORMATION:
 ; APPLICANT: Cecch, Thomas R.
 ; ; Lingner, Joachim
 ; ; Nakamura, Toru
 ; ; Chapman, Karen B.
 ; ; Morin, Gregg B.
 ; ; Harley, Calvin B.
 ; ; Andrews, William H.
 ; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 ; NUMBER OF SEQUENCES: 727
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/721,456
 ; FILING DATE: 22-NOV-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/974,549A
 ; FILING DATE: 19-NOV-1997
 ; APPLICATION NUMBER: US 08/724,643
 ; FILING DATE: 01-OCT-1996
 ; APPLICATION NUMBER: US 08/844,419
 ; FILING DATE: 18-APR-1997
 ; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997
 ; APPLICATION NUMBER: US 08/851,843
 ; FILING DATE: 06-MAY-1997
 ; APPLICATION NUMBER: US 08/854,050
 ; FILING DATE: 09-MAY-1997
 ; APPLICATION NUMBER: US 08/911,312
 ; FILING DATE: 14-AUG-1997
 ; APPLICATION NUMBER: US 08/912,951
 ; FILING DATE: 14-AUG-1997
 ; APPLICATION NUMBER: US 08/915,503
 ; FILING DATE: 14-AUG-1997
 ; APPLICATION NUMBER: WO PCT/US97/17618
 ; FILING DATE: 01-OCT-1997
 ; APPLICATION NUMBER: WO PCT/US97/17885
 ; FILING DATE: 01-OCT-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Apple, Randolph Ted
 ; REGISTRATION NUMBER: 36,429
 ; REFERENCE/DOCKET NUMBER: 015389--002610US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 344:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1132 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 344:
 US-09-721-456-344

Query Match 100.0%; Score 5963; DB 4; Length 1132;
 Best Local Similarity 100.0%; Pred. 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MPAPRCRAVRSLRSHYREVLPATFVRRLDPQGRVLVQSGDPAAFRALVAQCLVCPW 60
 Db 1 MPAPRCRAVRSLRSHYREVLPATFVRRLDPQGRVLVQSGDPAAFRALVAQCLVCPW 60
 Qy 61 DARPAPAPSPFROVSLCKELVARVLRQLCERAKVLAAGFALDQARQGPPEAFTTSVR 120
 Db 61 DARPAPAPSPFROVSLCKELVARVLRQLCERAKVLAAGFALDQARQGPPEAFTTSVR 120
 Qy 121 SYLNTVTDLRSGSGAMGILLRRVGGDVLVHLARCALFVLVAPSCAVQVCPPIYOLGA 180
 Db 121 SYLNTVTDLRSGSGAMGILLRRVGGDVLVHLARCALFVLVAPSCAVQVCPPIYOLGA 180
 Qy 181 ATQARPPHASPGRRLGCERAMNHSVRAGVPLGIPAGARRRQGSASRLPLPRPRR 240
 Db 181 ATQARPPHASPGRRLGCERAMNHSVRAGVPLGIPAGARRRQGSASRLPLPRPRR 240
 Qy 241 GAAPPEERTPVQGGSAHPCRTGSPDRGFCVSPAPAEATSLGALSGTRHSPVSG 300
 Db 241 GAAPPEERTPVQGGSAHPCRTGSPDRGFCVSPAPAEATSLGALSGTRHSPVSG 300
 Qy 301 ROHHAGPSTSRPDPMDTFCPPVYAEYKFLYSSGDKQLRPSPLLSRLSLTGARRL 360
 Db 301 ROHHAGPSTSRPDPMDTFCPPVYAEYKFLYSSGDKQLRPSPLLSRLSLTGARRL 360
 Qy 361 VETIFLGSRPWNGTFRRLPRLPORWQMRPLFLETLGHAQCPGVLTCTCPPLRAVT 420
 Db 361 VETIFLGSRPWNGTFRRLPRLPORWQMRPLFLETLGHAQCPGVLTCTCPPLRAVT 420
 Qy 421 PAAGVAREKPPQGSVAAPBEDTDPRLVQLLRQSSPQVGYFVACLRILVPPGLWGS 480
 Db 421 PAAGVAREKPPQGSVAAPBEDTDPRLVQLLRQSSPQVGYFVACLRILVPPGLWGS 480
 Qy 481 RHNERFLNTKKFISLGGAKLSLQELTWKMSVDDCARLSPGVGCVPAAEHRLREI 540
 Db 481 RHNERFLNTKKFISLGGAKLSLQELTWKMSVDDCARLSPGVGCVPAAEHRLREI 540
 Qy 541 LAKFLHMLSVVVELLRSEFFVETTFPQKRLFFYRPSVMSKLSIGIRQLKQVLE 600
 Db 541 LAKFLHMLSVVVELLRSEFFVETTFPQKRLFFYRPSVMSKLSIGIRQLKQVLE 600

Query	Subject	Similarity	Score	DB	Length	Matches	Consecutive	Mismatches	Indels	Gaps
QY	1 MPRAIDCRVAVSLIRSHYREVLPLATFVRRLPGCGWRLVQGDPPAPFALVAQCLVCVPM	100.0%	5963	DB 3	1407	1132	0	0	0	0
QY	276 MPRAIDCRVAVSLIRSHYREVLPLATFVRRLPGCGWRLVQGDPPAPFALVAQCLVCVPM	100.0%	5963	DB 3	1407	1132	0	0	0	0
QY	61 DARPDPAPSPRQVSCKEIVARVLQRCERGAQNVLAFGALLDGGARGPPEATTTSVR	100.0%	5963	DB 3	1407	1132	0	0	0	0
QY	336 DARPDPAPSPRQVSCKEIVARVLQRCERGAQNVLAFGALLDGGARGPPEATTTSVR	100.0%	5963	DB 3	1407	1132	0	0	0	0
QY	121 SYLNTVTDALRSGGAWGLLIRVGDVVLVHLLARCALFVLVAASCAVQVCGPPIYQIGA	100.0%	5963	DB 3	1407	1132	0	0	0	0
QY	396 SYLNTVTDALRSGGAWGLLIRVGDVVLVHLLARCALFVLVAASCAVQVCGPPIYQIGA	100.0%	5963	DB 3	1407	1132	0	0	0	0
QY	181 ATQARPPPHASGPPRRRLGCEBAMHVSREAGVPLGLPAPGARRRGGASRSLPLPKPRR	100.0%	5963	DB 3	1407	1132	0	0	0	0
QY	456 ATQARPPPHASGPPRRRLGCEBAMHVSREAGVPLGLPAPGARRRGGASRSLPLPKPRR	100.0%	5963	DB 3	1407	1132	0	0	0	0
QY	241 GAAPERTPTVGGQSWAPGRTGPDSDRGCVVSPAPPAEATSLLEGALSGTRSHPEVG	100.0%	5963	DB 3	1407	1132	0	0	0	0
QY	516 GAAPERTPTVGGQSWAPGRTGPDSDRGCVVSPAPPAEATSLLEGALSGTRSHPEVG	100.0%	5963	DB 3	1407	1132	0	0	0	0

```

QY 301 ROHAGPSTSRPPRPMWDTCPVYAEKHFLYSGDKEQRPFSLLSLRPSLTGARL 360
DB 576 ROHAGPSTSRPPRPMWDTCPVYAEKHFLYSGDKEQRPFSLLSLRPSLTGARL 635
QY 361 VETIFLGSRRPWPMTGTPRLPRLPQRYWQMRPLFELLGNHAQCYGVLLKTHCPLRAVT 420
DB 636 VETIFLGSRRPWPMTGTPRLPRLPQRYWQMRPLFELLGNHAQCYGVLLKTHCPLRAVT 695
QY 421 PAAGCAEKEKPGQSVAAPEEBEDTPRLVOLLROHSSPMQYGFACLRPLVPGMGS 480
DB 696 PAAGCAEKEKPGQSVAAPEEBEDTPRLVOLLROHSSPMQYGFACLRPLVPGMGS 755
QY 481 RANERFLNRTKFFISLGKHAFLSQELTWMSVDCAMLRSPDQVCVPAAEHRLBEI 540
DB 756 RANERFLNRTKFFISLGKHAFLSQELTWMSVDCAMLRSPDQVCVPAAEHRLBEI 815
QY 541 LAKFJHMLMSVYVVELLSFFVYTTTQKRLFFRPSVWSKOSIGIRHKLRYQURE 600
DB 816 LAKFJHMLMSVYVVELLSFFVYTTTQKRLFFRPSVWSKOSIGIRHKLRYQURE 875
QY 601 LSEAEVQREARPPALTSRLRFPKPDGLRPIVMDYVVGARTFRREKRAERLTSRYKA 660
DB 876 LSEAEVQREARPPALTSRLRFPKPDGLRPIVMDYVVGARTFRREKRAERLTSRYKA 935
QY 661 LFSVLYNERARRPPGLIGASVIGLDDIHRAMRTFVLRAODPPBELYFVKYDVTGADTI 720
DB 936 LFSVLYNERARRPPGLIGASVIGLDDIHRAMRTFVLRAODPPBELYFVKYDVTGADTI 995
QY 721 PODRLTEVASTIKQNTYCVARVAVVOKAAGHVRKAFKSHVSTLTLQRYMGOFAVHL 780
DB 996 PODRLTEVASTIKQNTYCVARVAVVOKAAGHVRKAFKSHVSTLTLQRYMGOFAVHL 1055
QY 781 QETSPLRDAVLEIOSSSLNEASSGLFDVFLRPMCHAVRIRGKSYVQCGIPQGSILSTL 840
DB 1056 QETSPLRDAVLEIOSSSLNEASSGLFDVFLRPMCHAVRIRGKSYVQCGIPQGSILSTL 1115
QY 841 LLSLCYGMENKLPAGIRDDGLLLVDDPLVTHLTHAKTEFLTVIRGVRGVCVNL 900
DB 1116 LLSLCYGMENKLPAGIRDDGLLLVDDPLVTHLTHAKTEFLTVIRGVRGVCVNL 1175
QY 901 KRTVNFPEDEBALGCTAFVQMPAHGLPFMCGLLIDRTLEVOSSYVARTSIRASYTF 960
DB 1176 KRTVNFPEDEBALGCTAFVQMPAHGLPFMCGLLIDRTLEVOSSYVARTSIRASYTF 1235
QY 961 NRGFKAGRMRRKLFQVLRKCHSLFDLQVNSLQVCTNLYKILLQAYRFAVCVQLP 1020
DB 1236 NRGFKAGRMRRKLFQVLRKCHSLFDLQVNSLQVCTNLYKILLQAYRFAVCVQLP 1295
QY 1021 FHOQWKNPTFLRIVSDTASLCYSILKXKNAGSLGAKGAGPLPSAVOMLCHQAFLL 1080
DB 1296 FHOQWKNPTFLRIVSDTASLCYSILKXKNAGSLGAKGAGPLPSAVOMLCHQAFLL 1355
QY 1081 KLTRHRVTYVPLGLSLRTAQOLSRKLPCTTLTALBAANPALPSDFXTIID 1132
DB 1356 KLTRHRVTYVPLGLSLRTAQOLSRKLPCTTLTALBAANPALPSDFXTIID 1407

```

```

CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
City: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 03-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 334:
SEQUENCE CHARACTERISTICS:
LENGTH: 1407 amino acids
STRANDNESS:
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-951-334
Query Match 100.0%; Score 5963; DB 4; Length 1407;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAPRCRAVRSILRSHYREVLPATFVRRLGQGRVLYVGQDPAAFRALVAGCLVCVW 60
DB 276 MPRAPRCRAVRSILRSHYREVLPATFVRRLGQGRVLYVGQDPAAFRALVAGCLVCVW 335
QY 61 DARRPPAARFROVSLCKELVAVLQRLCERGAKNVLAFGPALLDARGAPPEAFPTSVR 120
DB 336 DARRPPAARFROVSLCKELVAVLQRLCERGAKNVLAFGPALLDARGAPPEAFPTSVR 395
QY 121 SYLPNTVTDALRSGAGMGLLRVGDVILVHLARCALFVLVAPSCAYVCGPPIYOLGA 180
DB 396 SYLPNTVTDALRSGAGMGLLRVGDVILVHLARCALFVLVAPSCAYVCGPPIYOLGA 455
QY 181 ATQARPPHAGSGRRRLGCRANMHSVREAGVGLGPAAGARRGGSASRSILPKRPPR 240
DB 456 ATQARPPHAGSGRRRLGCRANMHSVREAGVGLGPAAGARRGGSASRSILPKRPPR 515
QY 241 GAAPPEPRTVQGSMAHPGRTGPDGRFCVSPARPAEATSLEGALSGTRHSPVVG 300

```

```

Db 516 GAAPERTITVGGGSMHPRGTGSPDRGCVVSPAPAEATSLGALSGTHSHSPSVG 575
QY 301 ROHAGPSTSPDRPMDTPCPVYATETKHFVSSGKEDLRPSFLSLRPSLTGABRL 360
Db 576 ROHAGPSTSPDRPMDTPCPVYATETKHFVSSGKEDLRPSFLSLRPSLTGABRL 635
QY 361 VETIFLGSRPMWPGTPRLRLPQRYWQMPLELIGNHAQCPYGLLKTGCPILAAVT 420
Db 636 VETIFLGSRPMWPGTPRLRLPQRYWQMPLELIGNHAQCPYGLLKTGCPILAAVT 695
QY 421 PAAGVCAREKPOQSVAAPEEDDPRLVOLLROHSPMVQVGFVACRLRVPPLKMS 480
Db 696 PAAGVCAREKPOQSVAAPEEDDPRLVOLLROHSPMVQVGFVACRLRVPPLKMS 755
QY 481 RHNERRELTNTKKEISLGGKAKLSLOELTWKMSVRCAMLRSPGVGCVAAERHREBI 540
Db 756 RHNERRELTNTKKEISLGGKAKLSLOELTWKMSVRCAMLRSPGVGCVAAERHREBI 815
QY 541 LAFLHMLMSVYVELLSRFYVTEFTTPOKRLFFRPSVMSKLOSTIGIRHOKVQLRE 600
Db 816 LAFLHMLMSVYVELLSRFYVTEFTTPOKRLFFRPSVMSKLOSTIGIRHOKVQLRE 875
QY 601 LSAEAYQREARPAALITSLRFLPKPDGLRPIYVNDYVVGARTFRREKAEELTSRYKA 660
Db 876 LSAEAYQREARPAALITSLRFLPKPDGLRPIYVNDYVVGARTFRREKAEELTSRYKA 935
QY 661 LBSVLNERARRRPGGLGASVGLGDIHRAMRTVLRAADPPPELYFYKVDVTGAYDTI 720
Db 936 LBSVLNERARRRPGGLGASVGLGDIHRAMRTVLRAADPPPELYFYKVDVTGAYDTI 995
QY 721 POBRLEFVIAIITKPONTYCVRRYAYVQKAAHGVAKAFKSHVSTLTDIOPYMEOPVAHL 780
Db 996 POBRLEFVIAIITKPONTYCVRRYAYVQKAAHGVAKAFKSHVSTLTDIOPYMEOPVAHL 1055
QY 781 QETSPLRADAVIIOSSSLNBAASGLFVPLRFMCHAVRIKGSYVQCGIIPGGSILSTL 840
Db 1056 QETSPLRADAVIIOSSSLNBAASGLFVPLRFMCHAVRIKGSYVQCGIIPGGSILSTL 1115
QY 841 LGSLOCYGDMEKRLFAGIRRDGILLRLVDDCLVTPHLLTHAKTFLRLVGVPEYGVVNL 900
Db 1116 LGSLOCYGDMEKRLFAGIRRDGILLRLVDDCLVTPHLLTHAKTFLRLVGVPEYGVVNL 1175
QY 901 RKTIVNFPVEDEALGTAFAVOMPAGHGFPCGILLDTRILEVOSDSSYARSISIRASYTF 960
Db 1176 RKTIVNFPVEDEALGTAFAVOMPAGHGFPCGILLDTRILEVOSDSSYARSISIRASYTF 1235
QY 961 NRGFKAQRNRKRLFVYLRKCHSLFLDQVNSLOVCTNINIKYKILLLOAYRPHACVLOLP 1020
Db 1236 NRGFKAQRNRKRLFVYLRKCHSLFLDQVNSLOVCTNINIKYKILLLOAYRPHACVLOLP 1295
QY 1021 FHOQWKNPFTFPRVISTDTSALCYSLIKAKNAGMSGAKGAGPLPSEAVOMLCHOAFL 1080
Db 1296 FHOQWKNPFTFPRVISTDTSALCYSLIKAKNAGMSGAKGAGPLPSEAVOMLCHOAFL 1355
QY 1081 KLTRHRTVYVPLIGSLRTAQTLRSKLPGLTTLTALEAANPALPSDFKTLTD 1132
Db 1356 KLTRHRTVYVPLIGSLRTAQTLRSKLPGLTTLTALEAANPALPSDFKTLTD 1407

```

RESULT 6
US-09-402-181B-628
Sequence 628, Application US/09402181B
Patent No. 6610839

GENERAL INFORMATION:

APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morth, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit

```

NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/951,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Auehush, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015385-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 628:
SEQUENCE CHARACTERISTICS:
LENGTH: 1407 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1407
OTHER INFORMATION: /note= "fusion protein composed of
enhanced green fluorescent protein
(EGFP) residues, residues encoded by the
5' untranslated region of hTERT mRNA and
hTERT protein sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 628:
US-09-402-181B-628
Query Match 100.0%; Score 5963; DB 4; Length 1407;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Gaps 0;
QY 1 MPBAPRCAYSLRSHRYEVLPLATFRRRLGPGWRLVQSGDPAARPAALVAGCVCVPM 60
Db 276 MPBAPRCAYSLRSHRYEVLPLATFRRRLGPGWRLVQSGDPAARPAALVAGCVCVPM 335
QY 61 DARPAPAPSFROYSCLEIYARVLORLCERGANVLAFGFALIDGARGGPEAFTTSVR 120
Db 336 DARPAPAPSFROYSCLEIYARVLORLCERGANVLAFGFALIDGARGGPEAFTTSVR 395

```

QY 121 SYLPTVTVDALRGSGAMGILLRVDVYLHLLACALFVLVAPGCAVGVGCPPLYQIGA 180
 DB 396 SYLPTVTVDALRGSGAMGILLRVDVYLHLLACALFVLVAPGCAVGVGCPPLYQIGA 455
 QY 181 ATQAAPPPHAGSPRRRLGCEBAMNHSVEAGVGLDLPAGARRGSGASRLPKRRR 240
 DB 456 ATQAAPPPHAGSPRRRLGCEBAMNHSVEAGVGLDLPAGARRGSGASRLPKRRR 515
 QY 241 GAAPPERTPVQGSWAPHGRTRGSDRGFCVSPAPPAEATSLGALSOTRSHSPVG 300
 DB 516 GAAPPERTPVQGSWAPHGRTRGSDRGFCVSPAPPAEATSLGALSOTRSHSPVG 575
 QY 301 RGHAGPPTSPRPPTPCPPVYAETKHFVSSGDKQLRPSFLSLRPSLTGARL 360
 DB 576 RGHAGPPTSPRPPTPCPPVYAETKHFVSSGDKQLRPSFLSLRPSLTGARL 635
 QY 361 VETIFGSPMPGCPRRRLPRLPQRYQWRPLFELIGNHACCPGVLLKTHCPRAVY 420
 DB 636 VETIFGSPMPGCPRRRLPRLPQRYQWRPLFELIGNHACCPGVLLKTHCPRAVY 695
 QY 421 PAAGVAREKPGGSVAAPBEDTDPRLVQLIRHSSFWOYGVYRACLRLVPPGLWGS 480
 DB 696 PAAGVAREKPGGSVAAPBEDTDPRLVQLIRHSSFWOYGVYRACLRLVPPGLWGS 755
 QY 481 RHNERFLANTKKFTSLGKAKLSLOELTWKMSVDCAMLRSPGVGCPAAERHRLREI 540
 DB 756 RHNERFLANTKKFTSLGKAKLSLOELTWKMSVDCAMLRSPGVGCPAAERHRLREI 815
 QY 541 LAKFLHMLSVYVLELRSPFYVETTPQKRLFFYRPSVMSKLSIGIRHLKRVQIRE 600
 DB 816 LAKFLHMLSVYVLELRSPFYVETTPQKRLFFYRPSVMSKLSIGIRHLKRVQIRE 875
 QY 601 LEEAEVROREARPALTSRLRFIPKPDGLRPIVMDYVVGARTREKRELRSLRKA 660
 DB 876 LEEAEVROREARPALTSRLRFIPKPDGLRPIVMDYVVGARTREKRELRSLRKA 935
 QY 661 LFSVLNVEARARRGLLGASVLDLDIRAMRTFVVRADPPPELYVVKYDVTGAYDTI 720
 DB 936 LFSVLNVEARARRGLLGASVLDLDIRAMRTFVVRADPPPELYVVKYDVTGAYDTI 995
 QY 721 PODRLTEVIASIIKPPONTYCVRRYAVVOKAAHGVKAFKSHVSTLTLQPYMRQFVAHL 780
 DB 996 PODRLTEVIASIIKPPONTYCVRRYAVVOKAAHGVKAFKSHVSTLTLQPYMRQFVAHL 1055
 QY 781 QETSPRLDVAVIEQSSSLNEASSGLFDVYLRFCMHAVRIRKGSYVQCGIPQGSILSTL 840
 DB 1056 QETSPRLDVAVIEQSSSLNEASSGLFDVYLRFCMHAVRIRKGSYVQCGIPQGSILSTL 1115
 QY 841 LCSLCYGDMENTKLFAGIRRDGLLLRLVDFLLVTHLTHAKTFLRTLYRGVPERGCVNL 900
 DB 1116 LCSLCYGDMENTKLFAGIRRDGLLLRLVDFLLVTHLTHAKTFLRTLYRGVPERGCVNL 1175
 QY 901 RRTVNVFPEDEALGGTAFAVQWPAHGLFPWCGLLDTRTLEVOQSYSSYARTSIRASVTF 960
 DB 1176 RRTVNVFPEDEALGGTAFAVQWPAHGLFPWCGLLDTRTLEVOQSYSSYARTSIRASVTF 1235
 QY 961 NGEFKAGRMARRKLFVGLRLKCHSLFLDIQVNSLOTVCTNIYKILLQAYRFHACVTLGP 1020
 DB 1236 NGEFKAGRMARRKLFVGLRLKCHSLFLDIQVNSLOTVCTNIYKILLQAYRFHACVTLGP 1295
 QY 1021 FHQOVKNTPTFLRYVSDTASLCYSILKAKNAGSLGAKGAAGPLPSAIVOMLCHQATLL 1080
 DB 1296 FHQOVKNTPTFLRYVSDTASLCYSILKAKNAGSLGAKGAAGPLPSAIVOMLCHQATLL 1355
 QY 1081 KLTRHRTVTVPLGLSLRTAQOTLSRKLPGTTLTALAANPALPSDFITIID 1132
 DB 1356 KLTRHRTVTVPLGLSLRTAQOTLSRKLPGTTLTALAANPALPSDFITIID 1407

RESULT 7
 US-09-721-456-628
 ; Sequence 628, Application US/09721456
 ; Patent No. 6617110

GENERAL INFORMATION:
 APPLICANT: Cecch, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Hatley, Calvin B.
 Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/721,456
 FILING DATE: 22-Nov-6617110-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,549A
 FILING DATE: 19-NOV-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: WO PCT/US97/17618
 FILING DATE: 01-OCT-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002610US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 628:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1407 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..1407
 OTHER INFORMATION: /note="fusion protein composed of
 enhanced green fluorescent protein
 (EGFP) residues, residues encoded by the
 5' untranslated region of hTERT mRNA and
 hTERT protein sequence"
 SEQUENCE DESCRIPTION: SEQ ID NO: 628:
 US-09-721-456-628

Query Match 100.0%; Score 5963; DB 4; Length 1407;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MPBAPRCRAVSLIRSHYREVLPATFVRRLGPGQWRLVORGDPAPRALVACLVCPW 60
 276 MPBAPRCRAVSLIRSHYREVLPATFVRRLGPGQWRLVORGDPAPRALVACLVCPW 335

QY 61 DABPPAPSPFQVSCIKELVAVYLQRLCERGAKNVLAFGFALLDAGRGPPAFTTSVR 120
 DB DABPPAPSPFQVSCIKELVAVYLQRLCERGAKNVLAFGFALLDAGRGPPAFTTSVR 395

QY 121 SYLPLNTDRLRSGAGMLLRVGDVYLHLLARCLFVLVAPSCAYQVCGPILYOLA 180
 DB SYLPLNTDRLRSGAGMLLRVGDVYLHLLARCLFVLVAPSCAYQVCGPILYOLA 455

QY 181 ATQARPPHAGSPRRRLGCRAMNHSYREAGVPLGAPAGARRGGSASRLPLPRPR 240
 DB ATQARPPHAGSPRRRLGCRAMNHSYREAGVPLGAPAGARRGGSASRLPLPRPR 515

QY 241 GAAPPEPRTVQGSMAHPERTGSPDRGCVVSPAPPAEATSLGALSGTRHSHPSVG 300
 DB GAAPPEPRTVQGSMAHPERTGSPDRGCVVSPAPPAEATSLGALSGTRHSHPSVG 575

QY 301 ROHHAGPSTSRPPMDTCCPPYATKHFVLSGGKQRLSPFLSLSPSLTGARL 360
 DB ROHHAGPSTSRPPMDTCCPPYATKHFVLSGGKQRLSPFLSLSPSLTGARL 635

QY 361 VETIFLGSRPWMDPTPRRLPLQRYWQMRPLFELIGNHACQPYGLLKTCHPLAAVT 420
 DB VETIFLGSRPWMDPTPRRLPLQRYWQMRPLFELIGNHACQPYGLLKTCHPLAAVT 695

QY 421 PAAGVCAREKPOGSVAPEEEDDPRLVOLLROHSPWQVGFVAACLRLVPLKMS 480
 DB PAAGVCAREKPOGSVAPEEEDDPRLVOLLROHSPWQVGFVAACLRLVPLKMS 755

QY 481 RHNERRLRNTKFFISLIGKHAKLSTLCTWMSVRCAMLRSPGVCPAAHRLREI 540
 DB RHNERRLRNTKFFISLIGKHAKLSTLCTWMSVRCAMLRSPGVCPAAHRLREI 815

QY 541 LAFLHLMVYVYVELLRFFVYTTETFOKNRLFIRPSPWSLQSIGTRHKLRYLRE 600
 DB LAFLHLMVYVYVELLRFFVYTTETFOKNRLFIRPSPWSLQSIGTRHKLRYLRE 875

QY 601 LSEAEVQHEEAPALITSLRFLPKPDGLRPIVNMDDYVAGTFRPREKAERLTSRVA 660
 DB LSEAEVQHEEAPALITSLRFLPKPDGLRPIVNMDDYVAGTFRPREKAERLTSRVA 935

QY 661 LFSVLNERARPPGLLGASVGLDIDHRAWRTVLRAADPPPELYFYKVDVTGAYDTI 720
 DB LFSVLNERARPPGLLGASVGLDIDHRAWRTVLRAADPPPELYFYKVDVTGAYDTI 995

QY 721 POORLIEVASIIRKPOVTVARVYAVYQKAHGVKAFKSHVSTLTDOPVROGVATL 780
 DB POORLIEVASIIRKPOVTVARVYAVYQKAHGVKAFKSHVSTLTDOPVROGVATL 1055

QY 781 QETSPLRDVAVIIOSSSLNEASSGLDVLRFMCHHAVIRGKSYVQCGIIPGGSILSTL 840
 DB QETSPLRDVAVIIOSSSLNEASSGLDVLRFMCHHAVIRGKSYVQCGIIPGGSILSTL 1115

QY 841 LGSCLYGDENKLPAGIRRDGLLRLVDDPLVTPHLTHAKTFLRLTVGVPYGVVNL 900
 DB LGSCLYGDENKLPAGIRRDGLLRLVDDPLVTPHLTHAKTFLRLTVGVPYGVVNL 1175

QY 901 RKTIVNPFVDEALGTAFAVQMPAHGLFPWCGLLDTRILEVSDSSYARTSIRASYTF 960
 DB RKTIVNPFVDEALGTAFAVQMPAHGLFPWCGLLDTRILEVSDSSYARTSIRASYTF 1235

QY 961 NRGFKAQRNRRKLFGLVRLKCHSLFLDLOVNSLQVTCNIVKILLLOAVRFHACVLOLP 1020
 DB NRGFKAQRNRRKLFGLVRLKCHSLFLDLOVNSLQVTCNIVKILLLOAVRFHACVLOLP 1295

QY 1021 FHQVWKNPTFFLRISTSLASLCVSIILKAKNAGSLGAKGAGPLPSRAVOMLCHQAFLL 1080
 DB FHQVWKNPTFFLRISTSLASLCVSIILKAKNAGSLGAKGAGPLPSRAVOMLCHQAFLL 1355

QY 1081 KLRHRVTVPLGLSRLCTAQTOLSRKLPGTTLTALAANPALPSDFKTIID 1132
 DB KLRHRVTVPLGLSRLCTAQTOLSRKLPGTTLTALAANPALPSDFKTIID 1407

RESULT 8
 US-08-851-843A-225
 ; Sequence 225, Application US/08851843A
 ; Patent No. 6093809
 ; GENERAL INFORMATION:
 ; APPLICANT: Cecch, Thomas R.
 ; APPLICANT: Ingner, Joachim
 ; APPLICANT: Nakamura, Toru
 ; APPLICANT: Chapman, Karen B.
 ; APPLICANT: Morin, Gregg B.
 ; APPLICANT: Harley, Calvin
 ; APPLICANT: Andrews, William H.
 ; TITLE OF INVENTION: No. 6093809e1 Telomerase
 ; NUMBER OF SEQUENCES: 225
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States of America
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/851.843A
 ; FILING DATE: 06-MAY-1997
 ; CLASSIFICATION:
 ; APPLICATION NUMBER: US 08/846,017
 ; FILING DATE: 25-APR-1997
 ; CLASSIFICATION:
 ; APPLICATION NUMBER: US 08/844,419
 ; FILING DATE: 18-APR-1997
 ; CLASSIFICATION:
 ; APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/724,643
 ; FILING DATE: 01-OCT-1996
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Apple, Randolph T.
 ; REGISTRATION NUMBER: 36,429
 ; REFERENCE/DOCKET NUMBER: 015389-002930US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 225:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1132 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-851-843A-225

Query Match 99.8%; Score 5952; DB 3; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 MPBAPRCRAVSLIRSHYREVLPATFVRRLGPGQWRLVORGDPAPRALVACLVCPW 60
 1 MPBAPRCRAVSLIRSHYREVLPATFVRRLGPGQWRLVORGDPAPRALVACLVCPW 60

QY 61 DARPPAASFRVQSCLEKELVARVILQRLCERGANVLAFFGALLDAGGPEEATTSVR 120
 DB 61 DARPPAASFRVQSCLEKELVARVILQRLCERGANVLAFFGALLDAGGPEEATTSVR 120
 QY 121 SYLNTVNTDALGSGMWGLLRRVGDVYLHLARCALFVLVAPSCAVQVCPYLQGA 180
 DB 121 SYLNTVNTDALGSGMWGLLRRVGDVYLHLARCALFVLVAPSCAVQVCPYLQGA 180
 QY 181 ATOARPPHAGSPRRRLGGERAMNHSVREAGVPLGAPGARRRGSGASRSJLPKRRR 240
 DB 181 ATOARPPHAGSPRRRLGGERAMNHSVREAGVPLGAPGARRRGSGASRSJLPKRRR 240
 QY 241 GAAPPEERTPVQGSVAHAGRTGSDRGFCVVSAPARPEEXTSLEGLSGTRSHSPVG 300
 DB 241 GAAPPEERTPVQGSVAHAGRTGSDRGFCVVSAPARPEEXTSLEGLSGTRSHSPVG 300
 QY 301 RQHAGPPSTSPPPMDTCCPPVVAETGHLFYSAGDEKQOLRPSLSLSLPSLTGARRL 360
 DB 301 RQHAGPPSTSPPPMDTCCPPVVAETGHLFYSAGDEKQOLRPSLSLSLPSLTGARRL 360
 QY 361 VETIFGSRPMNGTFRRLPLUPORYWQMRPLFELGNHACQPVGVLKTHCPRAAVT 420
 DB 361 VETIFGSRPMNGTFRRLPLUPORYWQMRPLFELGNHACQPVGVLKTHCPRAAVT 420
 QY 421 PAAGVAREKPOGSVAAPPEEDTDPRRLYQLROHSSPMQVGFYRACLRVPPGLMGS 480
 DB 421 PAAGVAREKPOGSVAAPPEEDTDPRRLYQLROHSSPMQVGFYRACLRVPPGLMGS 480
 QY 481 RHNERFLNTRKFFISLGHAHLSLQELTWKMSVDCAMLRSPGVCVPAEHLREI 540
 DB 481 RHNERFLNTRKFFISLGHAHLSLQELTWKMSVDCAMLRSPGVCVPAEHLREI 540
 QY 541 LAKFLHMLMSYVVELLSFEVYETTPCKNLPFYRPSVMSKOSIGRHLKRVORE 600
 DB 541 LAKFLHMLMSYVVELLSFEVYETTPCKNLPFYRPSVMSKOSIGRHLKRVORE 600
 QY 601 LSEAEVQREARPAALLTSRLRFLPKDGLRPIVMMDYVVGARTRREKRAERLTSRYKA 660
 DB 601 LSEAEVQREARPAALLTSRLRFLPKDGLRPIVMMDYVVGARTRREKRAERLTSRYKA 660
 QY 661 LPSVNLNEBARPGLLGASVGLDIDIRAMRTFVLVRAQDPPELVKVDVGAAYTI 720
 DB 661 LPSVNLNEBARPGLLGASVGLDIDIRAMRTFVLVRAQDPPELVKVDVGAAYTI 720
 QY 721 PODRLTEVASTIKPONTYCVARYAVOQKAHGRKAFKSHVSTLTLDQPYMRQFVAHL 780
 DB 721 PODRLTEVASTIKPONTYCVARYAVOQKAHGRKAFKSHVSTLTLDQPYMRQFVAHL 780
 QY 781 QETSPLRDAVIEOSSSLEASSGGLFDFVFLRPMCHAVIRKGSYVQCGIPQGSILSTL 840
 DB 781 QETSPLRDAVIEOSSSLEASSGGLFDFVFLRPMCHAVIRKGSYVQCGIPQGSILSTL 840
 QY 841 LGSICVGMENKLPAGIRRDGLLRLVDDFLLVTHLTHAKFTLTVRGVPEGCYVNL 900
 DB 841 LGSICVGMENKLPAGIRRDGLLRLVDDFLLVTHLTHAKFTLTVRGVPEGCYVNL 900
 QY 901 RKTUVNFPVEDALGGTAFCVMPAHGLFPWCGLLIDRTLEVOQSYSSVARTSIRASVTF 960
 DB 901 RKTUVNFPVEDALGGTAFCVMPAHGLFPWCGLLIDRTLEVOQSYSSVARTSIRASVTF 960
 QY 961 NGGFKAGRMRRKLFVULKCHSLFLDQVNSLQTVCMNYKILLQAYRFAHACVOLDP 1020
 DB 961 NGGFKAGRMRRKLFVULKCHSLFLDQVNSLQTVCMNYKILLQAYRFAHACVOLDP 1020
 QY 1021 FHQOVAKNFTFLRVIDSTASLCYSILKXKNGMSLGAKGAAGPLPSEAVOWLCHQATLL 1080
 DB 1021 FHQOVAKNFTFLRVIDSTASLCYSILKXKNGMSLGAKGAAGPLPSEAVOWLCHQATLL 1080
 QY 1081 KLTRHRYTVPLGLSIRTAQTOLSRKLPBTTLTALEAANPALPSDFXTIID 1132
 DB 1081 KLTRHRYTVPLGLSIRTAQTOLSRKLPBTTLTALEAANPALPSDFXTIID 1132

RESULT 9
 US-08-974-549A-2
 Sequence 2, Application US/08974549A
 Patent No. 6166178
 GENERAL INFORMATION:
 APPLICANT: Czech, Thomas R.
 APPLICANT: Lingner, Joachim
 APPLICANT: Nakamura, Toru
 APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Hartley, Calvin B.
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,549A
 FILING DATE: 19-NOV-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/854,843
 FILING DATE: 06-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: NO PCT/US97/117618
 FILING DATE: 01-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: NO PCT/US97/117885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002610US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0300
 TELEFAX: (415) 576-0200
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1132 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

Tue Dec 21 15:43:30 2004

us-08-974-584c-118.rai

Page 11

MOLECULE TYPE: protein
US-08-974-549A-2

Query Match 99.8%; Score 5952; DB 3; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAACRAVRSILRSYREVLPATFVRSILPGQWELVORGDPAAFRALVAQCLVCPM 60
DB 1 MPRAACRAVRSILRSYREVLPATFVRSILPGQWELVORGDPAAFRALVAQCLVCPM 60
QY 61 DARPPAPASFRQVSCIKELVARVLCRCERGAKNLAFALLDDARGPPPAFTTSR 120
DB 61 DARPPAPASFRQVSCIKELVARVLCRCERGAKNLAFALLDDARGPPPAFTTSR 120
QY 121 SYLPNTVTDALRGSGAGMLLRVGDVVLHLLARCALFVLVAPSCAYQCGPPLVQLGA 180
DB 121 SYLPNTVTDALRGSGAGMLLRVGDVVLHLLARCALFVLVAPSCAYQCGPPLVQLGA 180
QY 181 ATQARPPPHASGPPRRIGCBANMSYREAGVPLGLPACARRRGSGASLSLPPRPR 240
DB 181 ATQARPPPHASGPPRRIGCBANMSYREAGVPLGLPACARRRGSGASLSLPPRPR 240
QY 241 GAAPERTPYQGSQWHPGTRGSDRGFCVSPAPAEATSLGALSGTRHSPSYG 300
DB 241 GAAPERTPYQGSQWHPGTRGSDRGFCVSPAPAEATSLGALSGTRHSPSYG 300
QY 301 ROHHAGPSTSRPPRMDTCPVYATKHFVSSGKEQLRPSFLISSLRPSLTGAARL 360
DB 301 ROHHAGPSTSRPPRMDTCPVYATKHFVSSGKEQLRPSFLISSLRPSLTGAARL 360
QY 361 VETFLGSRPMGTPRRPLRPLRQVWOMRPLFELIGNNAOCPPYGLKTHGCLTAAYT 420
DB 361 VETFLGSRPMGTPRRPLRPLRQVWOMRPLFELIGNNAOCPPYGLKTHGCLTAAYT 420
QY 421 PAACVCAKREKQGSVAAPBEEDTDPRRLVOLLROHSSPMOYVGFVAACLRVLPGLMS 480
DB 421 PAACVCAKREKQGSVAAPBEEDTDPRRLVOLLROHSSPMOYVGFVAACLRVLPGLMS 480
QY 481 RHNERRLRLNTKRTISLGKAKLSLOELTWKMSYRDCAMLRSPGVCVAAHRLREEL 540
DB 481 RHNERRLRLNTKRTISLGKAKLSLOELTWKMSYRDCAMLRSPGVCVAAHRLREEL 540
QY 541 LAKELHMLMSYVVELRSFFVYVETTFQKNRLFFPYRPSWSKLSIGIQHLKRYOLRE 600
DB 541 LAKELHMLMSYVVELRSFFVYVETTFQKNRLFFPYRPSWSKLSIGIQHLKRYOLRE 600
QY 601 LSEAVEROHRERAPALLTSRLRFLPKDGLRPIVMDYVVGARTFRERKAERLTSRVA 660
DB 601 LSEAVEROHRERAPALLTSRLRFLPKDGLRPIVMDYVVGARTFRERKAERLTSRVA 660
QY 661 LFSVLYNERARRRPGLLASVGLDDIHRAMTFVLRAADPPPELIFVAVDTGADTI 720
DB 661 LFSVLYNERARRRPGLLASVGLDDIHRAMTFVLRAADPPPELIFVAVDTGADTI 720
QY 721 PODRLTEVIAIIRKONTVCYRRAVYVQKAHGHVRAKFSHVSTLTDLPYRQFVAHL 780
DB 721 PODRLTEVIAIIRKONTVCYRRAVYVQKAHGHVRAKFSHVSTLTDLPYRQFVAHL 780
QY 781 QETSPLEDAVITIESSSINEASSGLFDVPLRFPMCHNAVIRKGSYVOCOSIPQSIILSTL 840
DB 781 QETSPLEDAVITIESSSINEASSGLFDVPLRFPMCHNAVIRKGSYVOCOSIPQSIILSTL 840
QY 841 LCSLCYGDMEKRLFAGIRRDGILLRLVDDFLVTPHLTHAKFTLRLTVRGVPEYGVNL 900
DB 841 LCSLCYGDMEKRLFAGIRRDGILLRLVDDFLVTPHLTHAKFTLRLTVRGVPEYGVNL 900
QY 901 RKTIVNPFVDEALGGAFAVQMPAHGLPWCGLLIDRLTEVOSDYSSYARTSIRASLTF 960
DB 901 RKTIVNPFVDEALGGAFAVQMPAHGLPWCGLLIDRLTEVOSDYSSYARTSIRASLTF 960
QY 961 NRGFKAGNRMRKLFVILKCHSLFLDLQVNSLQTCNTNYKILLQAVRFHACVQLP 1020

DB 961 NRGFKAGNRMRKLFVILKCHSLFLDLQVNSLQTCNTNYKILLQAVRFHACVQLP 1020
QY 1021 FHQVWKNPTEFLRYISDTSALCYSLKAKNAGMSLGAKGAGPLPSBAVOMLCHQAFLL 1080
DB 1021 FHQVWKNPTEFLRYISDTSALCYSLKAKNAGMSLGAKGAGPLPSBAVOMLCHQAFLL 1080
QY 1081 KLTRHRVTVVPLGSLRFAQTOLSRKLPGLTTLTALEAANPALBSDFXTIID 1132
DB 1081 KLTRHRVTVVPLGSLRFAQTOLSRKLPGLTTLTALEAANPALBSDFXTIID 1132

RESULT 10
US-08-854-050-225
Sequence 225, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Linsner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Hartley, Calvin H.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854, 050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/851, 843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/846, 017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/844, 419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/724, 643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36, 429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 225:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-854-050-225
Query Match 99.8%; Score 5952; DB 3; Length 1132;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLSLRSHYREVLPLATFVRRLGPGNRLVQGDPAFRLVAQCLVCVPM 60
Db 1 MPAPRCRAVRSLSLRSHYREVLPLATFVRRLGPGNRLVQGDPAFRLVAQCLVCVPM 60

QY 61 DABPPAABSFRVSCLEKELVARVLOQLCEGAKVLAFGPALLGARGPPEAFTTSVR 120
Db 61 DABPPAABSFRVSCLEKELVARVLOQLCEGAKVLAFGPALLGARGPPEAFTTSVR 120

QY 121 SYLPNTVTDALRGSGAMGLLRRVGDVILWHILARCALFVLVAPSCAYQVCGPPLYOLGA 180
Db 121 SYLPNTVTDALRGSGAMGLLRRVGDVILWHILARCALFVLVAPSCAYQVCGPPLYOLGA 180

QY 181 ATGAPRPPHAGSGRRRLGGERAMNHSVRAGVPLGIPAGARRRGSGASRSLPLKRRR 240
Db 181 ATGAPRPPHAGSGRRRLGGERAMNHSVRAGVPLGIPAGARRRGSGASRSLPLKRRR 240

QY 241 GAAPERTPVGGGSAHSGRTGSPDRGFCVSPAPAEATSLGALSGTRHSPVG 300
Db 241 GAAPERTPVGGGSAHSGRTGSPDRGFCVSPAPAEATSLGALSGTRHSPVG 300

QY 301 RQHAGPSTSRPPRPWDTPCPPVYAEYHFLYSSGDKQLRPSRLSLSLTGARRL 360
Db 301 RQHAGPSTSRPPRPWDTPCPPVYAEYHFLYSSGDKQLRPSRLSLSLTGARRL 360

QY 361 VERIFGSRPMWGTERRLPRLPORWQMRPLFLELGNHACPYGLLTKTCPLRAVT 420
Db 361 VERIFGSRPMWGTERRLPRLPORWQMRPLFLELGNHACPYGLLTKTCPLRAVT 420

QY 421 PAAGVAREKPOGSAVAPEEDTDPRLVOLLROHSSPMQVYGFYACLRRLVPPGLMGS 480
Db 421 PAAGVAREKPOGSAVAPEEDTDPRLVOLLROHSSPMQVYGFYACLRRLVPPGLMGS 480

QY 481 RHNERPRLNTKFTSLGKHAKLSLOELTWKMSVDCALRRSPGVGCPAAEHRLREI 540
Db 481 RHNERPRLNTKFTSLGKHAKLSLOELTWKMSVDCALRRSPGVGCPAAEHRLREI 540

QY 541 LAKFLHMLSVYVVELLSRFYVTEETFPKXNLFYRPSVMSKLOSIGIRHLKEVORE 600
Db 541 LAKFLHMLSVYVVELLSRFYVTEETFPKXNLFYRPSVMSKLOSIGIRHLKEVORE 600

QY 601 LSAEVRQREARPAALITSLRFLIPKQDLRPIVNMDDYVGAARTRRERARLRSRYKA 660
Db 601 LSAEVRQREARPAALITSLRFLIPKQDLRPIVNMDDYVGAARTRRERARLRSRYKA 660

QY 661 LFSVLNERARRPGLIGASVGLGDDIHRAMRTFVLVRADPPPELYFKVDVTGAYDTI 720
Db 661 LFSVLNERARRPGLIGASVGLGDDIHRAMRTFVLVRADPPPELYFKVDVTGAYDTI 720

QY 721 PODRLTEVIASIIKPNNTYCVRRYAVVOCAHGHVAKAFKSHVSTLTDLOPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKPNNTYCVRRYAVVOCAHGHVAKAFKSHVSTLTDLOPYMRQFVAHL 780

QY 781 QERTSPRDAVVIQOSSSLNEASSGLFDVFLRFMCHAAVIRKSGSVOCOGIPQSSILSTL 840
Db 781 QERTSPRDAVVIQOSSSLNEASSGLFDVFLRFMCHAAVIRKSGSVOCOGIPQSSILSTL 840

QY 841 LCSLCYGDWENKLFAGIRRDGLLRLVDDFLLVTPHLLTHAKFTLRTLVAGVEYCVNVL 900
Db 841 LCSLCYGDWENKLFAGIRRDGLLRLVDDFLLVTPHLLTHAKFTLRTLVAGVEYCVNVL 900

QY 901 RKTUVNFPVEDALGTAFCVMPAHGLPWCGLLIDTTLTAVQSSYASRTSRASTF 960
Db 901 RKTUVNFPVEDALGTAFCVMPAHGLPWCGLLIDTTLTAVQSSYASRTSRASTF 960

QY 961 NNGFKAGNRMRRLFGVILRLKCHSLFLDQVNSLQTVCTNIYKILLQAYEFHACVLDLP 1020
Db 961 NNGFKAGNRMRRLFGVILRLKCHSLFLDQVNSLQTVCTNIYKILLQAYEFHACVLDLP 1020

QY 1021 FHQGVKNPTFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVOMLCHQAFLL 1080
Db 1021 FHQGVKNPTFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVOMLCHQAFLL 1080

Db 1021 FHQGVKNPTFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVOMLCHQAFLL 1080
QY 1081 KLTRHRTYVPLIGSLRTAQTOLSRKLPGLTTLALBAANPALPSPFKITLD 1132
Db 1081 KLTRHRTYVPLIGSLRTAQTOLSRKLPGLTTLALBAANPALPSPFKITLD 1132

RESULT 11
US-09-430-323-225
Sequence 225; Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 225:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 225:
US-09-430-323-225

Query Match 99.8%; Score 5952; DB 3; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLSLRSHYREVLPLATFVRRLGPGNRLVQGDPAFRLVAQCLVCVPM 60
Db 1 MPAPRCRAVRSLSLRSHYREVLPLATFVRRLGPGNRLVQGDPAFRLVAQCLVCVPM 60

QY 61 DABPPAABSFRVSCLEKELVARVLOQLCEGAKVLAFGPALLGARGPPEAFTTSVR 120

```

Db 61 DABPPAPAPFRQVSCLELVARVLQRLCERGAKNVLAFFGALLDAGRGPPAFTTSVR 120
Qy 121 SYLPTNTDALARSGAMGLLRVGGDVVHLLARCALFVLVAPSCAYQVCGPPLYQOLA 180
Db 121 SYLPTNTDALARSGAMGLLRVGGDVVHLLARCALFVLVAPSCAYQVCGPPLYQOLA 180
Qy 181 ATQARPPHASPGRRLCERAMNHSVREAGVPLGLPAPGARRGGSASRLPLPRPRR 240
Db 181 ATQARPPHASPGRRLCERAMNHSVREAGVPLGLPAPGARRGGSASRLPLPRPRR 240
Qy 241 GAAPPERTVPGQGSNAHPGRTGSDRGFCVSPAPPAEATSLGALSSTHSPSVG 300
Db 241 GAAPPERTVPGQGSNAHPGRTGSDRGFCVSPAPPAEATSLGALSSTHSPSVG 300
Qy 301 ROHHAQPPSTSRPPRMDTPCPRVYATKHFLLYSSGDEQLRSPFLSLRPSLTGARRL 360
Db 301 ROHHAQPPSTSRPPRMDTPCPRVYATKHFLLYSSGDEQLRSPFLSLRPSLTGARRL 360
Qy 361 VETIFLGSPPMGTGPRRLPLRPLQRYQWRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSPPMGTGPRRLPLRPLQRYQWRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVOLLRQSSPMQVYGFVACLRRLVPPGLMGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVOLLRQSSPMQVYGFVACLRRLVPPGLMGS 480
Qy 481 RHERRRLRMTKFTSLGKHAKTSLQELTWMSVDCAMLRSPGVCAVPAEHRREET 540
Db 481 RHERRRLRMTKFTSLGKHAKTSLQELTWMSVDCAMLRSPGVCAVPAEHRREET 540
Qy 541 LAKFLHMSVYVVELLSFFVYETETFOQNRLEFYKSWSKLOSGIRQHLKRYOLEB 600
Db 541 LAKFLHMSVYVVELLSFFVYETETFOQNRLEFYKSWSKLOSGIRQHLKRYOLEB 600
Qy 601 LSEAEVQHEARPAITSLRFLPKPDGLRPIYNDVYVVGASTPREKRAEELTSTRYKA 660
Db 601 LSEAEVQHEARPAITSLRFLPKPDGLRPIYNDVYVVGASTPREKRAEELTSTRYKA 660
Qy 661 LFSVLNERARBPGLIGASVLDGDIHRAMRTFVLRAADPPEELFYFVADVTGAYDTI 720
Db 661 LFSVLNERARBPGLIGASVLDGDIHRAMRTFVLRAADPPEELFYFVADVTGAYDTI 720
Qy 721 POBLTEVIASTIKPONTYCCRRYAAVQKAAHGVRAEFKSHYSTLTDLOPYRKQVAHL 780
Db 721 POBLTEVIASTIKPONTYCCRRYAAVQKAAHGVRAEFKSHYSTLTDLOPYRKQVAHL 780
Qy 781 QETSPLDAAVIEGSSSLNEASSGLFDVFLRFMCHNAVRIRGKSYYQCGQIPGGSILSTL 840
Db 781 QETSPLDAAVIEGSSSLNEASSGLFDVFLRFMCHNAVRIRGKSYYQCGQIPGGSILSTL 840
Qy 841 LCSTCYGDMENKLFAGIRRDGGLRLVYDVLVPHLTHAKTLRLTVRGVBEYCVANL 900
Db 841 LCSTCYGDMENKLFAGIRRDGGLRLVYDVLVPHLTHAKTLRLTVRGVBEYCVANL 900
Qy 901 RKTAVNPEVDEALGTAFAVQMPAHGLFPMCGLLDTRTLEVOSSDYSSVARTSIRASVF 960
Db 901 RKTAVNPEVDEALGTAFAVQMPAHGLFPMCGLLDTRTLEVOSSDYSSVARTSIRASVF 960
Qy 961 NRGFKAGRNMRKLFVLRKCHSLFLDLQVNSIQVCTNIYKILLIQAVRPAACVQLP 1020
Db 961 NRGFKAGRNMRKLFVLRKCHSLFLDLQVNSIQVCTNIYKILLIQAVRPAACVQLP 1020
Qy 1021 FHOQVKNPTEFLVISTDASLCYSILKAKNAGSLAKAKAGPLBEAOWMCHQAFLL 1080
Db 1021 FHOQVKNPTEFLVISTDASLCYSILKAKNAGSLAKAKAGPLBEAOWMCHQAFLL 1080
Qy 1081 KLTHRYTYVPLIGSLRTAQTOLSRKLGTTLTALBAANPALPSDEKTLID 1132
Db 1081 KLTHRYTYVPLIGSLRTAQTOLSRKLGTTLTALBAANPALPSDEKTLID 1132
RESULT 12

```

```

US-09-128-354-2
Sequence 2, Application US/09128354
Patent No. 6337200
GENERAL INFORMATION:
APPLICANT: Morin, Gregg B.
APPLICANT: Genon Corporation
TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
FILE REFERENCE: 015389-00310US
CURRENT APPLICATION NUMBER: US/09/128.354
EARLIER FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 08/851.843
EARLIER FILING DATE: 1997-05-06
EARLIER APPLICATION NUMBER: US 08/854.050
EARLIER FILING DATE: 1997-05-09
EARLIER APPLICATION NUMBER: US 08/911.312
EARLIER FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: US 08/912.951
EARLIER FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: US 08/915.503
EARLIER FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: WO PCT/US97/17618
EARLIER FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: WO PCT/US97/17618
EARLIER FILING DATE: 1997-10-01
EARLIER APPLICATION NUMBER: WO PCT/US97/17885
EARLIER FILING DATE: 1997-10-01
EARLIER APPLICATION NUMBER: US 08/974.549
EARLIER FILING DATE: 1997-11-19
EARLIER APPLICATION NUMBER: US 08/974.584
EARLIER FILING DATE: 1997-11-19
EARLIER APPLICATION NUMBER: US 09/052.864
EARLIER FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1132
TYPE: PRN
ORGANISM: Homo sapiens
US-09-128-354-2

Query Match 99.8%; Score 5952; DB 3; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPBARCRAVSLNLSHYREVLPLATFVRRLGPOQMRVLOSADPAFALVAOCIVCPW 60
Db 1 MPBARCRAVSLNLSHYREVLPLATFVRRLGPOQMRVLOSADPAFALVAOCIVCPW 60
Qy 61 DABPPAPAPFRQVSCLELVARVLQRLCERGAKNVLAFFGALLDAGRGPPAFTTSVR 120
Db 61 DABPPAPAPFRQVSCLELVARVLQRLCERGAKNVLAFFGALLDAGRGPPAFTTSVR 120
Qy 121 SYLPTNTDALARSGAMGLLRVGGDVVHLLARCALFVLVAPSCAYQVCGPPLYQOLA 180
Db 121 SYLPTNTDALARSGAMGLLRVGGDVVHLLARCALFVLVAPSCAYQVCGPPLYQOLA 180
Qy 181 ATQARPPHASPGRRLCERAMNHSVREAGVPLGLPAPGARRGGSASRLPLPRPRR 240
Db 181 ATQARPPHASPGRRLCERAMNHSVREAGVPLGLPAPGARRGGSASRLPLPRPRR 240
Qy 241 GAAPPERTVPGQGSNAHPGRTGSDRGFCVSPAPPAEATSLGALSSTHSPSVG 300
Db 241 GAAPPERTVPGQGSNAHPGRTGSDRGFCVSPAPPAEATSLGALSSTHSPSVG 300
Qy 301 ROHHAQPPSTSRPPRMDTPCPRVYATKHFLLYSSGDEQLRSPFLSLRPSLTGARRL 360
Db 301 ROHHAQPPSTSRPPRMDTPCPRVYATKHFLLYSSGDEQLRSPFLSLRPSLTGARRL 360
Qy 361 VETIFLGSPPMGTGPRRLPLRPLQRYQWRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSPPMGTGPRRLPLRPLQRYQWRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVOLLRQSSPMQVYGFVACLRRLVPPGLMGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVOLLRQSSPMQVYGFVACLRRLVPPGLMGS 480

```

QY 481 RHNERFLLNTKKTSLGKHALSLQELTWKMSVDCAMLRSPGVCPAAEHLREBI 540
DB 481 RHNERFLLNTKKTSLGKHALSLQELTWKMSVDCAMLRSPGVCPAAEHLREBI 540
QY 541 LAKFLHMLSVYVVELLRSEFFVYETETFOKNRLFYRPSVSKLOSIGRHLKRVQRE 600
DB 541 LAKFLHMLSVYVVELLRSEFFVYETETFOKNRLFYRPSVSKLOSIGRHLKRVQRE 600
QY 601 LSEAEVRQREARPAALITSLRLRFIPKPDGLRPIVMNDYVVGARTREKRAELTSRYKA 660
DB 601 LSEAEVRQREARPAALITSLRLRFIPKPDGLRPIVMNDYVVGARTREKRAELTSRYKA 660
QY 661 LFSVLNTERARPPGLIGASVLTGLDIDHRAMRTFVLVRADPPPELYFYKVDVTGAYDTI 720
DB 661 LFSVLNTERARPPGLIGASVLTGLDIDHRAMRTFVLVRADPPPELYFYKVDVTGAYDTI 720
QY 721 PODRLTEVIASTIKPONTYCVRRYAVVQKAHGHVAKAFKSHVSTLTDLOPYMRQFVAHL 780
DB 721 PODRLTEVIASTIKPONTYCVRRYAVVQKAHGHVAKAFKSHVSTLTDLOPYMRQFVAHL 780
QY 781 QETSPRDAVAVIEQSSSLNEASSGLFDVFLRFMCHAVIRGKSYVOCQGPQGSILSTL 840
DB 781 QETSPRDAVAVIEQSSSLNEASSGLFDVFLRFMCHAVIRGKSYVOCQGPQGSILSTL 840
QY 841 LLSLCYGDMMENKLFAGIRRDGLLRVDDFLLVTPHLLTHAKTFLRTLVRGVPEYGVVNL 900
DB 841 LLSLCYGDMMENKLFAGIRRDGLLRVDDFLLVTPHLLTHAKTFLRTLVRGVPEYGVVNL 900
QY 901 RKTIVNFPVEDALGATAVQMPAHGLFPWCGILLDTPTLEVOSSYASTSTIRASTF 960
DB 901 RKTIVNFPVEDALGATAVQMPAHGLFPWCGILLDTPTLEVOSSYASTSTIRASTF 960
QY 961 NRGFKAGRMRRRLFGVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYEFHACVLOLP 1020
DB 961 NRGFKAGRMRRRLFGVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYEFHACVLOLP 1020
QY 1021 FHQQWKNPTFFLRVISTDASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080
DB 1021 FHQQWKNPTFFLRVISTDASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080
QY 1081 KLTRHRTVTVPLIGSLRTAQOTLSRKLPGTTTLTALEAANPALPSPDFTIID 1132
DB 1081 KLTRHRTVTVPLIGSLRTAQOTLSRKLPGTTTLTALEAANPALPSPDFTIID 1132

RESULT 13
US-09-675-321-2
; Sequence 2, Application US/09675321
; Patent No. 6440735
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
; FILE REFERENCE: 015389-003500PC
; CURRENT APPLICATION NUMBER: US/09/675,321
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/112,006
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-675-321-2

Query Match 99.8%; Score 5952; DB 4; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAPCRARSLLRSHYREVLPLATFVRRLGQGWRLVORGDPAAFRALVQCLVCPM 60
DB 1 MPRAPCRARSLLRSHYREVLPLATFVRRLGQGWRLVORGDPAAFRALVQCLVCPM 60
QY 61 DARPAPAPSPROVSCIKELVAEVLQRLCERGANVLAEGFALLDGAAGPPEAFTTSVR 120
DB 61 DARPAPAPSPROVSCIKELVAEVLQRLCERGANVLAEGFALLDGAAGPPEAFTTSVR 120
QY 121 SYLPNTYTDLRSSGAMGLLRVSDVYVHLARCALVYVAPSCAYOCGPPLVQLA 180
DB 121 SYLPNTYTDLRSSGAMGLLRVSDVYVHLARCALVYVAPSCAYOCGPPLVQLA 180
QY 181 ATOARPPHAGSPRRRLGCERAMNHSVREAGVLTGLPAFGARRGGASRSPLPRPBR 240
DB 181 ATOARPPHAGSPRRRLGCERAMNHSVREAGVLTGLPAFGARRGGASRSPLPRPBR 240
QY 241 GAAPBEPRTVVGQSWAPRGRTGSDRGFCVSPARPBEATSLGALSGTRHSPSVG 300
DB 241 GAAPBEPRTVVGQSWAPRGRTGSDRGFCVSPARPBEATSLGALSGTRHSPSVG 300
QY 301 ROHHAGPSTSPRPMPDTCPPVYAEYKHFLYSSGDKQLRPSFLSLSLTGARL 360
DB 301 ROHHAGPSTSPRPMPDTCPPVYAEYKHFLYSSGDKQLRPSFLSLSLTGARL 360
QY 361 VETIFLGSRPMBDGTBRRLPLRQRYWQRPFLLELLGNHAOCPYGLLKHCPLEBAVT 420
DB 361 VETIFLGSRPMBDGTBRRLPLRQRYWQRPFLLELLGNHAOCPYGLLKHCPLEBAVT 420
QY 421 PAAGVCAKREKQGSVAAPBEBDTPRRLVOLLROHSPQOVYGFAPACRLRPLPGMKS 480
DB 421 PAAGVCAKREKQGSVAAPBEBDTPRRLVOLLROHSPQOVYGFAPACRLRPLPGMKS 480
QY 481 RHNERFLLNTKKTSLGKHALSLQELTWKMSVDCAMLRSPGVCPAAEHLREBI 540
DB 481 RHNERFLLNTKKTSLGKHALSLQELTWKMSVDCAMLRSPGVCPAAEHLREBI 540
QY 541 LAKFLHMLSVYVVELLRSEFFVYETETFOKNRLFYRPSVSKLOSIGRHLKRVQRE 600
DB 541 LAKFLHMLSVYVVELLRSEFFVYETETFOKNRLFYRPSVSKLOSIGRHLKRVQRE 600
QY 601 LSEAEVRQREARPAALITSLRLRFIPKPDGLRPIVMNDYVVGARTREKRAELTSRYKA 660
DB 601 LSEAEVRQREARPAALITSLRLRFIPKPDGLRPIVMNDYVVGARTREKRAELTSRYKA 660
QY 661 LFSVLNTERARPPGLIGASVLTGLDIDHRAMRTFVLVRADPPPELYFYKVDVTGAYDTI 720
DB 661 LFSVLNTERARPPGLIGASVLTGLDIDHRAMRTFVLVRADPPPELYFYKVDVTGAYDTI 720
QY 721 PODRLTEVIASTIKPONTYCVRRYAVVQKAHGHVAKAFKSHVSTLTDLOPYMRQFVAHL 780
DB 721 PODRLTEVIASTIKPONTYCVRRYAVVQKAHGHVAKAFKSHVSTLTDLOPYMRQFVAHL 780
QY 781 QETSPRDAVAVIEQSSSLNEASSGLFDVFLRFMCHAVIRGKSYVOCQGPQGSILSTL 840
DB 781 QETSPRDAVAVIEQSSSLNEASSGLFDVFLRFMCHAVIRGKSYVOCQGPQGSILSTL 840
QY 841 LLSLCYGDMMENKLFAGIRRDGLLRVDDFLLVTPHLLTHAKTFLRTLVRGVPEYGVVNL 900
DB 841 LLSLCYGDMMENKLFAGIRRDGLLRVDDFLLVTPHLLTHAKTFLRTLVRGVPEYGVVNL 900
QY 901 RKTIVNFPVEDALGATAVQMPAHGLFPWCGILLDTPTLEVOSSYASTSTIRASTF 960
DB 901 RKTIVNFPVEDALGATAVQMPAHGLFPWCGILLDTPTLEVOSSYASTSTIRASTF 960
QY 961 NRGFKAGRMRRRLFGVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYEFHACVLOLP 1020
DB 961 NRGFKAGRMRRRLFGVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYEFHACVLOLP 1020
QY 1021 FHQQWKNPTFFLRVISTDASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080
DB 1021 FHQQWKNPTFFLRVISTDASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080

QY 1081 KLTRHRTVYVLLGSLRTAQTQJ:SRKLPSTTLTALBAAANPALPSPDKTILD 1132
 Db 1081 KLTRHRTVYVLLGSLRTAQTQJ:SRKLPSTTLTALBAAANPALPSPDKTILD 1132

RESULT 14

US-09-052-919-2

Sequence 2, Application US/9052919

Patent No. 6444650

GENERAL INFORMATION:

APPLICANT: Cecch, Thomas R.

APPLICANT: Lingner, Joachim

APPLICANT: Nakamura, Toru

APPLICANT: Chapman, Karen B.

APPLICANT: Morin, Gregg B.

APPLICANT: Harley, Calvin B.

APPLICANT: Andrews, William H.

TITLE OF INVENTION: Antisense Compositions for Detecting and

TITLE OF INVENTION: Inhibiting Telomerase Reverse Transcriptase

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/052,919

FILING DATE: 31-MAR-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/974,549

FILING DATE: 19-NOV-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/974,584

FILING DATE: 19-NOV-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

PRIOR APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:

NAME: Parent, Annette S.
 REGISTRATION NUMBER: 42,058
 REFERENCE/DOCKET NUMBER: 015389-003600US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1132 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-052-919-2

Query Match 99.8%; Score 5952; DB 4; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPBARCAVYVSLRSHYREVLPATFVRRRPGQWRLVORGDPAAPALVAOCLVCPW 60
 Db 1 MPBARCAVYVSLRSHYREVLPATFVRRRPGQWRLVORGDPAAPALVAOCLVCPW 60
 QY 61 DARPPAPSFROYSCLELVARVLOLCERGANVLAFGALLDARGGPEAFTTSVR 120
 Db 61 DARPPAPSFROYSCLELVARVLOLCERGANVLAFGALLDARGGPEAFTTSVR 120
 QY 121 SYLPNTVTDALRGSGAWGLLRVGGDVLVHLLARCALFVTVARSCAYVCGPPLVQUGA 180
 Db 121 SYLPNTVTDALRGSGAWGLLRVGGDVLVHLLARCALFVTVARSCAYVCGPPLVQUGA 180
 QY 121 SYLPNTVTDALRGSGAWGLLRVGGDVLVHLLARCALFVTVARSCAYVCGPPLVQUGA 180
 Db 121 SYLPNTVTDALRGSGAWGLLRVGGDVLVHLLARCALFVTVARSCAYVCGPPLVQUGA 180
 QY 181 ATQARPPHAGSPRRRLCERAMNHSVEAGVPLGPAPGARSGASRSRLPKRPRR 240
 Db 181 ATQARPPHAGSPRRRLCERAMNHSVEAGVPLGPAPGARSGASRSRLPKRPRR 240
 QY 181 ATQARPPHAGSPRRRLCERAMNHSVEAGVPLGPAPGARSGASRSRLPKRPRR 240
 Db 181 ATQARPPHAGSPRRRLCERAMNHSVEAGVPLGPAPGARSGASRSRLPKRPRR 240
 QY 241 GAAPPERTPVGGGSAHPGSTRGSDRGFCVSPAPAEATSLLEGALSTRTSHSPVG 300
 Db 241 GAAPPERTPVGGGSAHPGSTRGSDRGFCVSPAPAEATSLLEGALSTRTSHSPVG 300
 QY 301 ROHAGPSTSRPPPMPTPCPPVYAEKTHFLYSGDGEOLRPSFLSLRPSLTGARL 360
 Db 301 ROHAGPSTSRPPPMPTPCPPVYAEKTHFLYSGDGEOLRPSFLSLRPSLTGARL 360
 QY 301 ROHAGPSTSRPPPMPTPCPPVYAEKTHFLYSGDGEOLRPSFLSLRPSLTGARL 360
 Db 301 ROHAGPSTSRPPPMPTPCPPVYAEKTHFLYSGDGEOLRPSFLSLRPSLTGARL 360
 QY 361 VETIFLGRPMWPGTPRRLPRLPQRYWQMRPLFELLGNHACCPGYLLKTHCPRAAVT 420
 Db 361 VETIFLGRPMWPGTPRRLPRLPQRYWQMRPLFELLGNHACCPGYLLKTHCPRAAVT 420
 QY 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLRQSSSWQYGVFRACLRRLVPGGLMS 480
 Db 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLRQSSSWQYGVFRACLRRLVPGGLMS 480
 QY 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLRQSSSWQYGVFRACLRRLVPGGLMS 480
 Db 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLRQSSSWQYGVFRACLRRLVPGGLMS 480
 QY 481 RHNERFLRNTKFKFISLGHAKLSLOELTWKASVDCAMLRSPGVGCVPAEARELRREI 540
 Db 481 RHNERFLRNTKFKFISLGHAKLSLOELTWKASVDCAMLRSPGVGCVPAEARELRREI 540
 QY 541 LAKFLHMTMSVYVVELLSFFVYETTFQKRLLPFRYSVWSKOSIGIRQHLKRVQURE 600
 Db 541 LAKFLHMTMSVYVVELLSFFVYETTFQKRLLPFRYSVWSKOSIGIRQHLKRVQURE 600
 QY 541 LAKFLHMTMSVYVVELLSFFVYETTFQKRLLPFRYSVWSKOSIGIRQHLKRVQURE 600
 Db 541 LAKFLHMTMSVYVVELLSFFVYETTFQKRLLPFRYSVWSKOSIGIRQHLKRVQURE 600
 QY 601 LSEAVERQHREARPPALTSRLRFLPKPGGLRPIVMDVYVAGARTFRERKARELRITSRYKA 660
 Db 601 LSEAVERQHREARPPALTSRLRFLPKPGGLRPIVMDVYVAGARTFRERKARELRITSRYKA 660
 QY 601 LSEAVERQHREARPPALTSRLRFLPKPGGLRPIVMDVYVAGARTFRERKARELRITSRYKA 660
 Db 601 LSEAVERQHREARPPALTSRLRFLPKPGGLRPIVMDVYVAGARTFRERKARELRITSRYKA 660
 QY 661 LFSVINYERRARRPGLLGASVIGLDDIRHAWTFVLRVAQDPPEPLRYKVDVTGAYDTI 720
 Db 661 LFSVINYERRARRPGLLGASVIGLDDIRHAWTFVLRVAQDPPEPLRYKVDVTGAYDTI 720
 QY 721 PODRLTEVIASIKQNTYCVRRYAVVQKAHGHVKAFFKSHVSTLTLDQYMRQFVHL 780
 Db 721 PODRLTEVIASIKQNTYCVRRYAVVQKAHGHVKAFFKSHVSTLTLDQYMRQFVHL 780
 QY 721 PODRLTEVIASIKQNTYCVRRYAVVQKAHGHVKAFFKSHVSTLTLDQYMRQFVHL 780
 Db 721 PODRLTEVIASIKQNTYCVRRYAVVQKAHGHVKAFFKSHVSTLTLDQYMRQFVHL 780
 QY 781 QETSPLRDAVYIEQSSSLNEASGLFDFVLRPMCHAVRIKSGSYVQCGI:PGGIIISTL 840
 Db 781 QETSPLRDAVYIEQSSSLNEASGLFDFVLRPMCHAVRIKSGSYVQCGI:PGGIIISTL 840

QY 841 LGLCYGDMENKLFAGIRDDGLLLRLVDDFLLVTHLTHAKTFLTLVRCVPEYCVNL 900
DB 841 LGLCYGDMENKLFAGIRDDGLLLRLVDDFLLVTHLTHAKTFLTLVRCVPEYCVNL 900
QY 901 KTVVNFPEEDALGTAIVQMPAHGLPFGWGLLDPTRELVQSYSSYARTSIRASTF 960
DB 901 KTVVNFPEEDALGTAIVQMPAHGLPFGWGLLDPTRELVQSYSSYARTSIRASTF 960
QY 961 NRGFKAGNMRRKLFGLVRLKCHSLFDLDQVNSLQTVCTNIVKILLQAYRFAVCVGLP 1020
DB 961 NRGFKAGNMRRKLFGLVRLKCHSLFDLDQVNSLQTVCTNIVKILLQAYRFAVCVGLP 1020
QY 1021 FHQOVKNGNFFFLRYVSDTASLCSYLKAKXAGSLGKAGAPLPSAVOMLCHQAFLL 1080
DB 1021 FHQOVKNGNFFFLRYVSDTASLCSYLKAKXAGSLGKAGAPLPSAVOMLCHQAFLL 1080
QY 1081 KLTRHRYVPLGLSLRTAQTQLSRKLPGTTLTALAANPALPSPDFITLD 1132
DB 1081 KLTRHRYVPLGLSLRTAQTQLSRKLPGTTLTALAANPALPSPDFITLD 1132

RESULT 15
US-08-912-951-2
Sequence 2, Application US/08912951
Patent No. 6475789
GENERAL INFORMATION:
APPLICANT: Caech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
TITLE OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ. ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-951-2

Query Match 99.8%; Score 5952; DB 4; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLRSHYREVLPATFVRLPQGWRLVQRGDPAAFRLVAQCLVCPM 60
DB 1 MPAPRCRAVRSLLRSHYREVLPATFVRLPQGWRLVQRGDPAAFRLVAQCLVCPM 60
QY 61 DAPPPAABSFROVSCLELVAVYVLCERGAKNVLAFGPALLDARGGPEAFTTSVR 120
DB 61 DAPPPAABSFROVSCLELVAVYVLCERGAKNVLAFGPALLDARGGPEAFTTSVR 120
QY 121 SYLPNTVDALRGSGAMGILLRVEDVYLHLARCALFVLAPSCAVOCPPHYOLGA 180
DB 121 SYLPNTVDALRGSGAMGILLRVEDVYLHLARCALFVLAPSCAVOCPPHYOLGA 180
QY 181 ATQARPFPASGRRRLGGERAMNHSVREAGVPLGIPAGARRGGASASRLPLKPRRR 240
DB 181 ATQARPFPASGRRRLGGERAMNHSVREAGVPLGIPAGARRGGASASRLPLKPRRR 240
QY 241 GAAPPEERTPVQGSAAHGRTRGPDRCFCVSPAPRPEETSLEALSGRRHSPVG 300
DB 241 GAAPPEERTPVQGSAAHGRTRGPDRCFCVSPAPRPEETSLEALSGRRHSPVG 300
QY 301 RQHAGPSTSPRRPMDTCCPVYAETGHPYSSODKQLRPSFLSLRPSLTGARRL 360
DB 301 RQHAGPSTSPRRPMDTCCPVYAETGHPYSSODKQLRPSFLSLRPSLTGARRL 360
QY 361 VETIFGSRPMWGTFRRLPLPORYWQRPPLFELIGNHAOCPPVYLKTCPRPAVT 420
DB 361 VETIFGSRPMWGTFRRLPLPORYWQRPPLFELIGNHAOCPPVYLKTCPRPAVT 420
QY 421 PAAGVCAKPKQGSVAAPREEDTDPRLVQLRQHSPPQVGYFRACTRLVPPGLMGS 480
DB 421 PAAGVCAKPKQGSVAAPREEDTDPRLVQLRQHSPPQVGYFRACTRLVPPGLMGS 480
QY 481 RANRRPLNTKFKISLGGAKLSLOELTWKNSVDCAMLRSPGVGCYPAAEHRLREBI 540
DB 481 RANRRPLNTKFKISLGGAKLSLOELTWKNSVDCAMLRSPGVGCYPAAEHRLREBI 540
QY 541 LAKEFLWMSVYVVELRSPFVVTETTPQKNLFFRPSVMSKLSIGIRQHLKRVOLRE 600
DB 541 LAKEFLWMSVYVVELRSPFVVTETTPQKNLFFRPSVMSKLSIGIRQHLKRVOLRE 600
QY 601 LSEAEVQREARPAALTSRLRFIPKPDGLRPIVMNDYVVGARTFRREKARLTSRYKA 660
DB 601 LSEAEVQREARPAALTSRLRFIPKPDGLRPIVMNDYVVGARTFRREKARLTSRYKA 660
QY 661 LPSVLYNERARRPGLLGASVLDIDIRAWRFFVLRVRAQDDPPLVFYKXVDTAYDTI 720
DB 661 LPSVLYNERARRPGLLGASVLDIDIRAWRFFVLRVRAQDDPPLVFYKXVDTAYDTI 720
QY 721 PODRLTEVLAIIKPPNTYCVARYAVVQKAAGHAKFKASHVSTLTDLPYMRQFVAHL 780
DB 721 PODRLTEVLAIIKPPNTYCVARYAVVQKAAGHAKFKASHVSTLTDLPYMRQFVAHL 780
QY 781 QETSPLRDAVITEOSSSLEASSGLFDVFLRVCYCHAVIRKSYVCCGIPQSSILSTL 840

Db 781 QETSPRLDAVIVEQSSSLNEASSGLFDVFLRFMCHHAVIRIGSKSYVCCGIGPQSGILSTL 840
QY 841 LGLSLGDMENKLFAGIRRDGLLLRLVDDDLVTPHITAKTTLRLVNGVPEYGCNVNL 900
Db 841 LGLSLGDMENKLFAGIRRDGLLLRLVDDDLVTPHITAKTTLRLVNGVPEYGCNVNL 900
QY 901 RKTIVNPFVDEALGTAFAVQMPAHGLFPMCGLLDTRTEVQSDYSVARTIRASVTF 960
Db 901 RKTIVNPFVDEALGTAFAVQMPAHGLFPMCGLLDTRTEVQSDYSVARTIRASVTF 960
QY 961 NRGFKAGRNRRKLFVGLRLKCHSLFLDLQVNSLQVCTNIVKILLQAVRPAVQLQIP 1020
Db 961 NRGFKAGRNRRKLFVGLRLKCHSLFLDLQVNSLQVCTNIVKILLQAVRPAVQLQIP 1020
QY 1021 FHOQWKNPTEFLRVISDTASLCYSILKAKNAGMSLGAKGAPLPSEAVQMLCHQAFIL 1080
Db 1021 FHOQWKNPTEFLRVISDTASLCYSILKAKNAGMSLGAKGAPLPSEAVQMLCHQAFIL 1080
QY 1081 KLTRHRVTVPLLSLRTAQTLQSRKLPCTTLTALLEANPALPSPDKTILD 1132
Db 1081 KLTRHRVTVPLLSLRTAQTLQSRKLPCTTLTALLEANPALPSPDKTILD 1132

RESULT 16

US-09-402-181B-2
Sequence 2, Application US/09402181B
Patent No. 6610839

GENERAL INFORMATION:

APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 633

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
City: San Francisco
STATE: California
COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/402,181B

FILING DATE: 29-Sep-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:

NAME: Ausehus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 013389-0026200S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-402-181B-2

Query Match 99.8%; Score 5952; DB 4; Length 1132;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPARPCRAVRSILRSHRYEVLPLATEFVRRLGPQGMRLVQGDPAFAFALVAQCLVCPW 60
Db 1 MPARPCRAVRSILRSHRYEVLPLATEFVRRLGPQGMRLVQGDPAFAFALVAQCLVCPW 60
QY 61 DARPPAAPSTROYSCLEKELVAVYLQRLCERGANVLAFGFALLDGRGSPPEAFTTSVR 120
Db 61 DARPPAAPSTROYSCLEKELVAVYLQRLCERGANVLAFGFALLDGRGSPPEAFTTSVR 120
QY 121 SYLPNTVTDALRGSGAMGLLRVYGDVYLVAHLARCALFVLVAPSCAVQVGGPFLYQOLA 180
Db 121 SYLPNTVTDALRGSGAMGLLRVYGDVYLVAHLARCALFVLVAPSCAVQVGGPFLYQOLA 180
QY 181 ATQARPPHAGSPRRRLCERANMNSVREAGVPLGLPAPGARRRGASASRLPLPKSPRR 240
Db 181 ATQARPPHAGSPRRRLCERANMNSVREAGVPLGLPAPGARRRGASASRLPLPKSPRR 240
QY 241 GAAPPERTPVQGGSMAPGRTGRSDRGFCVSPAPAEATSLGALSTGRSHSVG 300
Db 241 GAAPPERTPVQGGSMAPGRTGRSDRGFCVSPAPAEATSLGALSTGRSHSVG 300
QY 301 RQHNAGPSTSRPRPMDTPCPVYAEIKHFLYSSGDKEQLRPSFLSSLPSTLGARL 360
Db 301 RQHNAGPSTSRPRPMDTPCPVYAEIKHFLYSSGDKEQLRPSFLSSLPSTLGARL 360
QY 361 VETITLSRPPMPTGTPRLPLPQRYWOMRPLFELLGNHACQCYVYLKTHCGLRAVLT 420
Db 361 VETITLSRPPMPTGTPRLPLPQRYWOMRPLFELLGNHACQCYVYLKTHCGLRAVLT 420
QY 421 PAAGCAHEKPOGSAABEEDTPRRVLQRLRQSSWQYGVFVACRLRVPPGLMGS 480
Db 421 PAAGCAHEKPOGSAABEEDTPRRVLQRLRQSSWQYGVFVACRLRVPPGLMGS 480
QY 481 RHNERFLRNTKKTISLQKHAHLSLQELTWKMSYVDCAMLRSPGVGCVPAEHRLEBEI 540
Db 481 RHNERFLRNTKKTISLQKHAHLSLQELTWKMSYVDCAMLRSPGVGCVPAEHRLEBEI 540
QY 541 LAKFLHMLMSYVVEILASFFVYMETTFQKRLTFEYSPVSKXLSIGIRHLRVOYRE 600
Db 541 LAKFLHMLMSYVVEILASFFVYMETTFQKRLTFEYSPVSKXLSIGIRHLRVOYRE 600
QY 601 LSEAEVRQREARPALTLRLFTPKPDGLAPVNMVYVGARTFRREKRAERLTSRYKA 660
Db 601 LSEAEVRQREARPALTLRLFTPKPDGLAPVNMVYVGARTFRREKRAERLTSRYKA 660
QY 661 LFSVINYRARRPGLGASVGLDDIRAWMTFTLRRRAQDPPPELTVKXDVYGAVYTI 720
Db 661 LFSVINYRARRPGLGASVGLDDIRAWMTFTLRRRAQDPPPELTVKXDVYGAVYTI 720
QY 721 PODRLTEVIASIIKIPONTYCVRYAVVOKAAGHVRKAFKSHVSTLTDLPQYMGQVAHL 780
Db 721 PODRLTEVIASIIKIPONTYCVRYAVVOKAAGHVRKAFKSHVSTLTDLPQYMGQVAHL 780
QY 781 QETSPRLDAVIVEQSSSLNEASSGLFDVFLRFMCHHAVIRIGSKSYVCCGIGPQSGILSTL 840

Db 781 QETSPRDVAVIEOSSSINEASSGLDFVLEFRMCHHAVRIGKSYVOCQIGIPQGSILSTL 840
 QY 841 LLSLCGDMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVGVPEYGVNVL 900
 Db 841 LSLGCGDMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVGVPEYGVNVL 900
 QY 901 KRTVNFVEDEALGTAFCVQMPAHGLFPWCGLLIDRTLEVQSDSYASTSIRASVTF 960
 Db 901 KRTVNFVEDEALGTAFCVQMPAHGLFPWCGLLIDRTLEVQSDSYASTSIRASVTF 960
 QY 961 NNGFKAARMRKLLGVRLKCHSLFLDLQVNSLQVCTNLYKILLQAYFFHACVQLP 1020
 Db 961 NNGFKAARMRKLLGVRLKCHSLFLDLQVNSLQVCTNLYKILLQAYFFHACVQLP 1020
 QY 1021 FHQOVKNPTEFLRYISDTASLCYSILKAKNAGSLGAKGAAPLPSBAVQMLCHQAFLL 1080
 Db 1021 FHQOVKNPTEFLRYISDTASLCYSILKAKNAGSLGAKGAAPLPSBAVQMLCHQAFLL 1080
 QY 1081 KLTRHRTVTVPLGSLRTAQQLSRKLGTTTLTALEANPALBDEFTIIL 1132
 Db 1081 KLTRHRTVTVPLGSLRTAQQLSRKLGTTTLTALEANPALBDEFTIIL 1132

RESULT 17

US-09-721-456-2

Sequence 2, Application US/09721456

Patent No. 6617110

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Langner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSER: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/721,456

FILING DATE: 22-NOV-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A

FILING DATE: 19-NOV-1997

APPLICATION NUMBER: US/08/724,643

FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US/08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US/08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US/08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US/08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US/08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US/08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US/08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1132 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-721-456-2

Query Match 99.8%; Score 5952; DB 4; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	MPRAPRCRAVRSILRSHREVLP	ATFVRLPGQGRVYQGDPAFPAFVAQCLVCPM	60
Db	1	MPRAPRCRAVRSILRSHREVLP	ATFVRLPGQGRVYQGDPAFPAFVAQCLVCPM	60
QY	61	DARPPAASPROVSCLELVARV	QRLCEKRAKVLAAGFALLDGAAGPEAFTSVR	120
Db	61	DARPPAASPROVSCLELVARV	QRLCEKRAKVLAAGFALLDGAAGPEAFTSVR	120
QY	121	SVLPNTVDRSGAMGILLRRV	DDVLAHLAALFVLAAPSCAYVCGPPVYOLGA	180
Db	121	SVLPNTVDRSGAMGILLRRV	DDVLAHLAALFVLAAPSCAYVCGPPVYOLGA	180
QY	181	ATQARPPHAGSGRRRLGGER	AMNHSVREAGVPLGAPGARRRGSGASRLPLPKRPR	240
Db	181	ATQARPPHAGSGRRRLGGER	AMNHSVREAGVPLGAPGARRRGSGASRLPLPKRPR	240
QY	241	GAAPEERTPVGGSAHNGTR	SGDRGCVVSPAPAEATSLGALSGTRHSPVSG	300
Db	241	GAAPEERTPVGGSAHNGTR	SGDRGCVVSPAPAEATSLGALSGTRHSPVSG	300
QY	301	ROHAGPPTSRPPRMDTCCP	PVVAETGFLYSSGDKQLRPSFLSLRPSLTGARL	360
Db	301	ROHAGPPTSRPPRMDTCCP	PVVAETGFLYSSGDKQLRPSFLSLRPSLTGARL	360
QY	361	VERIFGSRPMWGTGRRLPL	PQRYWQMRPLFELGNAACCPGVLLKTCPLRAAVT	420
Db	361	VERIFGSRPMWGTGRRLPL	PQRYWQMRPLFELGNAACCPGVLLKTCPLRAAVT	420
QY	421	PAAGVAREKPOGSVAAPED	ETDPRRLVQLRQHSFPQVGFVRACLRLVPGMGSG	480
Db	421	PAAGVAREKPOGSVAAPED	ETDPRRLVQLRQHSFPQVGFVRACLRLVPGMGSG	480
QY	481	RHNERPFLNRTKFFISLGH	AKLSLOELTWKQSVRDCAMLRSPGVGCVPALEHRLREI	540
Db	481	RHNERPFLNRTKFFISLGH	AKLSLOELTWKQSVRDCAMLRSPGVGCVPALEHRLREI	540
QY	541	LAKFLHMSVYVELLSFFVT	ETTFQKNRLFPRSPWSEKLSIGIRQLKESVQRE	600
Db	541	LAKFLHMSVYVELLSFFVT	ETTFQKNRLFPRSPWSEKLSIGIRQLKESVQRE	600
QY	601	LSEAEVRQREARPAALLTS	RLRPIPKPDGLPIVMDVYVGAARTRRERGAERLTSRYKA	660
Db	601	LSEAEVRQREARPAALLTS	RLRPIPKPDGLPIVMDVYVGAARTRRERGAERLTSRYKA	660
QY	661	LPSVLYVERARPGILGASV	LGLDIDHRAHMFVLRVRQDPPPELYPKVVTGAYDTI	720
Db	661	LPSVLYVERARPGILGASV	LGLDIDHRAHMFVLRVRQDPPPELYPKVVTGAYDTI	720
QY	721	PODLTEVIASIIKPNITYC	VRAYAVQKAHGHAKAFKSHVSTLTDLQPMROFVAHL	780
Db	721	PODLTEVIASIIKPNITYC	VRAYAVQKAHGHAKAFKSHVSTLTDLQPMROFVAHL	780

Db 721 PODRLTEVIAIISKONTYCVRRYAVVQKAAGHVAKAFKSHVSTLTDLPYMRQFVAHL 780
Qy 781 QETSPLEDAVITESSSLINENASSGLFVFLRFMCHAVRRKSGSYVOCCGIPQGSILSTL 840
Db 781 QETSPLEDAVITESSSLINENASSGLFVFLRFMCHAVRRKSGSYVOCCGIPQGSILSTL 840
Qy 841 LCLSLCYDMMENKLFAGIRRDGLLRLVDEFLVPHLTHAKTFLRLTVRGVPEYGVNL 900
Db 841 LCLSLCYDMMENKLFAGIRRDGLLRLVDEFLVPHLTHAKTFLRLTVRGVPEYGVNL 900
Qy 901 RKTIVNPFVDEDAIGTAFVQMPAHGLFPWCGLLDTRTEVQSDVSSVARTSIRASLTF 960
Db 901 RKTIVNPFVDEDAIGTAFVQMPAHGLFPWCGLLDTRTEVQSDVSSVARTSIRASLTF 960
Qy 961 NRGFKAGNRMRKLFVYLRLKCHSLFLDLQVNSIQVCTNIYKILLQAFRFACTLOLP 1020
Db 961 NRGFKAGNRMRKLFVYLRLKCHSLFLDLQVNSIQVCTNIYKILLQAFRFACTLOLP 1020
Qy 1021 FHQGVNKPTEFLRVISDTASLQVSIILKAKNAGMSLGAKGAPLSEAVQWLCHQAFLL 1080
Db 1021 FHQGVNKPTEFLRVISDTASLQVSIILKAKNAGMSLGAKGAPLSEAVQWLCHQAFLL 1080
Qy 1081 KLFHRVTVYPLIGSLRTAQTQSRKLPSTTLTLEAANPALPSPDKTILD 1132
Db 1081 KLFHRVTVYPLIGSLRTAQTQSRKLPSTTLTLEAANPALPSPDKTILD 1132

RESULT 18
US-09-953-052-2
Sequence 2, Application US/03953052
Patent No. 6627619
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Antisense Compositions for Detecting and Inhibiting Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/953,052
FILING DATE: 14-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: 09/052,919
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997

APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: MO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: MO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 015389-003600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-953-052-2

Query Match 99.8% Score 5952; DB 4; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MPRAPRCRAVSLSLSHREVLPATFVRLGPGQWLVQGDPAFAFALVAOCLVCPW 60
Db 1 MPRAPRCRAVSLSLSHREVLPATFVRLGPGQWLVQGDPAFAFALVAOCLVCPW 60
Qy 61 DARPPEAPSPFROVSCLELVAIVLQRLCERAGKAVLAFGALLDDGARGSPPEAFITSVR 120
Db 61 DARPPEAPSPFROVSCLELVAIVLQRLCERAGKAVLAFGALLDDGARGSPPEAFITSVR 120
Qy 121 SYLPNTVTDALRGSGAMILLRVQDDVYLHLLARCALFVLVAPSCAYQVCGPFLYQGA 180
Db 121 SYLPNTVTDALRGSGAMILLRVQDDVYLHLLARCALFVLVAPSCAYQVCGPFLYQGA 180
Qy 181 ATQARPPHAGSPRRRLCERAMNHSVREAGVPLGLPAPGARRRGASRLPLPKRRR 240
Db 181 ATQARPPHAGSPRRRLCERAMNHSVREAGVPLGLPAPGARRRGASRLPLPKRRR 240
Qy 241 GAAPPERTPVGQSGMAHGRTRGSPDRGFCVSPAPAPAEATSLGALSTRSHSVG 300
Db 241 GAAPPERTPVGQSGMAHGRTRGSPDRGFCVSPAPAPAEATSLGALSTRSHSVG 300
Qy 301 ROHAGPPTSRPPRPMDTPCPPVYAETKHEFLYSGGXEQLRPSFLLSLRPSLTGARL 360
Db 301 ROHAGPPTSRPPRPMDTPCPPVYAETKHEFLYSGGXEQLRPSFLLSLRPSLTGARL 360
Qy 361 VETTFELSGRPMPGTPRRLPRLPORVQMRLEFELIGNHAQCCYGVILKTHGCLRAVT 420
Db 361 VETTFELSGRPMPGTPRRLPRLPORVQMRLEFELIGNHAQCCYGVILKTHGCLRAVT 420
Qy 421 PAAGVCAERKQGSVAAPEEDTDPRLVOLLROHSSFWQYGVFVRACLRLVPPGLWGS 480
Db 421 PAAGVCAERKQGSVAAPEEDTDPRLVOLLROHSSFWQYGVFVRACLRLVPPGLWGS 480
Qy 481 RHNRRLPLRNTKRLISLGAKLSLQSLTYMKSTRDQMLRRSGVGVCPAAERLREBI 540
Db 481 RHNRRLPLRNTKRLISLGAKLSLQSLTYMKSTRDQMLRRSGVGVCPAAERLREBI 540
Qy 541 LAKFLHMLMSYVVELLSFFVYETTFQKNRLFFYPSPVMSKQSIGIRQHLRVOLRE 600
Db 541 LAKFLHMLMSYVVELLSFFVYETTFQKNRLFFYPSPVMSKQSIGIRQHLRVOLRE 600
Qy 601 LSEAENVQHREARALLTSRLRFLPKPDGLRPIYNDVYVGARTFRREKAERLTSVKA 660
Db 601 LSEAENVQHREARALLTSRLRFLPKPDGLRPIYNDVYVGARTFRREKAERLTSVKA 660

QY 661 LFSVLYNTERARRPGLIGASVILGLDIDHRAWRTFVLVRAADPPPELYFVKVDTGAVDTI 720
 Db 661 LFSVLYNTERARRPGLIGASVILGLDIDHRAWRTFVLVRAADPPPELYFVKVDTGAVDTI 720
 QY 721 PODRLTEVIASITIKQNTYCVRRVAVVQKAHGHVRFKSHVSTLTDLOVMQFVAHL 780
 Db 721 PODRLTEVIASITIKQNTYCVRRVAVVQKAHGHVRFKSHVSTLTDLOVMQFVAHL 780
 QY 781 OETSPLRPAVVEOSSSINEASSGLFDVFLFMCCHAVIRKGSVVOCGIPGSIISTL 840
 Db 781 OETSPLRPAVVEOSSSINEASSGLFDVFLFMCCHAVIRKGSVVOCGIPGSIISTL 840
 QY 841 LCSLCYGDWENKLFAGIRRDGILLRLVDDFLVPLTHAFTPLTLVGVPEYGVNLT 900
 Db 841 LCSLCYGDWENKLFAGIRRDGILLRLVDDFLVPLTHAFTPLTLVGVPEYGVNLT 900
 QY 901 RKTVMNFPEDBALGTAFCVQMPAHGLFPWCGILLDTFLEVOSSYSSATSTRASVTF 960
 Db 901 RKTVMNFPEDBALGTAFCVQMPAHGLFPWCGILLDTFLEVOSSYSSATSTRASVTF 960
 QY 961 NRGFXAGNRMRKRLFGVLRKCHSLFLDLOVNSLOTVCTNIYKILLQAYEFHACVQLP 1020
 Db 961 NRGFXAGNRMRKRLFGVLRKCHSLFLDLOVNSLOTVCTNIYKILLQAYEFHACVQLP 1020
 QY 1021 FHQQVWKNFTFLRYISDTASLCYSILKAKNAGMSLGAKGAGPLPSAVQWMLCHQAFLL 1080
 Db 1021 FHQQVWKNFTFLRYISDTASLCYSILKAKNAGMSLGAKGAGPLPSAVQWMLCHQAFLL 1080
 QY 1081 KTRHRVTVVPLGLSIRTAQOTLSRKLPGTTLTALEAANPALPSDFKTIID 1132
 Db 1081 KTRHRVTVVPLGLSIRTAQOTLSRKLPGTTLTALEAANPALPSDFKTIID 1132

RESULT 19

US-09-042-460-3
 ; Sequence 3, Application US/09042460
 ; Patent No. 6767719

GENERAL INFORMATION:

APPLICANT: Morin, Gregg B.
 APPLICANT: Allsopp, Richard
 APPLICANT: DePinho, Ronald
 APPLICANT: Greenberg, Roger
 TITLE OF INVENTION: Mouse Telomerase Reverse Transcriptase
 NUMBER OF SEQUENCES: 101
 CORRESPONDENCE ADDRESS:
 ADDRESSES: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/042,460
 FILING DATE: 16-MAR-1998
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997

QY 1 MPAPRCRAVRSILRSHYREVLPLATFVRRLGFGWRVLYVORGDPAAFRALVAQCLVCVM 60
 Db 1 MPAPRCRAVRSILRSHYREVLPLATFVRRLGFGWRVLYVORGDPAAFRALVAQCLVCVM 60
 QY 61 DABPPPAAPSFROVSCIKELVAVVLORLCERGAKNVLAEGFALLDARGGPPAFTSVR 120
 Db 61 DABPPPAAPSFROVSCIKELVAVVLORLCERGAKNVLAEGFALLDARGGPPAFTSVR 120
 QY 121 SYLPNTVTDALRSGAGMLLRVGDVVLHARCALFVLVAPSCAYVCGPFLYOLGA 180
 Db 121 SYLPNTVTDALRSGAGMLLRVGDVVLHARCALFVLVAPSCAYVCGPFLYOLGA 180
 QY 181 ATQARPPPHASGPRRRLGECERAMNHSVREAGVPLGIPAGCARRGGSASRSJPLPRPRR 240
 Db 181 ATQARPPPHASGPRRRLGECERAMNHSVREAGVPLGIPAGCARRGGSASRSJPLPRPRR 240
 QY 241 GAAPPERTVVGGSNAHNGRTGPDROGCVVSPARPAAEATSLGALSGTRHSPVVG 300
 Db 241 GAAPPERTVVGGSNAHNGRTGPDROGCVVSPARPAAEATSLGALSGTRHSPVVG 300
 QY 301 RGHAGPPTSRPPRPWTDPCCPVYAETKXIFLYSSGDKQOLRPSFLLSLRSLTGARRL 360

Query Match 99.8%; Score 5952; DB 4; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSILRSHYREVLPLATFVRRLGFGWRVLYVORGDPAAFRALVAQCLVCVM 60
 Db 1 MPAPRCRAVRSILRSHYREVLPLATFVRRLGFGWRVLYVORGDPAAFRALVAQCLVCVM 60
 QY 61 DABPPPAAPSFROVSCIKELVAVVLORLCERGAKNVLAEGFALLDARGGPPAFTSVR 120
 Db 61 DABPPPAAPSFROVSCIKELVAVVLORLCERGAKNVLAEGFALLDARGGPPAFTSVR 120
 QY 121 SYLPNTVTDALRSGAGMLLRVGDVVLHARCALFVLVAPSCAYVCGPFLYOLGA 180
 Db 121 SYLPNTVTDALRSGAGMLLRVGDVVLHARCALFVLVAPSCAYVCGPFLYOLGA 180
 QY 181 ATQARPPPHASGPRRRLGECERAMNHSVREAGVPLGIPAGCARRGGSASRSJPLPRPRR 240
 Db 181 ATQARPPPHASGPRRRLGECERAMNHSVREAGVPLGIPAGCARRGGSASRSJPLPRPRR 240
 QY 241 GAAPPERTVVGGSNAHNGRTGPDROGCVVSPARPAAEATSLGALSGTRHSPVVG 300
 Db 241 GAAPPERTVVGGSNAHNGRTGPDROGCVVSPARPAAEATSLGALSGTRHSPVVG 300
 QY 301 RGHAGPPTSRPPRPWTDPCCPVYAETKXIFLYSSGDKQOLRPSFLLSLRSLTGARRL 360

```

Db 301 R0HAGSPSTSRPPRWDTPCPVYATKFLVSSGDXEQLRPSFLISSLRPSLTGARRL 360
Qy 361 VETIFLGSRRPMPGTPRRLPLPORYWQMRPLFELIGNAOCQYGVLLKTHCPRAVY 420
Db 361 VETIFLGSRRPMPGTPRRLPLPORYWQMRPLFELIGNAOCQYGVLLKTHCPRAVY 420
Qy 421 PAAYCAERKQGSVAAPBEEDTDPRLLVOLLRQHSPPWQYGFVRACLRVPGLWGS 480
Db 421 PAAYCAERKQGSVAAPBEEDTDPRLLVOLLRQHSPPWQYGFVRACLRVPGLWGS 480
Qy 481 RHNRRLRLTKKTSISGKAKLSLOELTWKMSVRDCAMLRSGVGCVAASHRLREI 540
Db 481 RHNRRLRLTKKTSISGKAKLSLOELTWKMSVRDCAMLRSGVGCVAASHRLREI 540
Qy 541 LAKFLHMLSVYVVELLRSPFYVTEFTFOKNRLFFYRPSVWSKLQSIGRQHLKRYQRE 600
Db 541 LAKFLHMLSVYVVELLRSPFYVTEFTFOKNRLFFYRPSVWSKLQSIGRQHLKRYQRE 600
Qy 541 LAKFLHMLSVYVVELLRSPFYVTEFTFOKNRLFFYRPSVWSKLQSIGRQHLKRYQRE 600
Db 541 LAKFLHMLSVYVVELLRSPFYVTEFTFOKNRLFFYRPSVWSKLQSIGRQHLKRYQRE 600
Qy 601 LSEAEVQHREARPAALLTSRLRTPKPDGLRPIYNDYVYGARFREREKAEELTSRYKA 660
Db 601 LSEAEVQHREARPAALLTSRLRTPKPDGLRPIYNDYVYGARFREREKAEELTSRYKA 660
Qy 661 LFSVLYNERARPPGLGASVGLDDIHRAMRTFVLRAODPPPELYFVAVDTGAYDTI 720
Db 661 LFSVLYNERARPPGLGASVGLDDIHRAMRTFVLRAODPPPELYFVAVDTGAYDTI 720
Qy 721 PODRLTVIASIIFPQNTYCYRRAYVQKAAHGVRKAFSHVSTLTDLPYKRYVAHL 780
Db 721 PODRLTVIASIIFPQNTYCYRRAYVQKAAHGVRKAFSHVSTLTDLPYKRYVAHL 780
Qy 781 QETSPLDVAVIEOSSSLNEASSGLFDPVLRFMCHAVRIRGKSYVQCSIPGSLSTL 840
Db 781 QETSPLDVAVIEOSSSLNEASSGLFDPVLRFMCHAVRIRGKSYVQCSIPGSLSTL 840
Qy 841 LCSTCYDMENKLPAGIRDDGLLRIVDPLVTPHLTHAKTFLRLVAGVPEYGVNL 900
Db 841 LCSTCYDMENKLPAGIRDDGLLRIVDPLVTPHLTHAKTFLRLVAGVPEYGVNL 900
Qy 901 RKTIVNFEVDEALGTAFAVQMPAHGLFPWCGILLDRTEVSDVSRYRTSRASVTF 960
Db 901 RKTIVNFEVDEALGTAFAVQMPAHGLFPWCGILLDRTEVSDVSRYRTSRASVTF 960
Qy 961 NRGEKAGNRNRKLPGLVLRKCHSLFLDLQVNSLQVCTNIYKILLDQAVRFACVQLP 1020
Db 961 NRGEKAGNRNRKLPGLVLRKCHSLFLDLQVNSLQVCTNIYKILLDQAVRFACVQLP 1020
Qy 1021 FHQQWKNPFFPLRVISDTSLCSILKAKNAQMSLGAKAAGPLDSEAVQWCHQAFLL 1080
Db 1021 FHQQWKNPFFPLRVISDTSLCSILKAKNAQMSLGAKAAGPLDSEAVQWCHQAFLL 1080
Qy 1081 KLTRHRVTVYPLIGSLRTAQTOLSRKLPSTTLALEAANPALPSDKTILD 1132
Db 1081 KLTRHRVTVYPLIGSLRTAQTOLSRKLPSTTLALEAANPALPSDKTILD 1132

```

```

RESULT 20
US-08-974-549A-611
; Sequence 611, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor

```

```

; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 611:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1154 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1154
; OTHER INFORMATION:
; OTHER INFORMATION: /note= "fusion protein composed of hTERT
; protein sequence, vector sequences, the
; Myc epitope and His6 tag"
US-08-974-549A-611

```

```

Qy 1 MPABRCRAVSLRSHREVLPATFVRLGPGMRLVQGDPAFAFRAVAQCLVCPW 60
Db 1 MPABRCRAVSLRSHREVLPATFVRLGPGMRLVQGDPAFAFRAVAQCLVCPW 60
Query Match 99.8% Score 5952; DB 3; Length 1154;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

QY 61 DARPAPABSFROVCLKELVARVLOLCEGAKNVLAFFGALLDAGGPPPEAFTTSVR 120
DB 61 DARPAPABSFROVCLKELVARVLOLCEGAKNVLAFFGALLDAGGPPPEAFTTSVR 120
QY 121 SYLPTVTDALGSGMGLLRVGDVYLHLLACALFVLVAPSCAQVCGPPLYOUGA 180
DB 121 SYLPTVTDALGSGMGLLRVGDVYLHLLACALFVLVAPSCAQVCGPPLYOUGA 180
QY 181 ATOGAPPPHAGSPRRRLGGERAMNHSVNBAGVPLCLPAPGARRGGSASRLPLPKRPR 240
DB 181 ATOGAPPPHAGSPRRRLGGERAMNHSVNBAGVPLCLPAPGARRGGSASRLPLPKRPR 240
QY 241 GAAPBERPVGOGSAHPRTRGSDGFCVVSAPAPAEATSTEGALSGTRSHSPVG 300
DB 241 GAAPBERPVGOGSAHPRTRGSDGFCVVSAPAPAEATSTEGALSGTRSHSPVG 300
QY 301 ROHAGPSTSRPPRWDTPCPVYAETGKPLVSSGDXEQLRPSLTLSPSLTGARL 360
DB 301 ROHAGPSTSRPPRWDTPCPVYAETGKPLVSSGDXEQLRPSLTLSPSLTGARL 360
QY 361 VETIFGSPMWPGRPRRLPRLPORYWQWRPLFELLGNHOCPPYVLLKTHCPRAVT 420
DB 361 VETIFGSPMWPGRPRRLPRLPORYWQWRPLFELLGNHOCPPYVLLKTHCPRAVT 420
QY 421 PAAGVAREKPOGSVAAPPEEDTDRRLVQLRQSHSPWOYGFYACLRRLVPPGLWGS 480
DB 421 PAAGVAREKPOGSVAAPPEEDTDRRLVQLRQSHSPWOYGFYACLRRLVPPGLWGS 480
QY 481 RHNERFLENTKFFISLGHAKLSLOELTWKMSVDCAMLRSPGVGCPAHEHLREI 540
DB 481 RHNERFLENTKFFISLGHAKLSLOELTWKMSVDCAMLRSPGVGCPAHEHLREI 540
QY 541 LAKFLHMLSVYVELLSFFVYETTFPOXNLFYRPSVMSKLOSIGRHLKRVQRE 600
DB 541 LAKFLHMLSVYVELLSFFVYETTFPOXNLFYRPSVMSKLOSIGRHLKRVQRE 600
QY 601 LSEAEVROHREARPALITSRLRFFPKDGLRPIVNDYVVGARTFRKKAERLTSRYKA 660
DB 601 LSEAEVROHREARPALITSRLRFFPKDGLRPIVNDYVVGARTFRKKAERLTSRYKA 660
QY 661 LRSVNLVEKARRPGLGASVGLDIDHRMRTFVLRAODPPEPLVYKVDVGAFTI 720
DB 661 LRSVNLVEKARRPGLGASVGLDIDHRMRTFVLRAODPPEPLVYKVDVGAFTI 720
QY 721 PODRLTEVIAIIPONTYCVRRYAVVOCAHGHYKAKFKSHVSTLTDLOPYMRQFVAHL 780
DB 721 PODRLTEVIAIIPONTYCVRRYAVVOCAHGHYKAKFKSHVSTLTDLOPYMRQFVAHL 780
QY 781 OETSPLRDAVVIQOSSSLNEASSGLFDVFLRMCHHAARIRKSYVQCGIPQSSILSTL 840
DB 781 OETSPLRDAVVIQOSSSLNEASSGLFDVFLRMCHHAARIRKSYVQCGIPQSSILSTL 840
QY 841 LCSLCYGDMENTKLFAGIRRDGILLRLVDDFLVTHLTAKTFLRLVAGVPEYCVVNL 900
DB 841 LCSLCYGDMENTKLFAGIRRDGILLRLVDDFLVTHLTAKTFLRLVAGVPEYCVVNL 900
QY 901 RKTVPNFPVEDEALGTAFAVQMPAGLFPWCGILLDTRLLEVOSSYSYARSISASTF 960
DB 901 RKTVPNFPVEDEALGTAFAVQMPAGLFPWCGILLDTRLLEVOSSYSYARSISASTF 960
QY 961 NRGFKAGRMRRKLFGLVLRKCHSLFLDQVNSLOVCNIXKILLQAYRHAQVLDLP 1020
DB 961 NRGFKAGRMRRKLFGLVLRKCHSLFLDQVNSLOVCNIXKILLQAYRHAQVLDLP 1020
QY 1021 FHOQVKNPFFLRVIDTASLCSYLKAKNAGMSIGAKGAGPLPSEAVQNLCHQAFLL 1080
DB 1021 FHOQVKNPFFLRVIDTASLCSYLKAKNAGMSIGAKGAGPLPSEAVQNLCHQAFLL 1080
QY 1081 KLTRHVVYVPLGLSRTAQTOUSRLPCTTTLTALAEANPMLPBDFTKIIL 1132
DB 1081 KLTRHVVYVPLGLSRTAQTOUSRLPCTTTLTALAEANPMLPBDFTKIIL 1132

RESULT 21
US-08-912-951-323
Sequence 323, Application US/08912951
Patent No. 6475789
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Linsner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Hatley, Calvin H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
TITLE OF INVENTION: THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-Aug-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-Oct-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 323:
SEQUENCE CHARACTERISTICS:
LENGTH: 1154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-951-323
Query March 99.8%; Score 5952; DB 4; Length 1154;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
1 MPRAPRCAVRSILRSYREVVLATFVRRLGQGRVIVQGRPAFALVACIVCPW 60

Db 1 MPAPRCRAVRSLLRSHREVLP LAFVFRRLGPGQWRVLVGRDPAFALVAQCLVCPW 60

Qy 61 DAPPAPAPSFROVSCIKELVAVLQRLCERGAKNVLAFGFALLDGAAGCPPEAFTTSVR 120

Db 61 DAPPAPAPSFROVSCIKELVAVLQRLCERGAKNVLAFGFALLDGAAGCPPEAFTTSVR 120

Qy 121 SYLPNTVTDLRSGGAGLLRRVGDVYVHLARCALPVLVPSGAYOCCGPLYQLQA 180

Db 121 SYLPNTVTDLRSGGAGLLRRVGDVYVHLARCALPVLVPSGAYOCCGPLYQLQA 180

Qy 181 ATQARPPHAGSPRRRLGGERAMNHSYREAGVPLGLPAGARRRGASASJLPLPRPRR 240

Db 181 ATQARPPHAGSPRRRLGGERAMNHSYREAGVPLGLPAGARRRGASASJLPLPRPRR 240

Qy 241 GAAPPEPRTVYGGGSAHPRTRGSPDRGCVVSPAPAEATSLGALSGTHSHSPVG 300

Db 241 GAAPPEPRTVYGGGSAHPRTRGSPDRGCVVSPAPAEATSLGALSGTHSHSPVG 300

Qy 301 ROHHAGPSTSPRPMDTCCPVYAETKHFILYSSGCKEOLRPSFLSLRPSLTGARBL 360

Db 301 ROHHAGPSTSPRPMDTCCPVYAETKHFILYSSGCKEOLRPSFLSLRPSLTGARBL 360

Qy 361 VETIFLGSRPMDGTPRRLPRLPORVQMRPLFLELIGNHAQCPYGLLKTGCPLEAAVT 420

Db 361 VETIFLGSRPMDGTPRRLPRLPORVQMRPLFLELIGNHAQCPYGLLKTGCPLEAAVT 420

Qy 421 PAAGVCAKREKPGOGVAAPPEEDDPRLVOLLRQSHSPMOVYGFVACRLRYVPGMGMS 480

Db 421 PAAGVCAKREKPGOGVAAPPEEDDPRLVOLLRQSHSPMOVYGFVACRLRYVPGMGMS 480

Qy 481 RHNERRLRNTKRFISLQKAKLSLQELTWKMSVDCAMLRSPGVGCPAPAEHRLREBT 540

Db 481 RHNERRLRNTKRFISLQKAKLSLQELTWKMSVDCAMLRSPGVGCPAPAEHRLREBT 540

Qy 541 LAKLHMLMSVYVVELLSFFVYETTFQCKNRLFFYRPSVWSKLQSIGRQHLKRVQLR 600

Db 541 LAKLHMLMSVYVVELLSFFVYETTFQCKNRLFFYRPSVWSKLQSIGRQHLKRVQLR 600

Qy 601 LSEAEVQOHEARFALLTSRLFIKPDGLRPIVNMVYVVGARTFRREKAEHLTSRVYA 660

Db 601 LSEAEVQOHEARFALLTSRLFIKPDGLRPIVNMVYVVGARTFRREKAEHLTSRVYA 660

Qy 661 LFSVYNERARRPGLILASVGLDDIHRAMRTFVLRAADPPPELYFVYVDTGAYDTI 720

Db 661 LFSVYNERARRPGLILASVGLDDIHRAMRTFVLRAADPPPELYFVYVDTGAYDTI 720

Qy 721 POBLTEVIASTIKPONTYCVRRAYVQKAAHGVRAKAFKSHVSTLTDLPYKROFVAHL 780

Db 721 POBLTEVIASTIKPONTYCVRRAYVQKAAHGVRAKAFKSHVSTLTDLPYKROFVAHL 780

Qy 781 QETSPLRDVAVIEQSSSLNEASGLFDVFLRPMCHAVRIRKSYVQCGIIPGSSILSTL 840

Db 781 QETSPLRDVAVIEQSSSLNEASGLFDVFLRPMCHAVRIRKSYVQCGIIPGSSILSTL 840

Qy 841 LCSI:CYGDMNKLFAGIRPDGLLRIYDDPLVTPHLLTHAKTLRTLVREVPYGVVNL 900

Db 841 LCSI:CYGDMNKLFAGIRPDGLLRIYDDPLVTPHLLTHAKTLRTLVREVPYGVVNL 900

Qy 901 RKTIVNPFVEDEALGTAFAVQMPAHGLFPMCGLLDTRTLEVOSSDYASVARTSIRASVTF 960

Db 901 RKTIVNPFVEDEALGTAFAVQMPAHGLFPMCGLLDTRTLEVOSSDYASVARTSIRASVTF 960

Qy 961 NRGKAGRNRRKLFGLYRLKCHSLFDLDQVNSIQVCTNIIYKLLIQARFFACVQLP 1020

Db 961 NRGKAGRNRRKLFGLYRLKCHSLFDLDQVNSIQVCTNIIYKLLIQARFFACVQLP 1020

Qy 1021 FHQGVNKNPTFFLAVISDTASLCYSILKAKAGMSLGAAGLPSSEAVOYLCHQAFLL 1080

Db 1021 FHQGVNKNPTFFLAVISDTASLCYSILKAKAGMSLGAAGLPSSEAVOYLCHQAFLL 1080

Qy 1081 KLTHRRVTVYVLLSLRTAQTOISRKLPGLTLLTALEAANPALPSDKITLD 1132

Db 1081 KLTHRRVTVYVLLSLRTAQTOISRKLPGLTLLTALEAANPALPSDKITLD 1132

RESULT 22
US-09-402-181B-611
Sequence 611, Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Czech, Thomas R.
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/117885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausemus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 611:
SEQUENCE CHARACTERISTICS:
LENGTH: 1154 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1154 /note= "fusion protein composed of hTERT
OTHER INFORMATION:
Protein sequence, vector sequences, the
Myc epitope and His6 tag"
SEQUENCE DESCRIPTION: SEQ ID NO: 611:
US-09-402-181B-611

Query Match 99.8%; Score 5952; DB 4; Length 1154;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAAPRCRAVRLSLRSHYREVLPLATFVRLPGQGRVLYQGRDPAPAFALVACCLVCPW 60
 DB 1 MPAAPRCRAVRLSLRSHYREVLPLATFVRLPGQGRVLYQGRDPAPAFALVACCLVCPW 60

QY 61 DAPPPAASFRQVSLCKELVARVLQRLCERGAKNVLAGFALLDGAAGPPEATTSVR 120
 DB 61 DAPPPAASFRQVSLCKELVARVLQRLCERGAKNVLAGFALLDGAAGPPEATTSVR 120

QY 121 SYLNTVTALRSGSGMGLLRRVGDVIVHLARCALVLAAPSCAVCGPPLVQLGA 180
 DB 121 SYLNTVTALRSGSGMGLLRRVGDVIVHLARCALVLAAPSCAVCGPPLVQLGA 180

QY 181 ATQAPRPPHAGSGRRRLGGERAMNHSVREAGVPLGLPAPGARRGGSASRSLPKRPRR 240
 DB 181 ATQAPRPPHAGSGRRRLGGERAMNHSVREAGVPLGLPAPGARRGGSASRSLPKRPRR 240

QY 241 GAAPBEERTPVGGSWAHPGRTGSDRGFCVSPAPPAEATSLGALSGTRHSPVG 300
 DB 241 GAAPBEERTPVGGSWAHPGRTGSDRGFCVSPAPPAEATSLGALSGTRHSPVG 300

QY 301 ROHHAAPSTSPRRPMDTCCPVYAEKHFYSSGDKQLRPSFLSLSTRSLTGARL 360
 DB 301 ROHHAAPSTSPRRPMDTCCPVYAEKHFYSSGDKQLRPSFLSLSTRSLTGARL 360

QY 361 VETIFLGSRRPMGTRRLPLRQRYWQMRPLFELIGNHACCPYVILKTHCPLRAAVT 420
 DB 361 VETIFLGSRRPMGTRRLPLRQRYWQMRPLFELIGNHACCPYVILKTHCPLRAAVT 420

QY 421 PAAGVACAREKPOGSVAAPBEDTDRRLVQLLRHSSPWQVGFPAACRLRVPBGLMS 480
 DB 421 PAAGVACAREKPOGSVAAPBEDTDRRLVQLLRHSSPWQVGFPAACRLRVPBGLMS 480

QY 481 RHEHREFLNTKFKFELGKHAKLLOELTWKMSVNDCAWLRSPGVGCPAAEHRLREI 540
 DB 481 RHEHREFLNTKFKFELGKHAKLLOELTWKMSVNDCAWLRSPGVGCPAAEHRLREI 540

QY 541 LAKEFLHMSVYVEILRSFYVETTFQKRLFFYRPSVMSKOSIGIRHLKRVQJRE 600
 DB 541 LAKEFLHMSVYVEILRSFYVETTFQKRLFFYRPSVMSKOSIGIRHLKRVQJRE 600

QY 601 LSEAEVRQREARBPALLTSLRFLRPKPDGLPIVNMDDVVGARTFRERERARLTSRKA 660
 DB 601 LSEAEVRQREARBPALLTSLRFLRPKPDGLPIVNMDDVVGARTFRERERARLTSRKA 660

QY 661 LFSVLNVERARERGLGASVGLDIDIRAMRTFVLRAQDPPELVKVDVTGAYDTI 720
 DB 661 LFSVLNVERARERGLGASVGLDIDIRAMRTFVLRAQDPPELVKVDVTGAYDTI 720

QY 721 PODRLTEVIASTIKPONTYCVRRYAVVOGAAGHVRKAFKSHVSTLTLOPVMQFVHL 780
 DB 721 PODRLTEVIASTIKPONTYCVRRYAVVOGAAGHVRKAFKSHVSTLTLOPVMQFVHL 780

QY 781 QETSPLRDAVLEOSSSLNEASSGLFDVFLRFMCHAVRIRKSYVQCGIPQGSILSTL 840
 DB 781 QETSPLRDAVLEOSSSLNEASSGLFDVFLRFMCHAVRIRKSYVQCGIPQGSILSTL 840

QY 841 LGSICVGMENKLFAGIRPDGLLRLVDDPILVTHLTHAKTFLTLVRCVPEVGCYNL 900
 DB 841 LGSICVGMENKLFAGIRPDGLLRLVDDPILVTHLTHAKTFLTLVRCVPEVGCYNL 900

QY 901 KATVNVFPEDEALGTAIVQMPAHGLFPMCGLLDTRTLEVOSSYASRTSRASVTF 960
 DB 901 KATVNVFPEDEALGTAIVQMPAHGLFPMCGLLDTRTLEVOSSYASRTSRASVTF 960

QY 961 NRGFYAGRNRRKLFQVRLKCHSLFLDIQVNSLQTVCTNIYKILLQAYFFHACVQLP 1020
 DB 961 NRGFYAGRNRRKLFQVRLKCHSLFLDIQVNSLQTVCTNIYKILLQAYFFHACVQLP 1020

QY 1021 FHQGVKNPTFFLRVISTDLSLCSYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
 DB 1021 FHQGVKNPTFFLRVISTDLSLCSYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080

QY 1081 KLTRHRTVYPLUGSLTAOTQLSRKLPCTTLTALBAANPALPSPFKTLLD 1132
 DB 1081 KLTRHRTVYPLUGSLTAOTQLSRKLPCTTLTALBAANPALPSPFKTLLD 1132

RESULT 23
 US-09-721-456-611
 ; Sequence 611, Application US/09721456
 ; Patent No. 6617110
 ; GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 ; Linguist, Joachim
 ; Nakamura, Toru
 ; Chapman, Karen B.
 ; Morin, Gregg B.
 ; Harley, Calvin B.
 ; Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/721,456
 FILING DATE: 22-Nov. 6617110-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,549A
 FILING DATE: 19-Nov-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-Oct-1996
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-Apr-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-Apr-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-May-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-May-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: WO PCT/US97/176,8
 FILING DATE: 01-Oct-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-Oct-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION/DOCKET NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002610US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 611:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1154 amino acids
 TYPE: amino acid

STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..1154
 OTHER INFORMATION: /note= "fusion protein composed of hTERT
 protein sequence, vector sequences, the
 Myc epitope and His6 tag"
 SEQUENCE DESCRIPTION: SEQ ID NO: 611:
 US-09-721-456-611

Query March 99.8%; Score 5952; DB 4; Length 1154;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAFCRAVRSLSRSHYREVLPATFVRSLGQGWRLVQGDPAAFRALVAQCLVCVPM 60
 Db 1 MPRAFCRAVRSLSRSHYREVLPATFVRSLGQGWRLVQGDPAAFRALVAQCLVCVPM 60
 QY 61 DARPPAPASFRQVSCLEKELVAVLQRLCERGAKNVLAEGFALLDQARCGPRAFTTSVR 120
 Db 61 DARPPAPASFRQVSCLEKELVAVLQRLCERGAKNVLAEGFALLDQARCGPRAFTTSVR 120
 QY 121 SYLPNTVTDALRGSGANGLLLRVGDVVLVHLARCALFVLVAPSCAYQCGPPLYQLGA 180
 Db 121 SYLPNTVTDALRGSGANGLLLRVGDVVLVHLARCALFVLVAPSCAYQCGPPLYQLGA 180
 QY 181 ATOARPPPHASGPPRRIGCEBAMNHSVREAGVPLGLPAPARRGGASASRLPLPRPR 240
 Db 181 ATOARPPPHASGPPRRIGCEBAMNHSVREAGVPLGLPAPARRGGASASRLPLPRPR 240
 QY 241 GAAPERTPVYGSGSMHPGRTGSPDRGCVVSPAPAEATSLGALSGTSHSPVY 300
 Db 241 GAAPERTPVYGSGSMHPGRTGSPDRGCVVSPAPAEATSLGALSGTSHSPVY 300
 QY 301 ROHHAGPSTSRPRPMDTCPPIVYAEKFLYSSGDKQLRPSFLISSRLPSLTGARSL 360
 Db 301 ROHHAGPSTSRPRPMDTCPPIVYAEKFLYSSGDKQLRPSFLISSRLPSLTGARSL 360
 QY 361 VERTIFLGSRPMMGTPRRLPRLPQRYWQMRPLLELLGNHACQPYGLKTHPEPLAAAT 420
 Db 361 VERTIFLGSRPMMGTPRRLPRLPQRYWQMRPLLELLGNHACQPYGLKTHPEPLAAAT 420
 QY 421 PAAGVCAERKPGQSVAAPEEDTDPRLVOLLRQSSPMQVYGFVBACTRLVPLPGLMS 480
 Db 421 PAAGVCAERKPGQSVAAPEEDTDPRLVOLLRQSSPMQVYGFVBACTRLVPLPGLMS 480
 QY 481 RHNRERRLRNTKKFISLGKIAKLSLQELTWKMSVRCAMLRSPGVGCVAEHRIRBEI 540
 Db 481 RHNRERRLRNTKKFISLGKIAKLSLQELTWKMSVRCAMLRSPGVGCVAEHRIRBEI 540
 QY 541 LAKPLHLMGVVYVELRSFFVYETETFOKNRLFEPVPSVMSKLOSIGIQHAKRYOLE 600
 Db 541 LAKPLHLMGVVYVELRSFFVYETETFOKNRLFEPVPSVMSKLOSIGIQHAKRYOLE 600
 QY 601 LSEAVERQHRDEARPAITSLRPLPKPDGLPIVNDYVVGASTFRREKAEELTSRYVA 660
 Db 601 LSEAVERQHRDEARPAITSLRPLPKPDGLPIVNDYVVGASTFRREKAEELTSRYVA 660
 QY 661 LFSVLANERARRPGLGASVGLDDIHRAWRTVLIRADDPPELYFVAVDTGAYDTI 720
 Db 661 LFSVLANERARRPGLGASVGLDDIHRAWRTVLIRADDPPELYFVAVDTGAYDTI 720
 QY 721 POBLTEVIAIIPQNTYCVRRYAVVQKAHGVKAFKFSHTLTDLPYKQCEVAHL 780
 Db 721 POBLTEVIAIIPQNTYCVRRYAVVQKAHGVKAFKFSHTLTDLPYKQCEVAHL 780
 QY 781 QETSPRLDAVYIESSSINASSGLFDVFLRFMHNAVRIRGSSVYOCQIGPGSILSTL 840
 Db 781 QETSPRLDAVYIESSSINASSGLFDVFLRFMHNAVRIRGSSVYOCQIGPGSILSTL 840
 QY 841 LCSLCYDMENKLFAGIRBDGLLRLVDDFLVTLVPLTHAKTFLRLTVRGVPEYGCVM 900

Db 841 LCSLCYDMENKLFAGIRBDGLLRLVDDFLVTLVPLTHAKTFLRLTVRGVPEYGCVM 900
 QY 901 RTIVNPFVEDEALAGTAFVQMPAHGLFPMCGLLDTRTEVQSDYSSYARTSIRASVTF 960
 Db 901 RTIVNPFVEDEALAGTAFVQMPAHGLFPMCGLLDTRTEVQSDYSSYARTSIRASVTF 960
 QY 961 NRGFAGKMRKILFGVRLKCHSLFDLQVNSIQVCTNIYKILLQAYRFHACVQLP 1020
 Db 961 NRGFAGKMRKILFGVRLKCHSLFDLQVNSIQVCTNIYKILLQAYRFHACVQLP 1020
 QY 1021 FHOQVKNPFFLRVISTASISYILKAKNAGSLGAKGAGPLSEAVOMLCHQAFIL 1080
 Db 1021 FHOQVKNPFFLRVISTASISYILKAKNAGSLGAKGAGPLSEAVOMLCHQAFIL 1080
 QY 1081 KLTRRRTVYVPLGSLRTAQQLSRKLPGTTLTALMAANPALPSDFKTIID 1132
 Db 1081 KLTRRRTVYVPLGSLRTAQQLSRKLPGTTLTALMAANPALPSDFKTIID 1132

RESULT 24
 US-08-974-549A-613
 ; Sequence 613, Application US/08974549A
 ; Patent No. 6166178
 ; GENERAL INFORMATION:
 ; APPLICANT: Cecch, Thomas R.
 ; APPLICANT: Lingner, Joachim
 ; APPLICANT: Nakamura, Toru
 ; APPLICANT: Chapman, Karen B.
 ; APPLICANT: Morlin, Gregg B.
 ; APPLICANT: Harley, Calvin B.
 ; APPLICANT: Andrews, William H.
 ; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 ; NUMBER OF SEQUENCES: 727
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/974, 549A
 ; FILING DATE: 19-NOV-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/724, 643
 ; FILING DATE: 01-OCT-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/844, 419
 ; FILING DATE: 18-APR-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/851, 843
 ; FILING DATE: 06-MAY-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/854, 050
 ; FILING DATE: 09-MAY-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/911, 312
 ; FILING DATE: 14-AUG-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/912, 951
 ; FILING DATE: 14-AUG-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/915, 503

```

FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: WO PCT/US97/17618
  FILING DATE: 01-OCT-1997
  PRIOR APPLICATION DATA: WO PCT/US97/17885
  APPLICATION NUMBER: NO PCT/US97/17885
  FILING DATE: 01-OCT-1997
  ATTORNEY/AGENT INFORMATION:
    NAME: Apple, Randolph Ted
    REGISTRATION NUMBER: 36,429
    REFERENCE/DOCKET NUMBER: 015389-002610US
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (415) 576-0200
    TELEFAX: (415) 576-0300
  INFORMATION FOR SEQ ID NO: 613:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 1189 amino acids
      TYPE: amino acid
      STRANDEDNESS:
      TOPOLOGY: linear
  MOLECULE TYPE: protein
  FEATURE:
  NAME/KEY: Protein
  LOCATION: 1..1189
  OTHER INFORMATION: /note="fusion protein composed of
  OTHER INFORMATION: melittin signal sequence and full length
  OTHER INFORMATION: h1rt protein
  US-08-974-549a-613

Query Match      99.8%; Score 5952; DB 3; Length 1189;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1180; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLSLRHREYVPLATFYARLPGQWELVQRDDPAFAFALVAQCVCVPM 60
DB 58 MPAPRCRAVRSLSLRHREYVPLATFYARLPGQWELVQRDDPAFAFALVAQCVCVPM 117
QY 61 DAPPPAASFRVQSCLEKELVARVLQRLCERGAQVLAFAFALLDGAAGPPEATTSVR 120
DB 118 DAPPPAASFRVQSCLEKELVARVLQRLCERGAQVLAFAFALLDGAAGPPEATTSVR 177
QY 121 SYLENTVTDLRGSGAMGILLRRVQDDVLVHLARCAFLVAAPSCAYQVCGPPLYLQGA 180
DB 178 SYLENTVTDLRGSGAMGILLRRVQDDVLVHLARCAFLVAAPSCAYQVCGPPLYLQGA 237
QY 181 ATOGAPPPAASGPRRLGGERAMNSVREAGVPLGIPAGARRGSGASRSLPLPKPRR 240
DB 238 ATOGAPPPAASGPRRLGGERAMNSVREAGVPLGIPAGARRGSGASRSLPLPKPRR 297
QY 241 GAAPBERTPVQGSVAHPRTRGSDRGFCVVSAPARPAEATSLGALSGTRHSHPSVG 300
DB 298 GAAPBERTPVQGSVAHPRTRGSDRGFCVVSAPARPAEATSLGALSGTRHSHPSVG 357
QY 301 RQHHAGPSTSPRPWDTPCEPPVAETGFIYSSGDYEQALPSSLSTSRSLTGARL 360
DB 358 RQHHAGPSTSPRPWDTPCEPPVAETGFIYSSGDYEQALPSSLSTSRSLTGARL 417
QY 361 VETIFLGSRRPMWGTFRRLPLRLPORYQWRPLFLELGNHACCPYGLLTKTCPLRAAVT 420
DB 418 VETIFLGSRRPMWGTFRRLPLRLPORYQWRPLFLELGNHACCPYGLLTKTCPLRAAVT 477
QY 421 PAAGVCAAREKPOGSVAPEEDTDRRLVQLLRQSSPMQYVGFYACLRILVPGMLGS 480
DB 478 PAAGVCAAREKPOGSVAPEEDTDRRLVQLLRQSSPMQYVGFYACLRILVPGMLGS 537
QY 481 RHNERFELNTKKFISLGHAKLSLOELTWKMSVDCAMLRSPVGVCAAEHRLREI 540
DB 538 RHNERFELNTKKFISLGHAKLSLOELTWKMSVDCAMLRSPVGVCAAEHRLREI 597
QY 541 LAKFLHMLSVYVVELLSFFVYVETTTQKNRLFFYRPSVMSKLOSIGIRHOLKRVQURE 600
DB 598 LAKFLHMLSVYVVELLSFFVYVETTTQKNRLFFYRPSVMSKLOSIGIRHOLKRVQURE 657

```

```

QY 601 LSEAENRQREARPAALITSLRFIPKPDGLRPIVNMDDYVGAFTFRERKAERLTSRVKA 660
DB 658 LSEAENRQREARPAALITSLRFIPKPDGLRPIVNMDDYVGAFTFRERKAERLTSRVKA 717
QY 661 LFSVLYNERARRPGLIGASVTLGDDIHRAMRTVLVRAQDPEPELYFVKVDTGAYDTI 720
DB 718 LFSVLYNERARRPGLIGASVTLGDDIHRAMRTVLVRAQDPEPELYFVKVDTGAYDTI 777
QY 721 PODRLTEVIAIIRKQNTYCVRRYAVYQKAHGVKAFKSHVSTLTDLOPNRQFVAHL 780
DB 778 PODRLTEVIAIIRKQNTYCVRRYAVYQKAHGVKAFKSHVSTLTDLOPNRQFVAHL 837
QY 781 QETSPLRDVAIVIOSSSLNASSGLFDVFLRFMCHAAVIRGSIYQCCGIPGGSITSLTL 840
DB 838 QETSPLRDVAIVIOSSSLNASSGLFDVFLRFMCHAAVIRGSIYQCCGIPGGSITSLTL 897
QY 841 LCSIYGDMMENKLPAGIRSDGLLRVLVDPLVTPHILHAKFRLTLVAGVEYGCYNL 900-
DB 898 LCSIYGDMMENKLPAGIRSDGLLRVLVDPLVTPHILHAKFRLTLVAGVEYGCYNL 957
QY 901 RKTIVANFVDEALGGTAFVQMAHGLFPWCGILLDRITLEVQSDYSYARISIRSLTF 960
DB 958 RKTIVANFVDEALGGTAFVQMAHGLFPWCGILLDRITLEVQSDYSYARISIRSLTF 1017
QY 961 NRGFKAGRRNRKLPGLYLRKCHSLFLDLQVNSLQVCTNIYKILLQAYRPHACVQLQP 1020
DB 1018 NRGFKAGRRNRKLPGLYLRKCHSLFLDLQVNSLQVCTNIYKILLQAYRPHACVQLQP 1077
QY 1021 FHOQWKNPFLPLRVISDTSALCYSLIKAKNAGMSIGAKGAAPLPSBAVQMLCHQAFLL 1080
DB 1078 FHOQWKNPFLPLRVISDTSALCYSLIKAKNAGMSIGAKGAAPLPSBAVQMLCHQAFLL 1137
QY 1081 KLTRHRVTYVPLIGSLRTQGLSRKLPGLTLTALBAANPALPSDFKITLD 1132
DB 1138 KLTRHRVTYVPLIGSLRTQGLSRKLPGLTLTALBAANPALPSDFKITLD 1189

RESULT 25
US-08-912-951-325
Sequence 325, Application US/08912951
Patent No. 6475789
GENERAL INFORMATION:
  APPLICANT: Cech, Thomas R.
  APPLICANT: Lingner, Joachim
  APPLICANT: Nakamura, Toru
  APPLICANT: Chapman, Karen B.
  APPLICANT: Morin, Gregg B.
  APPLICANT: Hailey, Calvin H.
  TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
  NUMBER OF SEQUENCES: 335
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend and Crew LLP
    STREET: Two Embarcadero Center, 8th Floor
    CITY: San Francisco
    STATE: California
    COUNTRY: United States of America
    ZIP: 94111
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/912,951
  FILING DATE: 14-AUG-1997
  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/854,050
  FILING DATE: 09-MAY-1997
  CLASSIFICATION: 435
  PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 325:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-951-325

Query Match 99.8%; Score 5952; DB 4; Length 1189;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAPRCAVRSLSIRSHYREYLPLATFVRRLPGQGMRLVORGDPAPRALVACLVCPM 60
DB 58 MPRAPRCAVRSLSIRSHYREYLPLATFVRRLPGQGMRLVORGDPAPRALVACLVCPM 117

QY 61 DAPPPAPSPFRQVSCIKELVARVYLQRLCERGANVLAFCFALLDGRGSPPEAFTTSVR 120
DB 118 DAPPPAPSPFRQVSCIKELVARVYLQRLCERGANVLAFCFALLDGRGSPPEAFTTSVR 177

QY 121 SYLPNTVTDLRSGAGMLLRVGDVLAHLARCLFTLVAPSCYVCGEPYQLQ 180
DB 178 SYLPNTVTDLRSGAGMLLRVGDVLAHLARCLFTLVAPSCYVCGEPYQLQ 237

QY 181 ATOARPPPHASGPRRLGCEAMNHSVREAGVPLGAPAGARRGGSASRSLFLPKRPR 240
DB 238 ATOARPPPHASGPRRLGCEAMNHSVREAGVPLGAPAGARRGGSASRSLFLPKRPR 297

QY 241 GAAPERTPTVYGQSMHAPGRTGPRSDRGFCVSPAPAEATSLGALSGTHSPSVG 300
DB 298 GAAPERTPTVYGQSMHAPGRTGPRSDRGFCVSPAPAEATSLGALSGTHSPSVG 357

QY 301 ROHAGPSTSRPRPMDTCPYPVATKFLVSSGDEQLRPSFLSLSPSLTGARL 360
DB 358 ROHAGPSTSRPRPMDTCPYPVATKFLVSSGDEQLRPSFLSLSPSLTGARL 417

QY 361 VETIFLGSRPMPGTPRRLPLRFQRYQMRPLFELIGNFAQCPYGLLTKHPPLAAVT 420
DB 418 VETIFLGSRPMPGTPRRLPLRFQRYQMRPLFELIGNFAQCPYGLLTKHPPLAAVT 477

QY 421 PAVGVCAREPQGVAAPEEDTPRRLVOLLROHSSPMOVYGVFVACRLRLPGLMGS 480
DB 478 PAVGVCAREPQGVAAPEEDTPRRLVOLLROHSSPMOVYGVFVACRLRLPGLMGS 537

QY 481 RHNERRLRLNTKPSISLQKAKSLQELTWKMSVRCAMLRSPGVCVPAASHRLREEL 540
DB 538 RHNERRLRLNTKPSISLQKAKSLQELTWKMSVRCAMLRSPGVCVPAASHRLREEL 597

QY 541 LAKFLHMLMSVYVELLSRFFVYVETTFQKNRLFFYRPSWMSKLQSIGIRHKLKVQURE 600

DB 598 LAKFLHMLMSVYVELLSRFFVYVETTFQKNRLFFYRPSWMSKLQSIGIRHKLKVQURE 657

QY 601 LSEAEVROHREARPALTLRLRFLPKPDGLAPVNMDDVVGARTRRERKRALTSRKA 660

DB 658 LSEAEVROHREARPALTLRLRFLPKPDGLAPVNMDDVVGARTRRERKRALTSRKA 717

QY 661 LFSVLNYSRARRPGLLGASVGLDIDHRAWTFVLVRAADPPPELYFVKYDVTGAYDTI 720

DB 718 LFSVLNYSRARRPGLLGASVGLDIDHRAWTFVLVRAADPPPELYFVKYDVTGAYDTI 777

QY 721 PODRLTEVIASIKQNTYCYRRYAVVOKAAHGRKAFKSHVSTLTLDQYMQFVAHL 780

DB 778 PODRLTEVIASIKQNTYCYRRYAVVOKAAHGRKAFKSHVSTLTLDQYMQFVAHL 837

QY 781 CETSPLRDAVVEQSSSINEASSGLFDVFLRFMCHHAVIRKGSYVCCGIPQGSISTL 840

DB 838 CETSPLRDAVVEQSSSINEASSGLFDVFLRFMCHHAVIRKGSYVCCGIPQGSISTL 897

QY 841 LCSLCYGMENKLPAGIRRDGLLRVDDFLLVTPHLLTHAKTFLRLTVRGVPEYGCYVNL 900

DB 898 LCSLCYGMENKLPAGIRRDGLLRVDDFLLVTPHLLTHAKTFLRLTVRGVPEYGCYVNL 957

QY 901 RKTIVNFPVEDBALDGTAFVQMPAHGLFPMCGLLDTRTLVQSDYSYARTSRASVTF 960

DB 958 RKTIVNFPVEDBALDGTAFVQMPAHGLFPMCGLLDTRTLVQSDYSYARTSRASVTF 1017

QY 961 NEGFAGSNMRKLFGLRLKCHSLFDLDQVNSIQTVCTNIYKILLQAFPHACVQLP 1020

DB 1018 NEGFAGSNMRKLFGLRLKCHSLFDLDQVNSIQTVCTNIYKILLQAFPHACVQLP 1077

QY 1021 EHQVWKKPTEFLRIVISDTASLQVSLKAKNAGMSLGKGAAPLPSAVQMLCHQATLL 1080

DB 1078 EHQVWKKPTEFLRIVISDTASLQVSLKAKNAGMSLGKGAAPLPSAVQMLCHQATLL 1137

QY 1081 KLTRHRTVYVPLGLSLRTAQQLSRKLPGLTLTLEAANPALPSDFETIILD 1132

DB 1138 KLTRHRTVYVPLGLSLRTAQQLSRKLPGLTLTLEAANPALPSDFETIILD 1189

RESULT 26
US-09-402-181B-613
Sequence 613, Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419

```

FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 23-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenius, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 613:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1189
OTHER INFORMATION: /note= "fusion protein composed of
melittin signal sequence and full length
hTERT protein"
SEQUENCE DESCRIPTION: SEQ ID NO: 613:
US-09-402-181B-613
Query Match          99.8%; Score 5952; DB 4; Length 1189;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRAPRCRAVRSLTSHREYVPLATFVRRLGPGMRVLVGRDPAFAFVAQCIVCPW 60
DB 58 MPAPRCRAVRSLTSHREYVPLATFVRRLGPGMRVLVGRDPAFAFVAQCIVCPW 117
QY 61 DARPPAPASFRQVSLKELVARVLQRLCERGAKNVLAFFGALLDGAAGPEAFTTSVR 120
DB 118 DARPPAPASFRQVSLKELVARVLQRLCERGAKNVLAFFGALLDGAAGPEAFTTSVR 177
QY 121 STLENTVTALNGSGWGLLLRRVGDVYLHLLACALFVLYABSCAYQVCPPLYQGA 180
DB 178 STLENTVTALNGSGWGLLLRRVGDVYLHLLACALFVLYABSCAYQVCPPLYQGA 237
QY 181 ATQARPPHAGSGRRRLGGERAMNHSVBEAGVPLGLPAGARRRGSASRSLLPKRPR 240
DB 238 ATQARPPHAGSGRRRLGGERAMNHSVBEAGVPLGLPAGARRRGSASRSLLPKRPR 297
QY 241 GAAPERTIPVQGSNAHPGRTGPGSDRGFCVVASPARPAEATSLLEGALSGTRHSHSVG 300
DB 298 GAAPERTIPVQGSNAHPGRTGPGSDRGFCVVASPARPAEATSLLEGALSGTRHSHSVG 357
QY 301 RQHHAQPPSTSPRRPMDTPCPVVAETKHFLYSSGDKROLRPSFLLSLPSLTGARRL 360
DB 358 RQHHAQPPSTSPRRPMDTPCPVVAETKHFLYSSGDKROLRPSFLLSLPSLTGARRL 417
QY 361 VETIFLGSRRPMWPGTFRRLRPLRQRYWQNRPLFLELLGNHAQCPYVLLKTHCPRAAVT 420
DB 418 VETIFLGSRRPMWPGTFRRLRPLRQRYWQNRPLFLELLGNHAQCPYVLLKTHCPRAAVT 477
QY 421 PPAAGVARRKPGGSVAAPEEDTDPRRLVQLLRQSSPMQVYGFRACLRLRVPFGMLGS 480
DB 478 PPAAGVARRKPGGSVAAPEEDTDPRRLVQLLRQSSPMQVYGFRACLRLRVPFGMLGS 537

```

```

QY 481 RHNERRLRTKTKFISIGKAKISLOELTWKMSVRDCAMLRSPGVGVPAAEHRLREI 540
DB 538 RHNERRLRTKTKFISIGKAKISLOELTWKMSVRDCAMLRSPGVGVPAAEHRLREI 597
QY 541 LAKFLHMLSVYVELRSEFYVTEFTFOKNRLFRRPSPWSKLOSIGIRHLKRYOLRE 600
DB 598 LAKFLHMLSVYVELRSEFYVTEFTFOKNRLFRRPSPWSKLOSIGIRHLKRYOLRE 657
QY 601 LSEAEVQHEARPAALITSLRFLPKPDGRPLVNMDDYVGAATFRERGAELTSRYVA 660
DB 658 LSEAEVQHEARPAALITSLRFLPKPDGRPLVNMDDYVGAATFRERGAELTSRYVA 717
QY 661 LFSVLNTERARRPGLLGASVLDGDDIHRARMTVLRAADPEPELYFKVDVTGAYDTI 720
DB 718 LFSVLNTERARRPGLLGASVLDGDDIHRARMTVLRAADPEPELYFKVDVTGAYDTI 777
QY 721 PDRLTEVIAIITKPPONTVCVRRYAVVQKAHGHVAKFASVSTLTDIQPYMRQFVAHL 780
DB 778 PDRLTEVIAIITKPPONTVCVRRYAVVQKAHGHVAKFASVSTLTDIQPYMRQFVAHL 837
QY 781 QETSPLEDAVIVIOSSSLNFASSGLPDLFRFPGCHAVRIKGSYVQCGIIPGGSILSTL 840
DB 838 QETSPLEDAVIVIOSSSLNFASSGLPDLFRFPGCHAVRIKGSYVQCGIIPGGSILSTL 897
QY 841 LGSICYGDMENKLPAGIRBDGLLLRLVDDELVTPLHAKTFLRLTVRGPEYGCVNL 900
DB 898 LGSICYGDMENKLPAGIRBDGLLLRLVDDELVTPLHAKTFLRLTVRGPEYGCVNL 957
QY 901 RKTIVANFVDEALGGTAFAQWPAHGLFPWCGILLDTRILEVOSDSSYARSIRASVPE 960
DB 958 RKTIVANFVDEALGGTAFAQWPAHGLFPWCGILLDTRILEVOSDSSYARSIRASVPE 1017
QY 961 NRGFKAQRNRRLKFGVLRKCHSLFLDLQVNSLQTCVNTIYKILLQAYRFAVCLQUP 1020
DB 1018 NRGFKAQRNRRLKFGVLRKCHSLFLDLQVNSLQTCVNTIYKILLQAYRFAVCLQUP 1077
QY 1021 PHQQWKNPFFELRVISDTASLCLYLKAKNAGMSGANGAAGPLPSEAVQMLCHQAFLL 1080
DB 1078 PHQQWKNPFFELRVISDTASLCLYLKAKNAGMSGANGAAGPLPSEAVQMLCHQAFLL 1137
QY 1081 KLTRHRTVYVPLGSLRTAQOTLSRLPGTTLTALPAAANPALSPDFKILL 1132
DB 1138 KLTRHRTVYVPLGSLRTAQOTLSRLPGTTLTALPAAANPALSPDFKILL 1189

```

RESULT 27
 US-09-721-456-613
 Sequence 613, Application US/09721456
 Patent No. 6617110
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin B.
 Andrews, William H.
 TITLE OF INVENTION: Human telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

```

? APPLICATION NUMBER: US/09/721,456
? FILING DATE: 22-Nov. 6617110-2000
? CLASSIFICATION: <unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/974,549A
? FILING DATE: 19-NOV-1997
? APPLICATION NUMBER: US 08/724,643
? FILING DATE: 01-OCT-1996
? APPLICATION NUMBER: US 08/844,419
? FILING DATE: 18-APR-1997
? APPLICATION NUMBER: US 08/846,017
? FILING DATE: 25-APR-1997
? APPLICATION NUMBER: US 08/851,843
? FILING DATE: 06-MAY-1997
? APPLICATION NUMBER: US 08/854,050
? FILING DATE: 09-MAY-1997
? APPLICATION NUMBER: US 08/911,312
? FILING DATE: 14-AUG-1997
? APPLICATION NUMBER: US 08/912,951
? FILING DATE: 14-AUG-1997
? APPLICATION NUMBER: US 08/915,503
? FILING DATE: 14-AUG-1997
? APPLICATION NUMBER: WO PCT/US97/17618
? FILING DATE: 01-OCT-1997
? APPLICATION NUMBER: WO PCT/US97/17885
? FILING DATE: 01-OCT-1997
? ATTORNEY/AGENT INFORMATION:
? NAME: Apple, Randolph Ted
? REGISTRATION NUMBER: 36,429
? REFERENCE/DOCKET NUMBER: 015389-002610US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 576-0300
? TELEFAX: (415) 576-0300
? INFORMATION FOR SEQ ID NO: 613:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1189 amino acids
? TYPE: amino acid
? STRANDEDNESS: <unknown>
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? FEATURE:
? NAME/KEY: Protein
? LOCATION: 1..1189
? OTHER INFORMATION: /note="fusion protein composed of
? telitelin signal sequence and full length
? hprt protein"
? SEQUENCE DESCRIPTION: SEQ ID NO: 613:
US-09-721-456-613

Query Match 99.8%; Score 5952; DB 4; Length 1189;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRLSLRSHYREVLPPLATFVRRLGPGQWLVORGPAPAFRAIVACIVCPW 60
DB 58 MPAPRCRAVRLSLRSHYREVLPPLATFVRRLGPGQWLVORGPAPAFRAIVACIVCPW 117
QY 61 DAPPPAPSPFQVSCIKELVAVRLORLCGRGAKVLAEGFALLDARGGPPAFTTSVR 120
DB 118 DAPPPAPSPFQVSCIKELVAVRLORLCGRGAKVLAEGFALLDARGGPPAFTTSVR 177
QY 121 SYPLNTVTDLRSGGAWGLLRLRVGDDVLVHLIARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 178 SYPLNTVTDLRSGGAWGLLRLRVGDDVLVHLIARCALFVLVAPSCAYQVCGPPLYQLGA 237
QY 181 ATQARPPEHASGRRRLGCEBAMNHSVREGVPLIGPAPGARRGGASASRLPLPRRPR 240
DB 238 ATQARPPEHASGRRRLGCEBAMNHSVREGVPLIGPAPGARRGGASASRLPLPRRPR 297
QY 241 GAAPERTPTVGQGSVAHPGRTGRGSPDRGFCVSPAPPAEATSLGALSGTRHSHPSVG 300
DB 298 GAAPERTPTVGQGSVAHPGRTGRGSPDRGFCVSPAPPAEATSLGALSGTRHSHPSVG 357

QY 301 ROHNAPESTSRPPRMDTPGCPVYAETKHFLLYSSGDKEQLRPSLLSLRSLTGARL 360
DB 356 ROHNAPESTSRPPRMDTPGCPVYAETKHFLLYSSGDKEQLRPSLLSLRSLTGARL 417
QY 361 VETITLGRPMWPGTPRRRLPLPQRYQWRPLFLLELNNHAQCPYGVLLKTHCPRLAAVT 420
DB 418 VETITLGRPMWPGTPRRRLPLPQRYQWRPLFLLELNNHAQCPYGVLLKTHCPRLAAVT 477
QY 421 PAGVCAEKPQGSVAAPBEEDTPRRRLVOLLROHSPWQYGFAPRACLRRLVPPGLGGS 480
DB 478 PAGVCAEKPQGSVAAPBEEDTPRRRLVOLLROHSPWQYGFAPRACLRRLVPPGLGGS 537
QY 481 RHNERFRLNTKFTSLGKHAQLSIQELTWKMSVDCAMLRSPQVGCVPAAEHLREBI 540
DB 538 RHNERFRLNTKFTSLGKHAQLSIQELTWKMSVDCAMLRSPQVGCVPAAEHLREBI 597
QY 541 LAKFLHMLMSVYVVELASFPYVETTFOKRLPFYRSVWSKLSIGIRHLKVCQJRE 600
DB 598 LAKFLHMLMSVYVVELASFPYVETTFOKRLPFYRSVWSKLSIGIRHLKVCQJRE 657
QY 601 LSEAEVRQHRERAPALTSRLRFLPKPDGLRPVMMDYVGARTFRERKAERLTSRYKA 660
DB 658 LSEAEVRQHRERAPALTSRLRFLPKPDGLRPVMMDYVGARTFRERKAERLTSRYKA 717
QY 661 LFSVUNYERARRPGLLGASVIGLDDIHRAMRTFYLRAVAQDPPELRYVKVDYGAVTI 720
DB 718 LFSVUNYERARRPGLLGASVIGLDDIHRAMRTFYLRAVAQDPPELRYVKVDYGAVTI 777
QY 721 PODRLTEYIASIKPQNTYCYRRAVVOKAAGHVRKAFKSHVSTLTLOPYMRQFVAHL 780
DB 778 PODRLTEYIASIKPQNTYCYRRAVVOKAAGHVRKAFKSHVSTLTLOPYMRQFVAHL 837
QY 781 QETSPLRDAVVIQSSSINERASSGLFDVFLRFMCHHAVRIRGKSYVQCGIPQGSII STL 840
DB 838 QETSPLRDAVVIQSSSINERASSGLFDVFLRFMCHHAVRIRGKSYVQCGIPQGSII STL 897
QY 841 LCSLCYGMENKLPFGIRBDGLLRVDDFLVLPHTATFRLTVRGVEGCVNLT 900
DB 898 LCSLCYGMENKLPFGIRBDGLLRVDDFLVLPHTATFRLTVRGVEGCVNLT 957
QY 901 RKTVPNFEVDEBALGTAFAVQMPAHGLFPWCGLLDFTLEVOSSYARTSIRASVTF 960
DB 958 RKTVPNFEVDEBALGTAFAVQMPAHGLFPWCGLLDFTLEVOSSYARTSIRASVTF 1017
QY 961 NRGFKAGNNMRKLPGVRLKCHSLFLDLQVNSIQYVCTINIKYKILLQAYRFHACVQLP 1020
DB 1018 NRGFKAGNNMRKLPGVRLKCHSLFLDLQVNSIQYVCTINIKYKILLQAYRFHACVQLP 1077
QY 1021 FHQYVWKPTFFLRVISTDASLSYLKAKNAGSLGAKGAGLPSEAVQMLCHQAFLL 1080
DB 1078 FHQYVWKPTFFLRVISTDASLSYLKAKNAGSLGAKGAGLPSEAVQMLCHQAFLL 1137
QY 1081 KLTRRRVTVVPLGSLRTAQOTLSRKLPPTTLTLEBAANPALPSDEKTIID 1132
DB 1138 KLTRRRVTVVPLGSLRTAQOTLSRKLPPTTLTLEBAANPALPSDEKTIID 1189

RESULT 28
US-08-974-549A-612
Sequence 612, Application US/08974549A
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morley, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
```

STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,549A
 FILING DATE: 19-NOV-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: NO PCT/US97/17618
 FILING DATE: 01-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: NO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002610US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 612:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1200 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..1200
 OTHER INFORMATION: /note="fusion protein composed of His6
 and Anti-Xpress tags, enterokinase
 OTHER INFORMATION: cleavage site and full length mrt
 OTHER INFORMATION: protein"
 US-08-974-549A-612

Query Match 99.8%; Score 5952; DB 3; Length 1200;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1100; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 MPAPRCRAVRSLSLRSHYREVLPLATFVRLRLOPQGMRLVQRGDPAPAFALVAQCCLVCPW 60
 |||||

Db 69 MPAPRCRAVRSLSLRSHYREVLPLATFVRLRLOPQGMRLVQRGDPAPAFALVAQCCLVCPW 128
 Qy 61 DAAPPAPASFRQVSCLELVARVLTQRLCEGAKVLAFGFALLDQAGCGPEPATTSVR 120
 Db 129 DAAPPAPASFRQVSCLELVARVLTQRLCEGAKVLAFGFALLDQAGCGPEPATTSVR 188
 Qy 121 SYLPLNTVALRSGGAMGILLIRVGDVYLHLARCALVLAASCAVOVCPPLYQGA 180
 Db 189 SYLPLNTVALRSGGAMGILLIRVGDVYLHLARCALVLAASCAVOVCPPLYQGA 248
 Qy 181 ATQARPPHAGSGRRRLGGERAMNHSVREAGVPLGIPAGARRGGASASLPLPKRPR 240
 Db 249 ATQARPPHAGSGRRRLGGERAMNHSVREAGVPLGIPAGARRGGASASLPLPKRPR 308
 Qy 241 GAAPPEERTPVQGGSAHAGRTGRGSDRGFCVSPAPAEATSLLEGALSGTRHSPSG 300
 Db 309 GAAPPEERTPVQGGSAHAGRTGRGSDRGFCVSPAPAEATSLLEGALSGTRHSPSG 368
 Qy 301 RQHAGPPTSRPRPMDTCCPPVVAETGHLFYSSGDKQLRPSFLSLRSLTGARRL 360
 Db 369 RQHAGPPTSRPRPMDTCCPPVVAETGHLFYSSGDKQLRPSFLSLRSLTGARRL 428
 Qy 361 VETIFGSRPMWPGTTRRLPRLPQRYWQMRPLFLELGNHAOCPPYVLLKTCPLRAAT 420
 Db 429 VETIFGSRPMWPGTTRRLPRLPQRYWQMRPLFLELGNHAOCPPYVLLKTCPLRAAT 488
 Qy 421 PAAGVAREKPGQSVAPAEEDTDPRLVQLRQHSPPQVYGFYACLRRLVPPGLMGS 480
 Db 489 PAAGVAREKPGQSVAPAEEDTDPRLVQLRQHSPPQVYGFYACLRRLVPPGLMGS 548
 Qy 481 RHNERPFLRNTKKEISLGAKLSLOELTWKMSVRDCAILRSRGVGCYPAAEHRLREI 540
 Db 549 RHNERPFLRNTKKEISLGAKLSLOELTWKMSVRDCAILRSRGVGCYPAAEHRLREI 608
 Qy 541 LAPELWMSVYVVELLRSEFYVTEETPOKNLFFPRSPVMSKLSIGIRQLKRYQARE 600
 Db 609 LAPELWMSVYVVELLRSEFYVTEETPOKNLFFPRSPVMSKLSIGIRQLKRYQARE 668
 Qy 601 LSEAEVQRHREARPALTSRLRFIPKPDGLRPIVMNDVYVAGARTREKRAELTSRYKA 660
 Db 669 LSEAEVQRHREARPALTSRLRFIPKPDGLRPIVMNDVYVAGARTREKRAELTSRYKA 728
 Qy 661 LSEVLYERARRRGLLGASVLTGDDTHRAMRTFVLRYRAQDDPPELYFQVNVTAQYDI 720
 Db 729 LSEVLYERARRRGLLGASVLTGDDTHRAMRTFVLRYRAQDDPPELYFQVNVTAQYDI 788
 Qy 721 PQDLTEVLASITKPNQTYCVRRYAVVQKAAGHAKAKFSVSTLTDLPYMRQFAHL 780
 Db 789 PQDLTEVLASITKPNQTYCVRRYAVVQKAAGHAKAKFSVSTLTDLPYMRQFAHL 848
 Qy 781 QETSPLRDVAVTBOSSSLNABSSGLFDVFLRFMCHNAVIRKGSYVQCGGIRQSGILSTL 840
 Db 849 QETSPLRDVAVTBOSSSLNABSSGLFDVFLRFMCHNAVIRKGSYVQCGGIRQSGILSTL 908
 Qy 841 LGSLEYGDMENKLFAGIRRDGLLRVDDFLVYTPHLTHAKTFLRLTVRGVEYGVNL 900
 Db 909 LGSLEYGDMENKLFAGIRRDGLLRVDDFLVYTPHLTHAKTFLRLTVRGVEYGVNL 968
 Qy 901 RKTIVNFPVEDEALGSTAFVQMPAGLFPWCGILLDTLRLLEVQSDYSYARSISRASTF 960
 Db 969 RKTIVNFPVEDEALGSTAFVQMPAGLFPWCGILLDTLRLLEVQSDYSYARSISRASTF 1028
 Qy 961 NRGFTKGRNNRRKLFVLLKCHSLFLDQVNSLQVVCNINIKILLLOAYRFHACVLOLP 1020
 Db 1029 NRGFTKGRNNRRKLFVLLKCHSLFLDQVNSLQVVCNINIKILLLOAYRFHACVLOLP 1088
 Qy 1021 FHOQVWKNPFFLRVISTDASLCYSILKAKNAGMSLGAGAAPLSEAVQWLCHQAFLL 1080
 Db 1089 FHOQVWKNPFFLRVISTDASLCYSILKAKNAGMSLGAGAAPLSEAVQWLCHQAFLL 1148
 Qy 1081 KLTRHRVTVPLIGSLRTAQTQSRKLBGTTLTALFAANPPLPSFKITLD 1132
 Db 1149 KLTRHRVTVPLIGSLRTAQTQSRKLBGTTLTALFAANPPLPSFKITLD 1200

RESULT 29
US-08-912-951-324
Sequence 324, Application US/08912951
Patent No. 6475789
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Hartley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
APPLICATION DATA:
APPLICATION NUMBER: 36,429
REGISTRATION NUMBER: 015389-003600US
REFERENCE/DOCKET NUMBER: 015389-003600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ. ID NO.: 324:
SEQUENCE CHARACTERISTICS:
LENGTH: 1200 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-951-324

Query Match 99.8%; Score 5952; DB 4; Length 1200;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	MPRAPRCVAVNSLSHSHREVLP	60
DB	69	MPRAPRCVAVNSLSHSHREVLP	128
QY	61	DARPPAPSPFROVSCUKEIVARV	120
DB	129	DARPPAPSPFROVSCUKEIVARV	188
QY	121	SYLPNTVTDALRGSGAMGILLR	180
DB	189	SYLPNTVTDALRGSGAMGILLR	248
QY	181	ATQARPAPHASGPRRLGCEPAA	240
DB	249	ATQARPAPHASGPRRLGCEPAA	308
QY	241	GAAPPERTPVGGSGMAHPRGR	300
DB	309	GAAPPERTPVGGSGMAHPRGR	368
QY	301	ROHNAAGPSTSRPPRPMDT	360
DB	369	ROHNAAGPSTSRPPRPMDT	428
QY	361	VETIFLGRPMWPGTFRRLPRL	420
DB	429	VETIFLGRPMWPGTFRRLPRL	488
QY	421	PAAGVCAEKPQGSVAABEEDT	480
DB	489	PAAGVCAEKPQGSVAABEEDT	548
QY	481	RHNERFRLNTKFTSLGKHA	540
DB	549	RHNERFRLNTKFTSLGKHA	608
QY	541	LAKFLHMLMSYVVELLSFF	600
DB	609	LAKFLHMLMSYVVELLSFF	668
QY	601	LSEAEVRQHRAPRALTLRL	660
DB	669	LSEAEVRQHRAPRALTLRL	728
QY	661	LFSVINYERARPGILGASV	720
DB	729	LFSVINYERARPGILGASV	788
QY	721	PODRLTEVIASIIKPONTY	780
DB	789	PODRLTEVIASIIKPONTY	848
QY	781	QETSRLRAVVIIEOSSS	840
DB	849	QETSRLRAVVIIEOSSS	908
QY	841	LCSLCYGMENKTLFAGIR	900
DB	909	LCSLCYGMENKTLFAGIR	968
QY	901	RKTYYNPFVEDEALGTA	960
DB	969	RKTYYNPFVEDEALGTA	1028
QY	961	NRGEVAGNMRKTLFVLR	1020
DB	1029	NRGEVAGNMRKTLFVLR	1088
QY	1021	FHQQVWKNPTFFLRAV	1080
DB	1089	FHQQVWKNPTFFLRAV	1148
QY	1081	KLTRHRYVYVLLGSLRTA	1132

Db 1149 KLTRRHYVPLGSLRTAQTLQSLRKLPGTLTLLALEAANPALPSDFKTLID 1200

RESULT 30

US-09-402-181B-612
Sequence 612, Application US/09402181B

Patent No. 6610839

GENERAL INFORMATION:

APPLICANT: Cecch, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

ADDRESS: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/402,181B

FILING DATE: 29-Sep-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-Oct-1996

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-Apr-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-Apr-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-May-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-May-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-Oct-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ausenius, Scott L.

REGISTRATION NUMBER: 42,271

REFERENCE/DOCKET NUMBER: 015389-002620US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 612:

SEQUENCE CHARACTERISTICS:

LENGTH: 1200 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Protein

LOCATION: 1..1200

OTHER INFORMATION: /note= "fusion protein composed of His6

and Anti-Xpress tags, enterokinase

cleavage site and full length hprt

;

SEQUENCE DESCRIPTION: SEQ ID NO: 612:
US-09-402-181B-612

Query Match 99.8%; Score 5952; DB 4; Length 1200;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MPRAPRCRAVRSILSRSHREVLPLATFVRRLCPQGRVLYQDGPAAFPALVAQCCVCPW	60
Db	69	MPRAPRCRAVRSILSRSHREVLPLATFVRRLCPQGRVLYQDGPAAFPALVAQCCVCPW	128
Qy	61	DARPPAPSPFQVSCLEKELVARVYLQRLCERGAQVLAAGFALLDQARGPEAFTTSVR	120
Db	129	DARPPAPSPFQVSCLEKELVARVYLQRLCERGAQVLAAGFALLDQARGPEAFTTSVR	188
Qy	121	SYLPNTVDALRSGAMGILLRVDGVVHLIARCALFVLAAPCAVQCGPPYQIGA	180
Db	189	SYLPNTVDALRSGAMGILLRVDGVVHLIARCALFVLAAPCAVQCGPPYQIGA	248
Qy	181	ATQARPPAPSGRRRLGGERAMNSVRAQVPLGPAAGARRGSGASRSLPLKPRPR	240
Db	249	ATQARPPAPSGRRRLGGERAMNSVRAQVPLGPAAGARRGSGASRSLPLKPRPR	308
Qy	241	GAAPERTPVQGGSWAHGRTGSPDRCFCVSPAPRAEATSLGALSGTRHSPVG	300
Db	309	GAAPERTPVQGGSWAHGRTGSPDRCFCVSPAPRAEATSLGALSGTRHSPVG	368
Qy	301	RQHAGPPTSPRPWDTPCPPVVAETHGFYSSGDKQLRPSFLSLRSLTGARL	360
Db	369	RQHAGPPTSPRPWDTPCPPVVAETHGFYSSGDKQLRPSFLSLRSLTGARL	428
Qy	361	VERTIFGSRPWWGTPRRPLRLPORWQMRPLFLELGNHACCPGVLLKTHCPRAAVT	420
Db	429	VERTIFGSRPWWGTPRRPLRLPORWQMRPLFLELGNHACCPGVLLKTHCPRAAVT	488
Qy	421	PAAGVAREKPGQSVAPAEEDTDPRLVQLIRQSSPMQVGYFVACLRILVPPGLWS	480
Db	489	PAAGVAREKPGQSVAPAEEDTDPRLVQLIRQSSPMQVGYFVACLRILVPPGLWS	548
Qy	481	RHNERELNRTKFTSLGKNAKLSLOELTWKSVRCALRRSPGVCPALAEHRLREBI	540
Db	549	RHNERELNRTKFTSLGKNAKLSLOELTWKSVRCALRRSPGVCPALAEHRLREBI	608
Qy	541	LAKFLHMSVYVELLRSPFYVTEETPOKNRLFYRPSWMSKLSIGIRQLKRYQRE	600
Db	609	LAKFLHMSVYVELLRSPFYVTEETPOKNRLFYRPSWMSKLSIGIRQLKRYQRE	668
Qy	601	LSAEVRQREARPAALTSLRLRPIPKDGLRPIVMNDVYGARTRRERARSLSRVA	660
Db	669	LSAEVRQREARPAALTSLRLRPIPKDGLRPIVMNDVYGARTRRERARSLSRVA	728
Qy	661	LFSLVNERARPPGLLGASVGLGDDIHRAMRTFVLRAQDPPPELYFVKVDVTGAYDTI	720
Db	729	LFSLVNERARPPGLLGASVGLGDDIHRAMRTFVLRAQDPPPELYFVKVDVTGAYDTI	788
Qy	721	PODLTEVIASIIKPNNTYCVRRYAVVQGAAGHRAKASHVSTLTDQPMRQFVAL	780
Db	789	PODLTEVIASIIKPNNTYCVRRYAVVQGAAGHRAKASHVSTLTDQPMRQFVAL	848
Qy	781	QETSPLRDAVIEQSSINBASGLFDVFLRFCHCAVIRIGKSYQCGGIPQGSILSTL	840
Db	849	QETSPLRDAVIEQSSINBASGLFDVFLRFCHCAVIRIGKSYQCGGIPQGSILSTL	908
Qy	841	LCSLCYGDMENKLPAGIRSDGLLRVLVDVFLVPHLTHAKTFLRTLVGVEYGCVNL	900
Db	909	LCSLCYGDMENKLPAGIRSDGLLRVLVDVFLVPHLTHAKTFLRTLVGVEYGCVNL	968
Qy	901	RKTVMNPVEDELAGTAFAVQPAHGLTFMCGLLDTRTLEVQSDVYSARISIRASVTF	960
Db	969	RKTVMNPVEDELAGTAFAVQPAHGLTFMCGLLDTRTLEVQSDVYSARISIRASVTF	1028
Qy	961	NRGFKAGRMWRKLPVLRKLKCHSLFLDQVNSLQTVCTNIYKILLQAYRFAACVQLQIP	1020

Db 1029 NRPFKGRNRRLFGVLRKCHSLFDLDVNSLQVCTNIVYKILLQAVRFACVLCIP 1088
 QY 1021 FHQWVKNPTFFLRVSDTASLTCYSILKAKNAGMSIGAKGAGPLPSEAVOMLCHQAFIL 1080
 Db 1089 FHQWVKNPTFFLRVSDTASLTCYSILKAKNAGMSIGAKGAGPLPSEAVOMLCHQAFIL 1148
 QY 1081 KLTRHRYTVPLIGSLRTAQTQSRKLPGLTTLTALEAANPALPSDFKTLID 1132
 Db 1149 KLTRHRYTVPLIGSLRTAQTQSRKLPGLTTLTALEAANPALPSDFKTLID 1200

RESULT 31
 US-09-721-456-612
 Sequence 612, Application US/09721456

GENERAL INFORMATION:

APPLICANT: Cecch, Thomas R.

NAME: Nakamura, Toru

Chapman, Karen B.

Martin, Gregg B.

Harley, Calvin B.

Andrews, William H.

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/721,456

FILING DATE: 22-Nov. 66/7110-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A

FILING DATE: 19-NOV-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 612:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1200 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURES:
 NAME/KEY: Protein
 LOCATION: 1..1200
 OTHER INFORMATION: /note="fusion protein composed of His6
 and Anti-Xpress tags, enterokinase
 cleavage site and full length hTTP
 protein"
 SEQUENCE DESCRIPTION: SEQ ID NO: 612:
 US-09-721-456-612

Query Match 99.8%; Score 5952; DB 4; Length 1200;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVSLIRSHYREVLPATFVRRIGPQGMRLVQGDPAAPRALVAQCLVCPW 60
 Db MPAPRCRAVSLIRSHYREVLPATFVRRIGPQGMRLVQGDPAAPRALVAQCLVCPW 128
 QY 61 DARPPAPSPROYSCLEKEIVARVLCRCERGANVLAFGPALLDGAAGGPPAEFTTSVR 120
 Db DARPPAPSPROYSCLEKEIVARVLCRCERGANVLAFGPALLDGAAGGPPAEFTTSVR 188
 QY 129 DARPPAPSPROYSCLEKEIVARVLCRCERGANVLAFGPALLDGAAGGPPAEFTTSVR 188
 Db DARPPAPSPROYSCLEKEIVARVLCRCERGANVLAFGPALLDGAAGGPPAEFTTSVR 248
 QY 121 SYLPRTVTDALRGSGAWGLIRVGDVLYHLARCAFLVLAAPSCAYQVGPPELYQIGA 180
 Db SYLPRTVTDALRGSGAWGLIRVGDVLYHLARCAFLVLAAPSCAYQVGPPELYQIGA 248
 QY 189 SYLPRTVTDALRGSGAWGLIRVGDVLYHLARCAFLVLAAPSCAYQVGPPELYQIGA 248
 Db SYLPRTVTDALRGSGAWGLIRVGDVLYHLARCAFLVLAAPSCAYQVGPPELYQIGA 308
 QY 181 ATQAPPPHAGGPRRLCCERAMNHVREAGVPLGLPAPGARRGGASASRLPLPKPRR 240
 Db ATQAPPPHAGGPRRLCCERAMNHVREAGVPLGLPAPGARRGGASASRLPLPKPRR 308
 QY 249 ATQAPPPHAGGPRRLCCERAMNHVREAGVPLGLPAPGARRGGASASRLPLPKPRR 308
 Db ATQAPPPHAGGPRRLCCERAMNHVREAGVPLGLPAPGARRGGASASRLPLPKPRR 368
 QY 241 GAAPPEPTPVQGSMAHFGRTGSPDRGFCVSPAPAEATSLLEGALSTRSHSVG 300
 Db GAAPPEPTPVQGSMAHFGRTGSPDRGFCVSPAPAEATSLLEGALSTRSHSVG 368
 QY 309 GAAPPEPTPVQGSMAHFGRTGSPDRGFCVSPAPAEATSLLEGALSTRSHSVG 368
 Db GAAPPEPTPVQGSMAHFGRTGSPDRGFCVSPAPAEATSLLEGALSTRSHSVG 428
 QY 301 ROHAGPSTSRPPRPMPTPCPPVYAEKHEPLYSKGKEDLRPSFLISSRLPTGARRL 360
 Db ROHAGPSTSRPPRPMPTPCPPVYAEKHEPLYSKGKEDLRPSFLISSRLPTGARRL 428
 QY 369 ROHAGPSTSRPPRPMPTPCPPVYAEKHEPLYSKGKEDLRPSFLISSRLPTGARRL 428
 Db ROHAGPSTSRPPRPMPTPCPPVYAEKHEPLYSKGKEDLRPSFLISSRLPTGARRL 488
 QY 361 VETIFLIGSRPMMPGPRRLPLPRVYOMRPLFELLGNNAQCYGVLLKTHCLRAVY 420
 Db VETIFLIGSRPMMPGPRRLPLPRVYOMRPLFELLGNNAQCYGVLLKTHCLRAVY 488
 QY 429 VETIFLIGSRPMMPGPRRLPLPRVYOMRPLFELLGNNAQCYGVLLKTHCLRAVY 488
 Db VETIFLIGSRPMMPGPRRLPLPRVYOMRPLFELLGNNAQCYGVLLKTHCLRAVY 548
 QY 421 PAAGVCAEKQGSVAAPBEEDTDPRLVOLLROHSSPMQVYGFVRACLRVPGLMG 480
 Db PAAGVCAEKQGSVAAPBEEDTDPRLVOLLROHSSPMQVYGFVRACLRVPGLMG 548
 QY 489 PAAGVCAEKQGSVAAPBEEDTDPRLVOLLROHSSPMQVYGFVRACLRVPGLMG 548
 Db PAAGVCAEKQGSVAAPBEEDTDPRLVOLLROHSSPMQVYGFVRACLRVPGLMG 608
 QY 481 RHNERPLRNTKRTISGKAKLSLOELTWKMSRDCAMLRSGVCCVPAERHRLTEE 540
 Db RHNERPLRNTKRTISGKAKLSLOELTWKMSRDCAMLRSGVCCVPAERHRLTEE 608
 QY 549 RHNERPLRNTKRTISGKAKLSLOELTWKMSRDCAMLRSGVCCVPAERHRLTEE 608
 Db RHNERPLRNTKRTISGKAKLSLOELTWKMSRDCAMLRSGVCCVPAERHRLTEE 660
 QY 541 LAKEFLHMTSMVYVELLRSFFVYETTFOKNRLEFPFYPSPVSKQSIGIRQHLRVOLRE 600
 Db LAKEFLHMTSMVYVELLRSFFVYETTFOKNRLEFPFYPSPVSKQSIGIRQHLRVOLRE 668
 QY 609 LAKEFLHMTSMVYVELLRSFFVYETTFOKNRLEFPFYPSPVSKQSIGIRQHLRVOLRE 668
 Db LAKEFLHMTSMVYVELLRSFFVYETTFOKNRLEFPFYPSPVSKQSIGIRQHLRVOLRE 728
 QY 601 LSEAEVROHREARAPALLTSRLRFLPKPDGLRPYNNMYYVGARFFREKAERLTSVKA 660
 Db LSEAEVROHREARAPALLTSRLRFLPKPDGLRPYNNMYYVGARFFREKAERLTSVKA 728
 QY 669 LSEAEVROHREARAPALLTSRLRFLPKPDGLRPYNNMYYVGARFFREKAERLTSVKA 728
 Db LSEAEVROHREARAPALLTSRLRFLPKPDGLRPYNNMYYVGARFFREKAERLTSVKA 788
 QY 661 LFSVLINERARPPGLGASVGLGDIHRAWTFELRAADPPPELFFVKVDVGAADTI 720
 Db LFSVLINERARPPGLGASVGLGDIHRAWTFELRAADPPPELFFVKVDVGAADTI 788
 QY 729 LFSVLINERARPPGLGASVGLGDIHRAWTFELRAADPPPELFFVKVDVGAADTI 788
 Db LFSVLINERARPPGLGASVGLGDIHRAWTFELRAADPPPELFFVKVDVGAADTI 848
 QY 721 PQRRLTEVIASIIKPQNTYCVRRYAVVQKAHGHVRAKFSHVSUFTLTDLPYMQPYAHL 780
 Db PQRRLTEVIASIIKPQNTYCVRRYAVVQKAHGHVRAKFSHVSUFTLTDLPYMQPYAHL 848
 QY 789 PQRRLTEVIASIIKPQNTYCVRRYAVVQKAHGHVRAKFSHVSUFTLTDLPYMQPYAHL 848
 Db PQRRLTEVIASIIKPQNTYCVRRYAVVQKAHGHVRAKFSHVSUFTLTDLPYMQPYAHL 912
 QY 781 QETSPRLDAVVIQSSSLNENASSGLPDVFLRFPMCHAVRLIRGKSYVQCQGIPOGSLISTL 840

```

Db      849  QETSLRAVYIEGSSLINEASSGLFVFLRPMCHHVRIGKSYVCCQGIPOCSILSTL
           |||
Qy      841  LCSLCYGMENKLFAGIRRDGLLRVDFLLVTPHLTHAKTFLTRVGVPEYCVNL
           |||
Db      909  LCSLCYGMENKLFAGIRRDGLLRVDFLLVTPHLTHAKTFLTRVGVPEYCVNL
           |||
Qy      901  RKTVPNFEVDEALGCTAFVQMPAHGLFPKCGLLDPTLTLEVQSDSYNATSTRASVTF
           |||
Db      969  RKTVPNFEVDEALGCTAFVQMPAHGLFPKCGLLDPTLTLEVQSDSYNATSTRASVTF
           |||
Qy      961  NRGFAGNRMRKLFQVRLKCHSLFLDLQVNSLQVCTNIYKILLQAYRFAVCVQLP
           |||
Db      1029  NRGFAGNRMRKLFQVRLKCHSLFLDLQVNSLQVCTNIYKILLQAYRFAVCVQLP
           |||
Qy      1021  FHQVWKPTEFLRVISSTASICYSILKAKNAGSLGAKGAGPLPSEAVOMLCHQAFLL
           |||
Db      1089  FHQVWKPTEFLRVISSTASICYSILKAKNAGSLGAKGAGPLPSEAVOMLCHQAFLL
           |||
Qy      1081  KLTRHRVYVPLGSLRTAQQLSRKLPGLTLLLEAANPALPSDFETIIL
           |||
Db      1149  KLTRHRVYVPLGSLRTAQQLSRKLPGLTLLLEAANPALPSDFETIIL
           |||

```

RESULT 32

```

US-08-974-549A-600
Sequence 600, Application US/08974549A
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:

```

```

APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 600:
SEQUENCE CHARACTERISTICS:
LENGTH: 1285 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1285
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-08-974-549A-600
/note="fusion protein composed of
enterokinase cleavable, His tagged
thioredoxin moiety and full length hTrr"

```

```

Query Match 99.8%; Score 5952; DB 3; Length 1285;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1  MPAPRCRAVRSILSRHREYVPLATFVRRLCPQGRRLVQRPDPAAFRLVQCICVQVW 60
Db      154  MPAPRCRAVRSILSRHREYVPLATFVRRLCPQGRRLVQRPDPAAFRLVQCICVQVW 213
Qy      61  DAPPPAASPROVSCLEKELVARVLQRLCERAKAVLAFGALLDGAARGPPEAFTTSVR 120
Db      214  DAPPPAASPROVSCLEKELVARVLQRLCERAKAVLAFGALLDGAARGPPEAFTTSVR 273
Qy      121  SYLNTVTDALRSGAWGLLRVGDVTVHLARCALFVLAFCAYVCGPPLYLQGA 180
Db      274  SYLNTVTDALRSGAWGLLRVGDVTVHLARCALFVLAFCAYVCGPPLYLQGA 333
Qy      181  ATQARPPHAGSRRLGGERAMNHSVRAGVPLGAPAGARRGGSASRLPLPKRPR 240
Db      334  ATQARPPHAGSRRLGGERAMNHSVRAGVPLGAPAGARRGGSASRLPLPKRPR 393
Qy      241  GAAPPERPTPVGGSNAPGRTGPGSDRGFCVYSPAPPAEATSLGALSTRHSHPSVG 300
Db      394  GAAPPERPTPVGGSNAPGRTGPGSDRGFCVYSPAPPAEATSLGALSTRHSHPSVG 453
Qy      301  RQHHAGPSTSRPPRPMDPCPPVATKHPFLYSSDCKQLPSPFLSLSLRSLNGARL 360
Db      454  RQHHAGPSTSRPPRPMDPCPPVATKHPFLYSSDCKQLPSPFLSLSLRSLNGARL 513
Qy      361  VETIFLGSRRPMPGTGPRRLPLRQRYWQMRPLFELILGNHAOCQPYVLLKTHCPRAAVT 420
Db      514  VETIFLGSRRPMPGTGPRRLPLRQRYWQMRPLFELILGNHAOCQPYVLLKTHCPRAAVT 573
Qy      421  PAAGVCAREKPGQSVAAPEBEDTDPRLVQLRQSSPMQYVGFYACLRRLVPPPLKWS 480
Db      574  PAAGVCAREKPGQSVAAPEBEDTDPRLVQLRQSSPMQYVGFYACLRRLVPPPLKWS 633
Qy      481  RHNERRLRNTKFKFISLGNKAKLSLDELTKMSVRCALRRSPGVGCVPAAEHRLREBI 540
Db      634  RHNERRLRNTKFKFISLGNKAKLSLDELTKMSVRCALRRSPGVGCVPAAEHRLREBI 693

```

QY 541 LAKELHMLSVYVVELLSRFFVYTTTFOQKRLFFYPSPVSKLQSIGRCHLKVQLRE 600
 Db 694 LAKELHMLSVYVVELLSRFFVYTTTFOQKRLFFYPSPVSKLQSIGRCHLKVQLRE 753
 QY 601 LSEAEVQHRREARPAALITSLRPLPKPDGLRPVNMDDYVGAATFRREKAEELISRVA 660
 Db 754 LSEAEVQHRREARPAALITSLRPLPKPDGLRPVNMDDYVGAATFRREKAEELISRVA 813
 QY 661 LFSVLNERARRRPGILGASVGLGDDIHRAMRTFVLRAADPPPELYFVAVDTGAYDT 720
 Db 814 LFSVLNERARRRPGILGASVGLGDDIHRAMRTFVLRAADPPPELYFVAVDTGAYDT 873
 QY 721 PDRLETVIASIIRKONTYCVRRYAVVQKAAHGVKAFKSHVSTLTDQPYMRQFVAHL 780
 Db 874 PDRLETVIASIIRKONTYCVRRYAVVQKAAHGVKAFKSHVSTLTDQPYMRQFVAHL 933
 QY 781 QETSPLDVAVIESSSLNEASSGLFVPLRFVCHAVRRRGSVVOCCGIPGGSILSTL 840
 Db 934 QETSPLDVAVIESSSLNEASSGLFVPLRFVCHAVRRRGSVVOCCGIPGGSILSTL 993
 QY 841 LCSLCYGDMMENKLFAGIRRDGLLRLVDPDLVTPHLTHAKTFLRLVSGVPEYGVNL 900
 Db 994 LCSLCYGDMMENKLFAGIRRDGLLRLVDPDLVTPHLTHAKTFLRLVSGVPEYGVNL 1053
 QY 901 RKTIVNPFVDEALGTAFFVQMPAHGLFPWCGILLDRILEVQSDVSSVARTISRSLTF 960
 Db 1054 RKTIVNPFVDEALGTAFFVQMPAHGLFPWCGILLDRILEVQSDVSSVARTISRSLTF 1113
 QY 961 NRGFKAGNRNRKLFGLRLCKSHLFLDLQVNSIQVCTNIYKILLQAVRFACVLOLP 1020
 Db 1114 NRGFKAGNRNRKLFGLRLCKSHLFLDLQVNSIQVCTNIYKILLQAVRFACVLOLP 1173
 QY 1021 FHOQVKNPFFFLRVISDTASLCYSILKAKNAGSLGAKAGAPLSEAVQMLCHQAFLL 1080
 Db 1174 FHOQVKNPFFFLRVISDTASLCYSILKAKNAGSLGAKAGAPLSEAVQMLCHQAFLL 1233
 QY 1081 KLTRHRVTYVPLIGSLPTAQTQSRKLPGLTTLALEAANPALPSPFKTLLD 1132
 Db 1234 KLTRHRVTYVPLIGSLPTAQTQSRKLPGLTTLALEAANPALPSPFKTLLD 1285

RESULT 33

US-08-912-951-314
 ; Sequence 314, Application US/08912951
 ; Patent No. 6475789

GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.
 ; APPLICANT: Lingner, Joachim
 ; APPLICANT: Nakamura, Toru
 ; APPLICANT: Chapman, Karen B.
 ; APPLICANT: Morin, Gregg B.
 ; APPLICANT: Harley, Calvin
 ; APPLICANT: Andrews, William H.
 ; TITLE OF INVENTION: HUMAN TELOWERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
 ; TITLE OF INVENTION: THERAPEUTIC METHODS
 ; NUMBER OF SEQUENCES: 335
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States of America
 ; ZIP: 94111

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/912,951
 ; FILING DATE: 14-AUG-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/854,050
 ; FILING DATE: 09-MAY-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/851,843
 ; FILING DATE: 06-MAY-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/846,017
 ; FILING DATE: 25-APR-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/844,419
 ; FILING DATE: 18-APR-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/724,643
 ; FILING DATE: 01-OCT-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Apple, Randolph T.
 ; REGISTRATION NUMBER: 36,429
 ; REFERENCE/DOCKET NUMBER: 015389-002600US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 314:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1285 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-912-951-314

Query Match 99.8%; Score 5952; DB 4; Length 1285;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRAPRCRAVRSLSHSHREVLPATFVRRLGPGMRLVQGDPAAPFALVAQCLVCPW 60
 Db 154 MRAPRCRAVRSLSHSHREVLPATFVRRLGPGMRLVQGDPAAPFALVAQCLVCPW 213
 QY 61 DARPPAAPSPROYSCLEIYVARVLQRLCERGAKNVLAFGALLDGAAGSEPEAFTSVR 120
 Db 214 DARPPAAPSPROYSCLEIYVARVLQRLCERGAKNVLAFGALLDGAAGSEPEAFTSVR 273
 QY 121 SYLPNTVTDALRGSGAWGLLRVGDVTVHLLARCALFVLVAPSCAYQVGPPLVYQGA 180
 Db 274 SYLPNTVTDALRGSGAWGLLRVGDVTVHLLARCALFVLVAPSCAYQVGPPLVYQGA 333
 QY 181 ATQARPPPHASGPRRLRCERAMNHSVREAGVPLGLPAPGARRGGSASRLPLPKPRRR 240
 Db 334 ATQARPPPHASGPRRLRCERAMNHSVREAGVPLGLPAPGARRGGSASRLPLPKPRRR 393
 QY 241 GAAPPERKTPVGGGWAHGRTRGSDRGFCVSPAPARAEATSLGALSSTRSHSPSVG 300
 Db 394 GAAPPERKTPVGGGWAHGRTRGSDRGFCVSPAPARAEATSLGALSSTRSHSPSVG 453
 QY 301 ROHAGPSTSRPPSPMDTPCPPVYAEIKHFLYSSGDKERQLRPSFLSLSPSLTGARRL 360
 Db 454 ROHAGPSTSRPPSPMDTPCPPVYAEIKHFLYSSGDKERQLRPSFLSLSPSLTGARRL 513
 QY 361 VETITLGRPMWPGPRRLPLRPORVWOMRPLFLGLGNHACQPYGLKTHCPRAAVT 420
 Db 514 VETITLGRPMWPGPRRLPLRPORVWOMRPLFLGLGNHACQPYGLKTHCPRAAVT 573
 QY 421 PAAGVCAEKPGQSVAAPEEDTDPRRLVOLLROHSSFWQYGFVRACLRLVPPGLWGS 480
 Db 574 PAAGVCAEKPGQSVAAPEEDTDPRRLVOLLROHSSFWQYGFVRACLRLVPPGLWGS 633
 QY 481 RHNERFLRNTKFTSLGKNAKLSIGELTWKQSVRDCAWLRSSGVGVPAEHRLEETI 540

Db 634 RINERBFLNNTKFTSLGKHAFLSLQELTWKSVFDCMLRSPGVCPAAHRLREI 693

QY 541 LAKFLHMLSVYVVELLSFFVYETETQKRLFFRPSWSKLQSIGIRHKLKVQRE 600

Db 694 LAKFLHMLSVYVVELLSFFVYETETQKRLFFRPSWSKLQSIGIRHKLKVQRE 753

QY 601 LSEAEVRQREARPAALTSRLAFIKPDGLRPIVMDYVGAFTREKREKRLSRKA 660

Db 754 LSEAEVRQREARPAALTSRLAFIKPDGLRPIVMDYVGAFTREKREKRLSRKA 813

QY 661 LFSVNIYERARRPGLGASVLGLDDIHPAMRTFVRAODPPPELYEVKVDVGYDTI 720

Db 814 LFSVNIYERARRPGLGASVLGLDDIHPAMRTFVRAODPPPELYEVKVDVGYDTI 873

QY 721 PODRLTEVYASIIKQNTYCVRRYAVVOKAAGHVRKAPKSHVSTLTLOPYMQFVNL 780

Db 874 PODRLTEVYASIIKQNTYCVRRYAVVOKAAGHVRKAPKSHVSTLTLOPYMQFVNL 933

QY 781 QETSPLRDAVYIEQSSSLNEASSGFLDYFLRFMCHAVRIRGKSYVQCQIPQSGILSTL 840

Db 934 QETSPLRDAVYIEQSSSLNEASSGFLDYFLRFMCHAVRIRGKSYVQCQIPQSGILSTL 993

QY 841 LCSLCYGMENKLPAGIRRDGLLLRLVDDFLVTLPHLTHAKTFLTLVGVPEYGVVNL 900

Db 994 LCSLCYGMENKLPAGIRRDGLLLRLVDDFLVTLPHLTHAKTFLTLVGVPEYGVVNL 1053

QY 901 RKTVVNPEVEDALGSTAFVOMPAHGLPFMCGLLDTSLEVOQDYSYASTSRASYTF 960

Db 1054 RKTVVNPEVEDALGSTAFVOMPAHGLPFMCGLLDTSLEVOQDYSYASTSRASYTF 1113

QY 961 NEGFKAGNMRRKLPGLVRLKCHSLFLDLQVNSLQVCTNIYKILLQAYRFAVCVQLP 1020

Db 1114 NEGFKAGNMRRKLPGLVRLKCHSLFLDLQVNSLQVCTNIYKILLQAYRFAVCVQLP 1173

QY 1021 FHQQWKNPTFFLRYISDTASLCYSIILKAKNAGSLGKGAAGLPSENAVOMLCHQARLL 1080

Db 1174 FHQQWKNPTFFLRYISDTASLCYSIILKAKNAGSLGKGAAGLPSENAVOMLCHQARLL 1233

QY 1081 KTRRHVTVPLGLSLRTAQOTLSRKLPGTTLTALEAANPALPSPDFITLD 1132

Db 1234 KTRRHVTVPLGLSLRTAQOTLSRKLPGTTLTALEAANPALPSPDFITLD 1285

RESULT 34

US-09-402-181B-600

Sequence 600, Application US/09402181B

Patent No. 6610839

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 633

CORRESPONDENCE ADDRESS:

ADDRESSER: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/09/402,181B

APPLICATION NUMBER: US/09/402,181B

FILING DATE: 29-Sep-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17865

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ausenbus, Scott L.

REGISTRATION NUMBER: 42,271

REFERENCE/DOCKET NUMBER: 015389-002620US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 600:

SEQUENCE CHARACTERISTICS:

LENGTH: 1285 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Protein

LOCATION: 1..1285

OTHER INFORMATION: /note="fusion protein composed of enterokinase cleavable, His tagged chondroxin moiety and full length hTERT"

SEQUENCE DESCRIPTION: SEQ ID NO: 600:

US-09-402-181B-600

Query Match 99.8%; Score 5952; DB 4; Length 1285;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSILRHRYEVLPLATFVRRLPGQWRVLYQDGPAPAFALVAQCLVCVM 60

Db 154 MPAPRCRAVRSILRHRYEVLPLATFVRRLPGQWRVLYQDGPAPAFALVAQCLVCVM 213

QY 61 DAREPPAARFROVSCLEKELVAVVYLQRLCERAKNVLACGFALLDQARGPPEAFTSVR 120

Db 214 DAREPPAARFROVSCLEKELVAVVYLQRLCERAKNVLACGFALLDQARGPPEAFTSVR 273

QY 121 SYLPNTVTDALRSGAGMLLRVGDVYLHLARCALFVLVAPSCAYVCGPPVYQLGA 180

Db 274 SYLPNTVTDALRSGAGMLLRVGDVYLHLARCALFVLVAPSCAYVCGPPVYQLGA 333

QY 181 ATQARPPHAGGRRRLGGERANNSVRBAQVPLGIPAGARRGGSARSPLPRLPRR 240

Db 334 ATQARPPHAGGRRRLGGERANNSVRBAQVPLGIPAGARRGGSARSPLPRLPRR 393

QY 241 GAAPPEPRTPVGGSWAHGRTGPGSDRGCVVSPAPPAEATSLGALSGTRHSPSVG 300

Db 394 GAAPPEPRTPVGGSWAHGRTGPGSDRGCVVSPAPPAEATSLGALSGTRHSPSVG 453

QY 301 ROHHAGPSTSRPPRMDTPCPVVAETGFLYSSGDKQLRPSFLSLRPSLTGARL 360

Db 454 ROHHAGPSTSRPPRMDTPCPVVAETGFLYSSGDKQLRPSFLSLRPSLTGARL 513

QY 361 VETIFLGSRRPMGCTRRRLPRLPQRYWQMRPLFLELLGNHACQPVYLLKTCPLBAAYT 420

Db 514 VETIFLGSRRPMGCTRRRLPRLPQRYWQMRPLFLELLGNHACQPVYLLKTCPLBAAYT 573

Tue Dec 21 15:43:30 2004

us-08-974-584c-118.txt

Page 37

421 PAAGVACAREKPGQSVAPAREEDTDPRLVOLLKROHSSPMQVGFVRACTRLVPLPGLMS 480
574 PAAGVACAREKPGQSVAPAREEDTDPRLVOLLKROHSSPMQVGFVRACTRLVPLPGLMS 633
481 RHNERRLRLNTKXKFIISGKAKLSLOGLTWKMSVDCAMLRSPGVCVPAARHRLREEL 540
634 RHNERRLRLNTKXKFIISGKAKLSLOGLTWKMSVDCAMLRSPGVCVPAARHRLREEL 693
541 LAKEFLHMLSVYVVELLSFEFFYTETTFQXNRLFFYRPSWSKLOSIGIRHOLKXQVLE 600
694 LAKEFLHMLSVYVVELLSFEFFYTETTFQXNRLFFYRPSWSKLOSIGIRHOLKXQVLE 753
601 LSEAEVQRHREARPAITSLRFLPKPDGLRPIVNDYVGAATFRERKAEELTSRVXA 660
754 LSEAEVQRHREARPAITSLRFLPKPDGLRPIVNDYVGAATFRERKAEELTSRVXA 813
661 LFSVLANERARRRPGGLGASVGLGDDHRAWRTVLVRAODPPPELYFYKVDTGAYDTI 720
814 LFSVLANERARRRPGGLGASVGLGDDHRAWRTVLVRAODPPPELYFYKVDTGAYDTI 873
721 PODRLTEVIAIIPQNTYCVRRYAVVQKAAHGVKAFKSHVSTLTDQPYMKQVAAH 780
874 PODRLTEVIAIIPQNTYCVRRYAVVQKAAHGVKAFKSHVSTLTDQPYMKQVAAH 933
781 QETSPLDVAVTEGSSSLNEASSGLFVFLRPMCHAVRIRGKSYYOCCGIPGGSILSTL 840
934 QETSPLDVAVTEGSSSLNEASSGLFVFLRPMCHAVRIRGKSYYOCCGIPGGSILSTL 993
841 LCSI.CYDGMENKLPAGIRRDGLLRLVDDPLVTLPHLTHAKTLRLVSGVPEYGVNL 900
994 LCSI.CYDGMENKLPAGIRRDGLLRLVDDPLVTLPHLTHAKTLRLVSGVPEYGVNL 1053
901 RKTYYNPFVEDEALGTAFAVQMPAHGJ.FPWCGILDLTRTELVEVSDYSSVARTSIRASVTF 960
1054 RKTYYNPFVEDEALGTAFAVQMPAHGJ.FPWCGILDLTRTELVEVSDYSSVARTSIRASVTF 1113
961 NRGKARNNRRKLFGLVRLKCHSLFLDLVNS.OTVCTNYITLILLOAFHACVLOLP 1020
1114 NRGKARNNRRKLFGLVRLKCHSLFLDLVNS.OTVCTNYITLILLOAFHACVLOLP 1173
1021 FHQGVNKPTEFFLRVISDLSLCSYLKAKNAGNSLGAKGAGPLPSEAVQWLCHQAFLL 1080
1174 FHQGVNKPTEFFLRVISDLSLCSYLKAKNAGNSLGAKGAGPLPSEAVQWLCHQAFLL 1233
1081 KLTRHRTTYVPLGLSLATAQTOQLSRKLPSTTLTALLEANPALPSPDKTILLD 1132
1234 KLTRHRTTYVPLGLSLATAQTOQLSRKLPSTTLTALLEANPALPSPDKTILLD 1285

RESULT 35
US-09-721-456-600
Sequence 600, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Inventor: Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721 456
FILING DATE: 22-NOV-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974, 549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724, 643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844, 419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846, 017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851, 843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854, 050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911, 312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912, 951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915, 503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 600:
SEQUENCE CHARACTERISTICS:
LENGTH: 1285 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1285
OTHER INFORMATION: /note= "fusion protein composed of
enterokinase cleavable, His tagged
thioredoxin moiety and full length hTERT"
SEQUENCE DESCRIPTION: SEQ ID NO: 600:
US-09-721-456-600

Query Match 99.8%; Score 5952; DB 4; Length 1285;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 MPARPCAVRSILSHRYEVPLATFVRRLGPOGMRIVQSGDPAFAFALVAQCIACVPM 60
154 MPARPCAVRSILSHRYEVPLATFVRRLGPOGMRIVQSGDPAFAFALVAQCIACVPM 213
61 DARPPAAPSPFQVSCLELVARVQLRCERAKNVLAFFGALLDGAAGGPEAATTISVR 120
214 DARPPAAPSPFQVSCLELVARVQLRCERAKNVLAFFGALLDGAAGGPEAATTISVR 273
121 SYLPTVTDALRGSGAMGILLRRVGDVYLHLARCALFVVAWSCAYOVCGPPLXYQGA 180
274 SYLPTVTDALRGSGAMGILLRRVGDVYLHLARCALFVVAWSCAYOVCGPPLXYQGA 333
181 ATQARPPPHASGPRRLRCERAMNHSVREAGVPLGLPAGARRRGSASRLPLPKRPRR 240
334 ATQARPPPHASGPRRLRCERAMNHSVREAGVPLGLPAGARRRGSASRLPLPKRPRR 393

```

QY 241 GAAPPEERTPVGGSWAHFGRTRGPDGFCVVSPPAPAEATSTSEALSGTRSHSPVVG 300
DB 394 GAAPPEERTPVGGSWAHFGRTRGPDGFCVVSPPAPAEATSTSEALSGTRSHSPVVG 453
QY 301 ROHHAAPPTSTSRPMDTFCPPVVAETGHPLYSSDQKQLPSPFLSLSLRSLGAPRL 360
DB 454 ROHHAAPPTSTSRPMDTFCPPVVAETGHPLYSSDQKQLPSPFLSLSLRSLGAPRL 513
QY 361 VETIFLGSSAPWMEGTBRRLPRLPQRYWQMRPLFELIGNHAOCPPYVILLKHCPLRAAVT 420
DB 514 VETIFLGSSAPWMEGTBRRLPRLPQRYWQMRPLFELIGNHAOCPPYVILLKHCPLRAAVT 573
QY 421 PAAGVAREKPOGQSVAPAEEDTPPRVLVOLRQSSPWQYGFACICRLRYPGGLMS 480
DB 574 PAAGVAREKPOGQSVAPAEEDTPPRVLVOLRQSSPWQYGFACICRLRYPGGLMS 633
QY 481 RHNERREFLNTKFFISLGHAKLSLOELTKMSVDCAWLRSPGVGCPVAERHREBEI 540
DB 634 RHNERREFLNTKFFISLGHAKLSLOELTKMSVDCAWLRSPGVGCPVAERHREBEI 693
QY 541 LAEFLHMLSVYVVELLRFPYVETETPQKRLFPYRPSVMSKOSIGIRQLKRVQURE 600
DB 694 LAEFLHMLSVYVVELLRFPYVETETPQKRLFPYRPSVMSKOSIGIRQLKRVQURE 753
QY 601 LSEAEVROHREARFALLTSRLRPIPKDGLRPIVMDYVVGARTPRERKARLTSRYKA 660
DB 754 LSEAEVROHREARFALLTSRLRPIPKDGLRPIVMDYVVGARTPRERKARLTSRYKA 813
QY 661 LBSVLNVERARRRPGLIGASVLDIHDHRAWRTFVLRADPPPELLFYKXDVTCAYDTI 720
DB 814 LBSVLNVERARRRPGLIGASVLDIHDHRAWRTFVLRADPPPELLFYKXDVTCAYDTI 873
QY 721 PODRLTEVASTIKPONTYCVRYAYVQKAAHGRKAKFSHVSTLTLDOPRMOQVANH 780
DB 874 PODRLTEVASTIKPONTYCVRYAYVQKAAHGRKAKFSHVSTLTLDOPRMOQVANH 933
QY 781 QETSPLRDAVVIQSSSLNEASSGLFDFVLRFMCHAVRIRKSSVYQCGIPQSSILSTL 840
DB 934 QETSPLRDAVVIQSSSLNEASSGLFDFVLRFMCHAVRIRKSSVYQCGIPQSSILSTL 993
QY 841 LCSLCYGDENKLPFAIRRDGILLRVDDELVTPLTHAKFELTLVRGVEYGCYNL 900
DB 994 LCSLCYGDENKLPFAIRRDGILLRVDDELVTPLTHAKFELTLVRGVEYGCYNL 1053
QY 901 RKTVMNFPVEDEALGTAFCVMPAGLFPWCGLLDTRTLEVOSSYASRTSIRASYTF 960
DB 1054 RKTVMNFPVEDEALGTAFCVMPAGLFPWCGLLDTRTLEVOSSYASRTSIRASYTF 1113
QY 961 NRGFKAGRMWRKTLFGVLRKCHSLFLDQVNSLQTVCTNIYKILLQAYRPHACVLDLP 1020
DB 1114 NRGFKAGRMWRKTLFGVLRKCHSLFLDQVNSLQTVCTNIYKILLQAYRPHACVLDLP 1173
QY 1021 FHQGVKNFTFLRVTSDTASLCYSTLKAKNAGMSLGAAGAAPPSEAVQWLCGQAFLL 1080
DB 1174 FHQGVKNFTFLRVTSDTASLCYSTLKAKNAGMSLGAAGAAPPSEAVQWLCGQAFLL 1233
QY 1081 KLTRHRTVYVPLIGSLRTAQOLSRKLPSTTVLTALBAANPALPSDFKTIID 1132
DB 1234 KLTRHRTVYVPLIGSLRTAQOLSRKLPSTTVLTALBAANPALPSDFKTIID 1285

```

RESULT 36
US-08-974-549A-5
Sequence 5, Application US/08974549A
Patent No. 6166178

GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Linsmet, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.

```

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17685
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-549A-5

```

Query Match 67.9%; Score 4046; DB 3; Length 807;
Best Local Similarity 99.9%; Pctd. No. 0;
Matches 762; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MPAPRCRAVRSLLSHYREVLPALFVRLIGQGRWLVORGDPAPAFRALVAGCLVCYVM 60
DB 1 MPAPRCRAVRSLLSHYREVLPALFVRLIGQGRWLVORGDPAPAFRALVAGCLVCYVM 60
QY 61 DAPPPAPSPFRCVSLKELVAVRLQRCGAKNVLAFCFALLDQAGCPPEAFTTVR 120

```

```

Db 61 DARPPAASFRQVSCLEKELVARVLQRLCEGAKNVLAFGFALLDGAAGPPEAFTTSVR 120
Qy 121 SYLPNTVTDALRGSGAMGLLRVGGDVLVHLLARCALFVVA8CAVQVCGPPLYQGA 180
Db 121 SYLPNTVTDALRGSGAMGLLRVGGDVLVHLLARCALFVVA8CAVQVCGPPLYQGA 180
Qy 181 ATQARPPPHASGPRRLGCEERAMNHSVREAGVPLGPAFGARRGSGASRSLPLPKRPR 240
Db 181 ATQARPPPHASGPRRLGCEERAMNHSVREAGVPLGPAFGARRGSGASRSLPLPKRPR 240
Qy 241 GAAPPERTPVQGGSWAHGRTGSDRGFCVSPAPAEATSLGALSGTRHSHPSVG 300
Db 241 GAAPPERTPVQGGSWAHGRTGSDRGFCVSPAPAEATSLGALSGTRHSHPSVG 300
Qy 301 ROHAGPSTSRPPRMDTCCPVYAETKHFLVSSGDKELRPSFLSSLRPSLTGARL 360
Db 301 ROHAGPSTSRPPRMDTCCPVYAETKHFLVSSGDKELRPSFLSSLRPSLTGARL 360
Qy 361 VETIFLGSRPWMPGTFRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRPWMPGTFRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEEDTDFRLVQLRQSHSPWQYGFVPAQLRLVPGLMGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTDFRLVQLRQSHSPWQYGFVPAQLRLVPGLMGS 480
Qy 481 RHNERRLRNTKKEFISLGKAKLSLOELTWKMSVRCAMLRSPGVGCVPAAHRLEBI 540
Db 481 RHNERRLRNTKKEFISLGKAKLSLOELTWKMSVRCAMLRSPGVGCVPAAHRLEBI 540
Qy 541 LAFLHMLSVVYVELLRSPFYVTTETTFQKNRLEFFRPSWSKLSQIGTFOHAKRYQLE 600
Db 541 LAFLHMLSVVYVELLRSPFYVTTETTFQKNRLEFFRPSWSKLSQIGTFOHAKRYQLE 600
Qy 601 LSEAEVQHRERAPALTSRLFPKPDGRPIVNMDDVVGARTFRERKAEELTSRYVA 660
Db 601 LSEAEVQHRERAPALTSRLFPKPDGRPIVNMDDVVGARTFRERKAEELTSRYVA 660
Qy 661 LFSVLYNERARRPGLIGASVGLDDIHRMRTFVLRAVADPPPELYFVAVDTGAYDTI 720
Db 661 LFSVLYNERARRPGLIGASVGLDDIHRMRTFVLRAVADPPPELYFVAVDTGAYDTI 720
Qy 721 POBLTEVIAIITKPONTCVREYAVVQKRAHGHVRAAFSHV 763
Db 721 POBLTEVIAIITKPONTCVREYAVVQKRAHGHVRAAFSHV 763

```

```

RESULT 37
US-08-912-951-5
Sequence 5, Application US/08912951
Patent No. 6475789
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Linsner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Hatley, Calvin H.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
TITLE OF INVENTION: THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-951-5
Query Match 67.9%; Score 4046; DB 4; Length 807;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 762; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MRARPCANVASLSRSHREVLPLATFYRRRGPGMRVYQGGDPAFAFALVAQCLVCPW 60
Db 1 MRARPCANVASLSRSHREVLPLATFYRRRGPGMRVYQGGDPAFAFALVAQCLVCPW 60
Qy 61 DARPPAASFRQVSCLEKELVARVLQRLCEGAKNVLAFGFALLDGAAGPPEAFTTSVR 120
Db 61 DARPPAASFRQVSCLEKELVARVLQRLCEGAKNVLAFGFALLDGAAGPPEAFTTSVR 120
Qy 121 SYLPNTVTDALRGSGAMGLLRVGGDVLVHLLARCALFVVA8CAVQVCGPPLYQGA 180
Db 121 SYLPNTVTDALRGSGAMGLLRVGGDVLVHLLARCALFVVA8CAVQVCGPPLYQGA 180
Qy 181 ATQARPPPHASGPRRLGCEERAMNHSVREAGVPLGPAFGARRGSGASRSLPLPKRPR 240
Db 181 ATQARPPPHASGPRRLGCEERAMNHSVREAGVPLGPAFGARRGSGASRSLPLPKRPR 240
Qy 241 GAAPPERTPVQGGSWAHGRTGSDRGFCVSPAPAEATSLGALSGTRHSHPSVG 300
Db 241 GAAPPERTPVQGGSWAHGRTGSDRGFCVSPAPAEATSLGALSGTRHSHPSVG 300
Qy 301 ROHAGPSTSRPPRMDTCCPVYAETKHFLVSSGDKELRPSFLSSLRPSLTGARL 360
Db 301 ROHAGPSTSRPPRMDTCCPVYAETKHFLVSSGDKELRPSFLSSLRPSLTGARL 360
Qy 361 VETIFLGSRPWMPGTFRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRPWMPGTFRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEEDTDFRLVQLRQSHSPWQYGFVPAQLRLVPGLMGS 480

```

```

Db 421 PAAGVAREKPOGSAVAPEEDTDRRLVQLRQHSPPQYGVFARACLRVPPGLWGS 480
QY 481 RHNERFFLNNTKFFISLGHAKLSLOELTWKMSVDCAMLRSPGVGCVPAAEHRLREI 540
Db 481 RHNERFFLNNTKFFISLGHAKLSLOELTWKMSVDCAMLRSPGVGCVPAAEHRLREI 540
QY 541 LAKFLMLMSVYVELLSFFVYETTFPOKNLFFRPSVMSKLSIGIRHKLKVQURE 600
Db 541 LAKFLMLMSVYVELLSFFVYETTFPOKNLFFRPSVMSKLSIGIRHKLKVQURE 600
QY 601 LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVNDVVGARTFRERKRAERLTSRYKA 660
Db 601 LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVNDVVGARTFRERKRAERLTSRYKA 660
QY 661 LFSVLNVEARARRRGLGASVLDGDIHRMRFVLRVRAQDPPPELYFKVDVTGAYDTI 720
Db 661 LFSVLNVEARARRRGLGASVLDGDIHRMRFVLRVRAQDPPPELYFKVDVTGAYDTI 720
QY 721 POURLTEVIASIIKPONTYCVRRYAVVQKAAHGHVKAFAKSHV 763
Db 721 POURLTEVIASIIKPONTYCVRRYAVVQKAAHGHVKAFAKSHV 763

```

RESULT 38

```

US-09-402-181B-5
Sequence 5, Application US/09402181B
Patent No. 6610839

```

GENERAL INFORMATION:

```

APPLICANT: Cech, Thomas R.
            Lingner, Joachim
            Nakamura, Toru
            Chapman, Karen B.
            Morin, Gregg B.
            Harley, Calvin B.
            Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESSES:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

```

COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

```

```

APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

```

```

ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-00262005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-402-181B-5

```

```

Query Match 67.3%; Score 4046; DB 4; Length 807;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 762; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 MPAPRCRAVRSILRSHYREVLPATFVRLPGQGRVLYORGPAPAFALVAQCLVCPW 60
Db 1 MPAPRCRAVRSILRSHYREVLPATFVRLPGQGRVLYORGPAPAFALVAQCLVCPW 60
QY 61 DAPPAPAPSPROVSCLEIVARVLOLCEGAKNYLAFGALLDAGRGPPAPFTSYR 120
Db 61 DAPPAPAPSPROVSCLEIVARVLOLCEGAKNYLAFGALLDAGRGPPAPFTSYR 120
QY 121 SYLPNTVTDALRGSGAGMLLRVGGDVLVHLARCALFVLVAPSCAYVCGPELYQLGA 180
Db 121 SYLPNTVTDALRGSGAGMLLRVGGDVLVHLARCALFVLVAPSCAYVCGPELYQLGA 180
QY 181 ATQARPPHAGRRRLGGERAMNSVREAGVPLGLPABGARRGGASRSLPLPKRPR 240
Db 181 ATQARPPHAGRRRLGGERAMNSVREAGVPLGLPABGARRGGASRSLPLPKRPR 240
QY 241 GAAPPEERTVGGSAHAGRTGPGSDRGFCVSPAPAEATSLGALSGRHSPPSG 300
Db 241 GAAPPEERTVGGSAHAGRTGPGSDRGFCVSPAPAEATSLGALSGRHSPPSG 300
QY 301 ROHHAGPSTSRPPRMDTPCPVVAETKPLFYSSGDKQLRPSFLSLSLTGARRL 360
Db 301 ROHHAGPSTSRPPRMDTPCPVVAETKPLFYSSGDKQLRPSFLSLSLTGARRL 360
QY 361 VETIFLGSRRPMGTTRRLPRLPQRYOMRPLFLELLGHNAOCPYVLKTHCPPLRAVT 420
Db 361 VETIFLGSRRPMGTTRRLPRLPQRYOMRPLFLELLGHNAOCPYVLKTHCPPLRAVT 420
QY 421 PAAGVAREKPOGSAVAPEEDTDRRLVQLRQHSPPQYGVFARACLRVPPGLWGS 480
Db 421 PAAGVAREKPOGSAVAPEEDTDRRLVQLRQHSPPQYGVFARACLRVPPGLWGS 480
QY 481 RHNERFFLNNTKFFISLGHAKLSLOELTWKMSVDCAMLRSPGVGCVPAAEHRLREI 540
Db 481 RHNERFFLNNTKFFISLGHAKLSLOELTWKMSVDCAMLRSPGVGCVPAAEHRLREI 540
QY 541 LAKFLMLMSVYVELLSFFVYETTFPOKNLFFRPSVMSKLSIGIRHKLKVQURE 600
Db 541 LAKFLMLMSVYVELLSFFVYETTFPOKNLFFRPSVMSKLSIGIRHKLKVQURE 600
QY 601 LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVNDVVGARTFRERKRAERLTSRYKA 660
Db 601 LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVNDVVGARTFRERKRAERLTSRYKA 660
QY 661 LFSVLNVEARARRRGLGASVLDGDIHRMRFVLRVRAQDPPPELYFKVDVTGAYDTI 720
Db 661 LFSVLNVEARARRRGLGASVLDGDIHRMRFVLRVRAQDPPPELYFKVDVTGAYDTI 720
QY 721 POURLTEVIASIIKPONTYCVRRYAVVQKAAHGHVKAFAKSHV 763
Db 721 POURLTEVIASIIKPONTYCVRRYAVVQKAAHGHVKAFAKSHV 763

```


Tue Dec 21 15:43:30 2004

us-08-974-584c-118.txt

Page 41

RESULT 39
US-09-721-456-5
Sequence 5, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cecchi, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
City: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17685
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-721-456-5
Query Match 67.9%; Score 4046; DB 4; Length 807;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 762; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAPRCVAVSLRSYREVLPLATFVRLGPGQMRIVQGDPAAPRALVAOCLVCVPM 60
DB 1 MPRAPRCVAVSLRSYREVLPLATFVRLGPGQMRIVQGDPAAPRALVAOCLVCVPM 60
QY 61 DARPPAPSPFRQVSLKELVAVLQRLCERGANVLAFGALLDGAAGPPEAFTTSVR 120
DB 61 DARPPAPSPFRQVSLKELVAVLQRLCERGANVLAFGALLDGAAGPPEAFTTSVR 120
QY 121 SYLPNTVTDALRGSGAWGLLRVYDVLVHLLARCALFVLVAPSCAYQVCGPPLYQGA 180
DB 121 SYLPNTVTDALRGSGAWGLLRVYDVLVHLLARCALFVLVAPSCAYQVCGPPLYQGA 180
QY 181 ATQAPPPHAGSPRRRLGCEPAMNHSVLAQVPLGPARRRGSGASRLPLPKRRR 240
DB 181 ATQAPPPHAGSPRRRLGCEPAMNHSVLAQVPLGPARRRGSGASRLPLPKRRR 240
QY 241 GAAPPERTPVQGGSMWHPGRTGSDRGFCVSPAPAPAEATSLGALSSTRSHPSVG 300
DB 241 GAAPPERTPVQGGSMWHPGRTGSDRGFCVSPAPAPAEATSLGALSSTRSHPSVG 300
QY 301 RQHNAGPPTSRPPRPMDTPCPVYAEKHLVYSSGDKQLRPSFLSLSPSLGARL 360
DB 301 RQHNAGPPTSRPPRPMDTPCPVYAEKHLVYSSGDKQLRPSFLSLSPSLGARL 360
QY 361 VETITLGRPMWPGTFRRLPRLPORWQMRPLELELGNHACQPGVLLKTHCPLEAAVT 420
DB 361 VETITLGRPMWPGTFRRLPRLPORWQMRPLELELGNHACQPGVLLKTHCPLEAAVT 420
QY 421 PAAGVCAEKPQGSVAAPDEEDTDBRLVQLLRHSSWQVYGFYACLRILVPPGLWS 480
DB 421 PAAGVCAEKPQGSVAAPDEEDTDBRLVQLLRHSSWQVYGFYACLRILVPPGLWS 480
QY 481 RNNRRPLRNTKFTSLGKAKLSQELTWKMSVDCMLRSPGVGCVPAEHLRREI 540
DB 481 RNNRRPLRNTKFTSLGKAKLSQELTWKMSVDCMLRSPGVGCVPAEHLRREI 540
QY 541 IAKFLHMLSVYVVELLSFFVYETTFQKNRLFYRPSWSKLSQSIGRHLKRVQURE 600
DB 541 IAKFLHMLSVYVVELLSFFVYETTFQKNRLFYRPSWSKLSQSIGRHLKRVQURE 600
QY 601 LSEAEVQRREARPLLTSLRLFIPKPGLRPIVMDVVGARTREKRAERLTSRYKA 660
DB 601 LSEAEVQRREARPLLTSLRLFIPKPGLRPIVMDVVGARTREKRAERLTSRYKA 660
QY 661 LFSVLYNERARRPGLLGASVGLDDIHRAMRTFVLRAQDPPEPLVYVKVDVTGAYDTI 720
DB 661 LFSVLYNERARRPGLLGASVGLDDIHRAMRTFVLRAQDPPEPLVYVKVDVTGAYDTI 720
QY 721 PODRLTEVIASIKPONTYCVRRYAVVQKAAGHVRKAFKSHV 763
DB 721 PODRLTEVIASIKPONTYCVRRYAVVQKAAGHVRKAFKSHV 763

RESULT 40
US-08-851-843A-217
Sequence 217, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cecchi, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: No. 6093809e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
City: San Francisco
STATE: California
COUNTRY: United States of America

```
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-8200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 217:
SEQUENCE CHARACTERISTICS:
LENGTH: 1003 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-851-843A-217

Query Match      63.9%; Score 3810.5; DB 3; Length 1003;
Best Local Similarity 78.5%; Pred. No. 0;
Matches 786; Conservative 24; Mismatches 124; Indels 67; Gaps 18;

QY 163 AHS-CAYVCGPPYLGLAATQAPPPHAGSPRRRL-----GCEAHNSVREAGVPLG 215
DB 39 APTXCAGRRRC-----TSSALXLRP-----GPRHTLXDPAHGIGRAMHNSVREAGVPLG 87
QY 216 LPAPGARRSGSASRLPLPKRPR--RGAARPEPRT--PVGGSMWHPGRT--GPSDRGFC 271
DB 88 CQ---PRVAGGAGVPAEVCRCPRGPGVALPLSISGRPLRG---PGPTRAGRLDR--VT 139
QY 272 VVS-----PARP-----AEEATSLGALSGTRSHSPSVGRQ--HHAGPPSTSRP 313
DB 140 VVSVMCHLPDPKPKPLMVRSLARATPTHPMAASTRAHPHGHVGHALSPGYR- 198
QY 314 PRPWDPCCPVYAETKHFVYSSGDKQLRPSFLSLSLTGARLVETIFLGRPMMP 373
DB 199 ----DQADPLLRQXHC-----XPPSYST-YLPSLTVGEVGVGDYLSGSRPMMP 244
QY 374 GTPRRRLPRLPQRYWQWRPLLELLGNHACCPYGVLLK--THCPLEAATVPAGVCAAREKP 431
DB 245 GPPAGCPACPSXTKGCGPCFWSCLGTTTSAPFGCSSRRTARCELSRPPQVPS--VPGSRP 302
QY 432 QGSVAAPREEDTDPRLVOLLRQSSPWCYVGFVACLRVLPGLMGSRNERRFLPNT 491
DB 303 RALMWRPPRRRNTDPRRLVOLLRQSSPWCYVGFVACLRVLPGLMGSRNERRFLPNT 362
QY 492 KKFISLGIKIAKLSLDELTKWMSVRCAMLRSPGVGCVPAAEHRLREELILAKFLHMLMSV 551
DB 363 KKFISLGIKIAKLSLDELTKWMSVRCAMLRSPGVGCVPAAEHRLREELILAKFLHMLMSV 422
QY 552 YVVELLRSEFFVYTTETTFQAKRLFFYRPSVMSKLOSIGIRQHKRYVOLRELSAEVROHRE 611
DB 423 YVVELLRSEFFVYTTETTFQAKRLFFYRPSVMSKLOSIGIRQHKRYVOLRELSAEVROHRE 482
```

```
QY 612 ARPALLTSRLRFIPKPDGLRPIVMNDYVGARTFRREKREKRLTSRYKALFSVLYNERAR 671
DB 483 ARPALLTSRLRFIPKPDGLRPIVMNDYVGARTFRREKREKRLTSRYKALFSVLYNERAR 542
QY 672 RPLGLGASVGLDDIHNAMRTFVLRAQDPPELIFVKYDVTGADTIPQDRLTEVIAS 731
DB 543 RPLGLGASVGLDDIHNAMRTFVLRAQDPPELIFVKYDVTGADTIPQDRLTEVIAS 602
QY 732 IIRPQNTCYRRYAVVQKAHGHVKAFKSHVSTLIDLPYMEQFVAHLQETSPLRDAVY 791
DB 603 IIRPQNTCYRRYAVVQKAHGHVKAFKSHVSTLIDLPYMEQFVAHLQETSPLRDAVY 662
QY 792 IEQSSSLNEASSGLFDVFLRFMCHAVRIFGKSIVYQCGIPQGSIIITLCSLCYGDMEH 851
DB 663 IEQSSSLNEASSGLFDVFLRFMCHAVRIFGKSIVYQCGIPQGSIIITLCSLCYGDMEH 722
QY 852 KLFAGIRDDGLLRLVYDPLVTPPHLTHAKTFLRTLVRGVEYGVNLRKTYVNFPEVD 911
DB 723 KLFAGIRDDGLLRLVYDPLVTPPHLTHAKTFLRTLVRGVEYGVNLRKTYVNFPEVD 782
QY 912 EALGGTAFVQMPAHGLFPWCGLLLDTRTLEVOGSYSSVARTSIRASVTNRRGFKAGRNR 971
DB 783 EALGGTAFVQMPAHGLFPWCGLLLDTRTLEVOGSYSSVARTSIRASVTNRRGFKAGRNR 842
QY 972 RKLPGVIRLKGSLFLIDVNSLQVCTNIYKILLQAYRFAVCVQLPEHQWKNQPTF 1031
DB 843 RKLPGVIRLKGSLFLIDVNSLQVCTNIYKILLQAYRFAVCVQLPEHQWKNQPTF 902
QY 1032 FLRVISDTASLCYSILKAKNAGMSLGAKAGPLPSEAVQMLCHQAFILKLTTRHRTYVP 1091
DB 903 FLRVISDTASLCYSILKAKNAGMSLGAKAGPLPSEAVQMLCHQAFILKLTTRHRTYVP 962
QY 1092 LLSGLRTAQQLSRKLPGLTTLTLEAANPALPBSDKTLID 1132
DB 963 LLSGLRTAQQLSRKLPGLTTLTLEAANPALPBSDKTLID 1003
```

Search completed: December 20, 2004, 16:02:03
Job time : 66 secs

Tue Dec 21 15:43:31 2004

us-08-974-584c-118.rapb

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

CM protein - protein search, using sw model

Run on: December 20, 2004, 15:56:51 ; Search time 166 Seconds
(without alignments)

2440.176 Million cell updates/sec

Title: US-08-974-584C-118

Perfect score: 5963
Sequence: 1 MPRAPRCRAVRSLRSHYRE.....TALEAANPALPSDFKTIID 1132Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 segs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 120 summaries

Database :

Published Applications AA:*

1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubppaa/PCR_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/prodata/1/pubppaa/US06_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubppaa/US07_NEW_PUB.pep:*
6: /cgn2_6/prodata/1/pubppaa/PCRTUS_PUBCOMB.pep:*
7: /cgn2_6/prodata/1/pubppaa/US08_NEW_PUB.pep:*
8: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
9: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
10: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
11: /cgn2_6/prodata/1/pubppaa/US09_NEW_PUB.pep:*
12: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
13: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep:*
14: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep:*
15: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep:*
16: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep:*
17: /cgn2_6/prodata/1/pubppaa/US10_NEW_PUB.pep:*
18: /cgn2_6/prodata/1/pubppaa/US11_NEW_PUB.pep:*
19: /cgn2_6/prodata/1/pubppaa/US60_NEW_PUB.pep:*
20: /cgn2_6/prodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5963	100.0	1132	14	US-10-325-810-344 Sequence 344, App
2	5963	100.0	1132	17	US-10-877-124-344 Sequence 344, App
3	5963	100.0	1132	17	US-10-877-022-344 Sequence 344, App
4	5963	100.0	1407	14	US-10-044-692-334 Sequence 334, App
5	5963	100.0	1407	14	US-10-044-539-334 Sequence 334, App
6	5963	100.0	1407	14	US-10-325-810-628 Sequence 628, App
7	5963	100.0	1407	17	US-10-877-124-628 Sequence 628, App
8	5963	100.0	1407	17	US-10-877-022-628 Sequence 628, App
9	5952	99.8	1132	9	US-09-990-080-2 Sequence 2, Appl1
10	5952	99.8	1132	9	US-09-749-728B-31 Sequence 31, Appl1
11	5952	99.8	1132	9	US-09-843-676-225 Sequence 225, App
12	5952	99.8	1132	9	US-09-953-052-2 Sequence 2, Appl1
13	5952	99.8	1132	11	US-09-788-110A-23 Sequence 23, Appl1

87 1565 26.2 538 17 US-10-877-022-602 Sequence 602, App
 88 1506 25.3 514 14 US-10-044-692-319 Sequence 319, App
 89 1506 25.3 514 14 US-10-044-539-319 Sequence 319, App
 90 1506 25.3 514 14 US-10-325-810-605 Sequence 605, App
 91 1506 25.3 514 17 US-10-877-124-605 Sequence 605, App
 92 1506 25.3 514 17 US-10-877-022-605 Sequence 605, App
 93 1484 24.9 291 14 US-10-282-960-3 Sequence 3, Appl
 94 1454 24.4 517 14 US-10-044-692-330 Sequence 330, App
 95 1454 24.4 517 14 US-10-044-539-330 Sequence 330, App
 96 1454 24.4 517 14 US-10-325-810-606 Sequence 606, App
 97 1454 24.4 517 14 US-10-877-124-606 Sequence 606, App
 98 1454 24.4 517 17 US-10-877-022-606 Sequence 606, App
 99 1447 24.3 530 14 US-10-044-692-317 Sequence 317, App
 100 1447 24.3 530 14 US-10-044-539-317 Sequence 317, App
 101 1447 24.3 530 14 US-10-325-810-603 Sequence 603, App
 102 1447 24.3 530 17 US-10-877-124-603 Sequence 603, App
 103 1447 24.3 530 17 US-10-877-022-603 Sequence 603, App
 104 1416 23.7 283 17 US-10-623-515-6 Sequence 6, Appl
 105 1386 23.2 515 14 US-10-044-692-318 Sequence 318, App
 106 1386 23.2 515 14 US-10-044-539-318 Sequence 318, App
 107 1386 23.2 515 14 US-10-325-810-604 Sequence 604, App
 108 1386 23.2 515 17 US-10-877-124-604 Sequence 604, App
 109 1386 23.2 515 17 US-10-877-022-604 Sequence 604, App
 110 1293 21.7 250 14 US-10-449-565-2 Sequence 2, Appl
 111 1243.5 20.9 364 14 US-10-304-095-41 Sequence 41, Appl
 112 1090 18.3 259 14 US-10-044-692-10 Sequence 10, Appl
 113 1090 18.3 259 14 US-10-044-539-10 Sequence 10, Appl
 114 1090 18.3 259 14 US-10-325-810-10 Sequence 10, Appl
 115 1090 18.3 259 17 US-10-877-124-10 Sequence 10, Appl
 116 1090 18.3 259 17 US-10-877-022-10 Sequence 10, Appl
 117 929 15.6 222 9 US-09-843-676-202 Sequence 202, App
 118 929 15.6 222 14 US-09-438-486-202 Sequence 202, App
 119 929 15.6 222 14 US-10-053-758-202 Sequence 202, App
 120 929 15.6 222 14 US-10-054-235-202 Sequence 202, App

ALIGNMENTS

RESULT 1
 US-10-325-810-344
 Sequence 344, Application US/10325810
 Publication No. US20030204069A1
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chakman, Karen B.
 Morin, Gregg B.
 Harley, Calvin B.
 Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 633
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/325,810
 FILING DATE: 20-Dec-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/402,181
 FILING DATE: 29-Sep-1997
 APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Ausenhus, Scott L.
 REGISTRATION NUMBER: 42,271
 REFERENCE/DOCKET NUMBER: 015389-002620US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 344:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1132 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 344:
 US-10-325-810-344

Query Match 100.0%; Score 5963; DB 14; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MPAPRCRAVSLIRSHYREVLPLATFVRRLGFGQWRLVQSGDPAFAALVAQCLVCPW 60
 1 MPAPRCRAVSLIRSHYREVLPLATFVRRLGFGQWRLVQSGDPAFAALVAQCLVCPW 60
 61 DAPPPAPSPFROVSCIKELVAVLQRLCERKANVLAAGFALLDQARGGPPEAFTTSR 120
 61 DAPPPAPSPFROVSCIKELVAVLQRLCERKANVLAAGFALLDQARGGPPEAFTTSR 120
 121 SYLPNTVTDLRSGAGWGLLRVGGDVLVHLARCALFVLVAPSCAYOVCGPFLYQLGA 180
 121 SYLPNTVTDLRSGAGWGLLRVGGDVLVHLARCALFVLVAPSCAYOVCGPFLYQLGA 180
 181 ATQARPPHAGRRRLGGERAMNHSVREAGVPLGPAFGARRGGASRSLLPPRRPR 240
 181 ATQARPPHAGRRRLGGERAMNHSVREAGVPLGPAFGARRGGASRSLLPPRRPR 240
 241 GAAPPEPRTPVGGGSAHAPRTGSPDRGFCVSPARPABEATSLGALSGTRHSPVG 300
 241 GAAPPEPRTPVGGGSAHAPRTGSPDRGFCVSPARPABEATSLGALSGTRHSPVG 300
 301 ROHHAGPPSTSPRRPMDTPCPVVAETKHFLYSSGDKQLRPSFLSLRSLTGARL 360
 301 ROHHAGPPSTSPRRPMDTPCPVVAETKHFLYSSGDKQLRPSFLSLRSLTGARL 360
 361 VETIFIGSRPMWGTPLRLPLPQRYWQRPFLFLILSHNAQCPYVLLKTCPLRAAT 420
 361 VETIFIGSRPMWGTPLRLPLPQRYWQRPFLFLILSHNAQCPYVLLKTCPLRAAT 420
 421 PAAGVCAAREKQSVAAPEEDTDPRRLVQLRQHSPPQVYGFVACLRRLVPPGLMS 480
 421 PAAGVCAAREKQSVAAPEEDTDPRRLVQLRQHSPPQVYGFVACLRRLVPPGLMS 480
 481 RHNERPRLENTKFFISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAHRLREI 540
 481 RHNERPRLENTKFFISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAHRLREI 540

QY 541 LAKPLHMLSVYVVELLSFFVYTTETTFOKNRLFFVRPSVMSKLOSLGIRQHLKRYOLRE 600
 DB 541 LAKPLHMLSVYVVELLSFFVYTTETTFOKNRLFFVRPSVMSKLOSLGIRQHLKRYOLRE 600
 QY 601 LSEAVERQHEARPAALLTSRLRFLPKPDGLRPIVNMDDYVVGARTFRREKKAERLTSRYKA 660
 DB 601 LSEAVERQHEARPAALLTSRLRFLPKPDGLRPIVNMDDYVVGARTFRREKKAERLTSRYKA 660
 QY 661 LFSVLANERARPPGLLASVGLDDIRHARMTFLVRADDPPELTFYVVDVGTAVDTI 720
 DB 661 LFSVLANERARPPGLLASVGLDDIRHARMTFLVRADDPPELTFYVVDVGTAVDTI 720
 QY 721 PODRLTEVIAIIRKQNTYCVRRYAVVQKAAHGHVRAKFSHVSTLTDLPYMRQFVAHL 780
 DB 721 PODRLTEVIAIIRKQNTYCVRRYAVVQKAAHGHVRAKFSHVSTLTDLPYMRQFVAHL 780
 QY 781 QETSPLRDYVIEQSSSLNEASSGLFVFLRPMCHAVRIRKGSYVOCQIPQGSILSTL 840
 DB 781 QETSPLRDYVIEQSSSLNEASSGLFVFLRPMCHAVRIRKGSYVOCQIPQGSILSTL 840
 QY 841 LCSLCYGDMEKRLPAGLRBDGLRLVDDPLVTPHILTHAKTFLRLVREGVPEYCVNL 900
 DB 841 LCSLCYGDMEKRLPAGLRBDGLRLVDDPLVTPHILTHAKTFLRLVREGVPEYCVNL 900
 QY 901 RKTIVNFPVEDEALGTAFAVQMPAHGLFPMCGLLDTRTLEVOSSDYSSVARTSIRASVTF 960
 DB 901 RKTIVNFPVEDEALGTAFAVQMPAHGLFPMCGLLDTRTLEVOSSDYSSVARTSIRASVTF 960
 QY 961 NRGKARBNMRKLFGLVRLKCHSLFLDLQVNSIQTCNTNRYKLLLOARFHACVLOLP 1020
 DB 961 NRGKARBNMRKLFGLVRLKCHSLFLDLQVNSIQTCNTNRYKLLLOARFHACVLOLP 1020
 QY 1021 FHQGVNKPFTFELVISTDASTLCYSILKAKXAGMSLAKAGAGLPSEAVOMLCHQAFLL 1080
 DB 1021 FHQGVNKPFTFELVISTDASTLCYSILKAKXAGMSLAKAGAGLPSEAVOMLCHQAFLL 1080
 QY 1081 KLTFRHRYTVPLLSLRTAQOLSRKLPGLTLLLEMAANPALPSDKITLD 1132
 DB 1081 KLTFRHRYTVPLLSLRTAQOLSRKLPGLTLLLEMAANPALPSDKITLD 1132

RESULT 2
 US-10-877-124-344
 Sequence 344, Application US/10877124
 Publication No. US2004024529A1
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 Linguist, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin B.
 Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/877,124
 FILING DATE: 24-Jun-2004
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/432,503

FILING DATE: 02-Nov-1999
 APPLICATION NUMBER: 08/974,549
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-Apr-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-Apr-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-May-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-May-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: WO PCT/US97/17618
 FILING DATE: 01-Oct-1997
 APPLICATION NUMBER: WO PCT/US97/17685
 FILING DATE: 01-Oct-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002610US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 344:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1132 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 344:
 US-10-877-124-344

Query Match 100.0%; Score 5963; DB 17; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLSRSHAEVLPATFVRRLQPGMRVLVORDDPAFPAVLAQCLVCPM 60
 DB 1 MPRAPRCRAVRSLLSRSHAEVLPATFVRRLQPGMRVLVORDDPAFPAVLAQCLVCPM 60
 QY 61 DARPPAASFRQVSCIKELVARVQLICERGAQVLAFGALLDGAAGGPEEATTVSR 120
 DB 61 DARPPAASFRQVSCIKELVARVQLICERGAQVLAFGALLDGAAGGPEEATTVSR 120
 QY 121 SYLPTNTDALRGSGAMGLLRVGGDYLVIHLARCALFVLAAPSCAYOVGPPPLYOQA 180
 DB 121 SYLPTNTDALRGSGAMGLLRVGGDYLVIHLARCALFVLAAPSCAYOVGPPPLYOQA 180
 QY 181 ATOAAPPPHAGSPRRRLIGCERAMNSVREAGVPLGLPAGARRGSGASRSLLPKRPRR 240
 DB 181 ATOAAPPPHAGSPRRRLIGCERAMNSVREAGVPLGLPAGARRGSGASRSLLPKRPRR 240
 QY 241 GAAPPEERTPVQGSNAHNGRTGRGSDGFCVYSAPRAPEATSLGALSGTRHSHPSVG 300
 DB 241 GAAPPEERTPVQGSNAHNGRTGRGSDGFCVYSAPRAPEATSLGALSGTRHSHPSVG 300
 QY 301 ROHHAAPPSTSRPPRPMDPCPPVYAETGHLFYSSGDKQLRPSLLSLRSLTGARRL 360
 DB 301 ROHHAAPPSTSRPPRPMDPCPPVYAETGHLFYSSGDKQLRPSLLSLRSLTGARRL 360
 QY 361 VETIFLGSFPMGCTPRRLRPLPORYWQMRPLFLLGNHACCPYGVLLKTHCPRAAYT 420
 DB 361 VETIFLGSFPMGCTPRRLRPLPORYWQMRPLFLLGNHACCPYGVLLKTHCPRAAYT 420
 QY 421 PAAGVCAKPKPGSGVAAPEEEDTDPRRLVQLRQHSFPMQVGFYRACLRVLPGLWGS 480
 DB 421 PAAGVCAKPKPGSGVAAPEEEDTDPRRLVQLRQHSFPMQVGFYRACLRVLPGLWGS 480

QY 481 RHNRERFLRNTKFKISLGKHAUQLSLOELTMKNSVRCDAWLRRSPGVGCPAAEHRLREI 540
 DB 481 RHNRERFLRNTKFKISLGKHAUQLSLOELTMKNSVRCDAWLRRSPGVGCPAAEHRLREI 540
 QY 541 LAFPLMWSVYVELLRSPFYVETTFPQXNRLFFYRPSVMSKLSQSIGRQHLKXVQRE 600
 DB 541 LAFPLMWSVYVELLRSPFYVETTFPQXNRLFFYRPSVMSKLSQSIGRQHLKXVQRE 600
 QY 601 LSAEVRORHREARPAALTSRLRFIPKPDGLRPVNMDDYVGARTPRERARLRSRYKA 660
 DB 601 LSAEVRORHREARPAALTSRLRFIPKPDGLRPVNMDDYVGARTPRERARLRSRYKA 660
 QY 661 LFSVLNVERARBPGLLGASVTLGLDTHRAMRTFVLVRAPDPPPELYFKVDVTGAYDTI 720
 DB 661 LFSVLNVERARBPGLLGASVTLGLDTHRAMRTFVLVRAPDPPPELYFKVDVTGAYDTI 720
 QY 721 PQRRLTEVLAISTIKPQNTYCVRRYAVVQKAHGHVAKAKSVSTLTDLPFMRQFVAML 780
 DB 721 PQRRLTEVLAISTIKPQNTYCVRRYAVVQKAHGHVAKAKSVSTLTDLPFMRQFVAML 780
 QY 781 QETSPLRDAVIEQSSSLNEASSGLFDVFLRFMCHHAVIRKSYVQCGIPQGSILSTL 840
 DB 781 QETSPLRDAVIEQSSSLNEASSGLFDVFLRFMCHHAVIRKSYVQCGIPQGSILSTL 840
 QY 841 LCSLCYGDMEKFKFAGIRRDGLLRVDFLVTPLTHAKTFLKTLVNGVPEYGCYVNL 900
 DB 841 LCSLCYGDMEKFKFAGIRRDGLLRVDFLVTPLTHAKTFLKTLVNGVPEYGCYVNL 900
 QY 901 RKTVPVFPEDDELGGTAFCVQMPAHGLFPMCGLLDTRLEVOQSYSSAATSIASATF 960
 DB 901 RKTVPVFPEDDELGGTAFCVQMPAHGLFPMCGLLDTRLEVOQSYSSAATSIASATF 960
 QY 961 NRGFKAQRNRRKLFVGLRLKCHSLFLDQVNSLQVTCTNIVKILLQAYRPHACVQLP 1020
 DB 961 NRGFKAQRNRRKLFVGLRLKCHSLFLDQVNSLQVTCTNIVKILLQAYRPHACVQLP 1020
 QY 1021 FHOQWKNPTEFLRVSDDTASLCVSLTKAKNAGMSIGAKGAGPLPSEAVQMLCHQAL 1080
 DB 1021 FHOQWKNPTEFLRVSDDTASLCVSLTKAKNAGMSIGAKGAGPLPSEAVQMLCHQAL 1080
 QY 1081 KLTRHRVTVVPLLSLRTAQTQSRKLPSTTLTALAAANPALPSPDFKTL 1132
 DB 1081 KLTRHRVTVVPLLSLRTAQTQSRKLPSTTLTALAAANPALPSPDFKTL 1132

RESULT 3
 US-10-877-022-344
 ; Sequence 344, Application US/10877022
 ; Publication No. US20040247613A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; Linsner, Joachim
 ; Nakamura, Toru
 ; Chapman, Karen B.
 ; Morin, Gregg B.
 ; Harley, Calvin B.
 ; Andrews, William H.
 ; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 ; NUMBER OF SEQUENCES: 727
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/877,022

; FILING DATE: 24-Jun-2004
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/432,503
 ; FILING DATE: 02-Nov-1999
 ; APPLICATION NUMBER: 08/974,549
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: US 08/844,419
 ; FILING DATE: 18-Apr-1997
 ; APPLICATION NUMBER: US 08/846,017
 ; FILING DATE: 25-Apr-1997
 ; APPLICATION NUMBER: US 08/851,843
 ; FILING DATE: 06-May-1997
 ; APPLICATION NUMBER: US 08/854,050
 ; FILING DATE: 09-May-1997
 ; APPLICATION NUMBER: US 08/911,312
 ; FILING DATE: 14-Aug-1997
 ; APPLICATION NUMBER: US 08/912,951
 ; FILING DATE: 14-Aug-1997
 ; APPLICATION NUMBER: US 08/915,503
 ; FILING DATE: 14-Aug-1997
 ; APPLICATION NUMBER: WO PCT/US97/17618
 ; FILING DATE: 01-Oct-1997
 ; APPLICATION NUMBER: WO PCT/US97/17885
 ; FILING DATE: 01-Oct-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Apple, Randolph Ted
 ; REGISTRATION NUMBER: 36,429
 ; REFERENCE/DOCKET NUMBER: 015389-002610US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 344:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1132 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 344:
 ; US-10-877-022-344

Query Match 100.0%; Score 5963; DB 17; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGQGRRLVQRGDPAAPRALVAQCLVCVW 60
 DB 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGQGRRLVQRGDPAAPRALVAQCLVCVW 60
 QY 61 DAPPPAPSPFROVSCIKELVARVLRQLCERGAQNVLAEGFALLDGAAGPPPAFTTSYR 120
 DB 61 DAPPPAPSPFROVSCIKELVARVLRQLCERGAQNVLAEGFALLDGAAGPPPAFTTSYR 120
 QY 121 SYLNTVTDALRSGAWGLLRVGDVIVHLIARCALFVLVAPSCAYVCGPPLYQLGA 180
 DB 121 SYLNTVTDALRSGAWGLLRVGDVIVHLIARCALFVLVAPSCAYVCGPPLYQLGA 180
 QY 181 ATQARPPHAGSPRRRLGCRAMNHSVREAGVPLGAPGARRRGGSARSLLPLRPPR 240
 DB 181 ATQARPPHAGSPRRRLGCRAMNHSVREAGVPLGAPGARRRGGSARSLLPLRPPR 240
 QY 241 GAAPBERPTVVGSGVAHPGRTGSPDRGFCVSPAPPAEATSLLEGALSGTRHSPSYG 300
 DB 241 GAAPBERPTVVGSGVAHPGRTGSPDRGFCVSPAPPAEATSLLEGALSGTRHSPSYG 300
 QY 301 RQHHAGPSTSRPPRWDTPCPVYAEKHFLLYSQDKEQLRPSFLSLRPSLTGARLL 360
 DB 301 RQHHAGPSTSRPPRWDTPCPVYAEKHFLLYSQDKEQLRPSFLSLRPSLTGARLL 360
 QY 361 VETIFGSRPMMGTGRRRLRLPQRYWQKRPFLLELIGNHAOCYPYGVLLKTHCPLRAAYT 420
 DB 361 VETIFGSRPMMGTGRRRLRLPQRYWQKRPFLLELIGNHAOCYPYGVLLKTHCPLRAAYT 420

QY 421 PAAGVCAAREKPOGSAVAPEEDTDPRRLVOLLRQSSPMQYGVFVACLRVLPGLMGS 480
 Db 421 PAAGVCAAREKPOGSAVAPEEDTDPRRLVOLLRQSSPMQYGVFVACLRVLPGLMGS 480
 QY 481 RHNRERRRLNTKRTISGKNAKSLQELTWKMSVRCAMIRSPFGVCPAABHRLREET 540
 Db 481 RHNRERRRLNTKRTISGKNAKSLQELTWKMSVRCAMIRSPFGVCPAABHRLREET 540
 QY 541 LAKELHLMMSYVVELLSFPHYVTETFEOKRBLFFYRPSVWSKQSIGIPIQHIXVQLRE 600
 Db 541 LAKELHLMMSYVVELLSFPHYVTETFEOKRBLFFYRPSVWSKQSIGIPIQHIXVQLRE 600
 QY 601 LSEAEVQOHRBAPALLTSRLRFLPKPDGLRPIVNMDDYVVGARTFRREKKAERLTSVKA 660
 Db 601 LSEAEVQOHRBAPALLTSRLRFLPKPDGLRPIVNMDDYVVGARTFRREKKAERLTSVKA 660
 QY 661 LFSVLNTERARBPCLLGASVLGLDDIRHAWRTFVLRRADDPPELTVFVVDVTGAYDTI 720
 Db 661 LFSVLNTERARBPCLLGASVLGLDDIRHAWRTFVLRRADDPPELTVFVVDVTGAYDTI 720
 QY 721 PODRLTEVIASIIKPONTYCVRYAVVQKAAHGVKAFKSHVSTLTDLPYMRQFVAHL 780
 Db 721 PODRLTEVIASIIKPONTYCVRYAVVQKAAHGVKAFKSHVSTLTDLPYMRQFVAHL 780
 QY 781 QETSPFLRDVAVIEOQSSLINEASGCLFDVFLRFVCHAVIRIGKSYVOCQGIPOGSIISTL 840
 Db 781 QETSPFLRDVAVIEOQSSLINEASGCLFDVFLRFVCHAVIRIGKSYVOCQGIPOGSIISTL 840
 QY 841 LCSLCYGMENKLPAGIRRDGLLRLVDDFLVLTPLTHAKTFLRTLVRGVEPGCVNL 900
 Db 841 LCSLCYGMENKLPAGIRRDGLLRLVDDFLVLTPLTHAKTFLRTLVRGVEPGCVNL 900
 QY 901 RKTIVNPFVEDEALGTAFAVQMPAHGLFPWCGLLDRLTEVSDVSYSVARTSIRASVTF 960
 Db 901 RKTIVNPFVEDEALGTAFAVQMPAHGLFPWCGLLDRLTEVSDVSYSVARTSIRASVTF 960
 QY 961 NRGFKAGRMNRKLFGLVRLKCHSLFLDLQVNSIQYCTNITYILLQARFHACVLOLP 1020
 Db 961 NRGFKAGRMNRKLFGLVRLKCHSLFLDLQVNSIQYCTNITYILLQARFHACVLOLP 1020
 QY 1021 FHQGVNKNPTFFLRVISDTASLCYSILKANAGMSLGAAGPLPSEAVQMLCHOAFLI 1080
 Db 1021 FHQGVNKNPTFFLRVISDTASLCYSILKANAGMSLGAAGPLPSEAVQMLCHOAFLI 1080
 QY 1081 KLTRRHRTVYVPLGLSLTAOTQLSRKLPQTTLTALLEANPALPSPDKTILD 1132
 Db 1081 KLTRRHRTVYVPLGLSLTAOTQLSRKLPQTTLTALLEANPALPSPDKTILD 1132

RESULT 4
 US-10-044-692-334
 Sequence 334, Application US/10044692
 Publication No. US20030096344A1
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 Lininger, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin
 Andrews, William H.
 TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
 THERAPEUTIC METHODS
 NUMBER OF SEQUENCES: 335
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: PatentIn Release #1.0, Version #1.30
 ?
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/10/044,692
 ? FILING DATE: 11-Jan-2002
 ? CLASSIFICATION: <Unknown>
 ?
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: 08/912,951
 ? FILING DATE: <Unknown>
 ? APPLICATION NUMBER: US 08/854,050
 ? FILING DATE: 09-MAY-1997
 ? APPLICATION NUMBER: US 08/851,843
 ? FILING DATE: 06-MAY-1997
 ? APPLICATION NUMBER: US 08/846,017
 ? FILING DATE: 25-APR-1997
 ? APPLICATION NUMBER: US 08/844,419
 ? FILING DATE: 18-APR-1997
 ? APPLICATION NUMBER: US 08/724,643
 ? FILING DATE: 01-OCT-1996
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Apple, Randolph T.
 ? REGISTRATION NUMBER: 36,429
 ? REFERENCE/DOCKET NUMBER: 015389-002600US
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (415) 576-0200
 ? TELEFAX: (415) 576-0300
 ?
 ? INFORMATION FOR SEQ ID NO: 334:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 1407 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: <Unknown>
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: protein
 ? SEQUENCE DESCRIPTION: SEQ ID NO: 334:
 ?
 ? US-10-044-692-334
 ?
 ? Query Match 100.0%; Score 5963; DB 14; Length 1407;
 ? Best Local Similarity 100.0%; Pred. No. 0;
 ? Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ?
 ? 1 MPARPCAVRSILMSHYREVLPATFVRRIGPOQMRVQSGDPAAPRALVAQCIVCPM 60
 ? 276 MPARPCAVRSILMSHYREVLPATFVRRIGPOQMRVQSGDPAAPRALVAQCIVCPM 335
 ?
 ? QY 61 DARPPEAPSPFRQVSCLELVAARVLOLRCERGANVLAFGALLDGAAGPPEAFTTSVR 120
 ? Db 336 DARPPEAPSPFRQVSCLELVAARVLOLRCERGANVLAFGALLDGAAGPPEAFTTSVR 395
 ?
 ? QY 121 SYLENTVDALRGSGAMGLLRRVGDVTLVHLARCALFVLVAPSCAYOVGPPLYOIGA 180
 ? Db 396 SYLENTVDALRGSGAMGLLRRVGDVTLVHLARCALFVLVAPSCAYOVGPPLYOIGA 455
 ?
 ? QY 181 ATQARPPHAGSPRRRLCERAMNHSVREAGVPLGLPAPGARRRGSGASRSLPLPKRRR 240
 ? Db 456 ATQARPPHAGSPRRRLCERAMNHSVREAGVPLGLPAPGARRRGSGASRSLPLPKRRR 515
 ?
 ? QY 241 GAAPPERTPVQGGWMAHPRGTRGSDRGFCVYSAPARPAEATLSLEGALSTRHSHPSVG 300
 ? Db 516 GAAPPERTPVQGGWMAHPRGTRGSDRGFCVYSAPARPAEATLSLEGALSTRHSHPSVG 575
 ?
 ? QY 301 RQHAAGPSTSRPPMDTPCPVYAEKHFYLSGDKQELRPSFLSSLRPSLTGASRL 360
 ? Db 576 RQHAAGPSTSRPPMDTPCPVYAEKHFYLSGDKQELRPSFLSSLRPSLTGASRL 635
 ?
 ? QY 361 VETIFLGRPMWPGTFRPLPLPQRYWQMRPLFELLAGNHAQCPYGVLLKTHCPRAAVT 420
 ? Db 636 VETIFLGRPMWPGTFRPLPLPQRYWQMRPLFELLAGNHAQCPYGVLLKTHCPRAAVT 695
 ?
 ? QY 421 PAAGVCAAREKPOGSAVAPEEDTDPRRLVOLLRQSSPMQYGVFVACLRVLPGLMGS 480
 ? Db 696 PAAGVCAAREKPOGSAVAPEEDTDPRRLVOLLRQSSPMQYGVFVACLRVLPGLMGS 755

481 RHNERFRLNTKFKFISLGGAKLSLOELTWKMSVBDCAWLRRSPGVGCVPAEHRRLREI 540
756 RHNERFRLNTKFKFISLGGAKLSLOELTWKMSVBDCAWLRRSPGVGCVPAEHRRLREI 815
541 LAKFLHMLMSYVVELLSRFYVETETTPKXNLFFYRPSWSKLSIGIRHKLKRVQURE 600
816 LAKFLHMLMSYVVELLSRFYVETETTPKXNLFFYRPSWSKLSIGIRHKLKRVQURE 875
601 LSAEVRORREARPAALTSRLRFIPKPDGLRPIVNMDDYVGARTFRREKRAERLRSRKA 660
876 LSAEVRORREARPAALTSRLRFIPKPDGLRPIVNMDDYVGARTFRREKRAERLRSRKA 935
661 LBSVLNVEBARRRPGLIGASVIGLDTIHRAMRTFVLRPAQDPPPELRYVQDVTGAYDTI 720
936 LBSVLNVEBARRRPGLIGASVIGLDTIHRAMRTFVLRPAQDPPPELRYVQDVTGAYDTI 995
721 PDORLEVIASIIKPNNTYCVRRYAVVOCAAHGVRKAFKSVSTLTLOPMRQFVAHL 780
996 PDORLEVIASIIKPNNTYCVRRYAVVOCAAHGVRKAFKSVSTLTLOPMRQFVAHL 1055
781 QETSPRLDAVIEOSSSLNEASSGLFDVFLRFMCHAVRIRGKSYVOCGIPQGSILSTL 840
1056 QETSPRLDAVIEOSSSLNEASSGLFDVFLRFMCHAVRIRGKSYVOCGIPQGSILSTL 1115
841 LGSGLCYGDMENKLFAGIRDDGILLRYVDELLVTBHLTHAKTFLRTYRGVPEYCVNL 900
1116 LGSGLCYGDMENKLFAGIRDDGILLRYVDELLVTBHLTHAKTFLRTYRGVPEYCVNL 1175
901 RKTIVNFPVEDBALGGTAFCVMPAHGLFPMCGILLDTITLVEQSDYSSYARTSIRASYTF 960
1176 RKTIVNFPVEDBALGGTAFCVMPAHGLFPMCGILLDTITLVEQSDYSSYARTSIRASYTF 1235
961 NRGFKAGRNRRKLFQVFLRKCHSLFLDIQVNSLOTCVCTNYKILLQAYRPAVLOLP 1020
1236 NRGFKAGRNRRKLFQVFLRKCHSLFLDIQVNSLOTCVCTNYKILLQAYRPAVLOLP 1295
1021 FHOQVKNPTFFLRVSDTASLCYSILKAKNAGMSLGAAGAPLPSEAVOLCHQAPL 1080
1296 FHOQVKNPTFFLRVSDTASLCYSILKAKNAGMSLGAAGAPLPSEAVOLCHQAPL 1355
1081 KLRHRVTYVPLLSLRTAQOLSRKLPQTTLTALBAANPALPSEDFXTIID 1132
1356 KLRHRVTYVPLLSLRTAQOLSRKLPQTTLTALBAANPALPSEDFXTIID 1407

RESULT 5
US-10-044-539-334
Sequence 334, Application US/10044539
Publication No. US2003010093A1
GENERAL INFORMATION:
APPLICANT: Czech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/044, 539
FILING DATE: 11-Jan-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912, 951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854, 050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851, 843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846, 017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844, 419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724, 643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 334:
SEQUENCE CHARACTERISTICS:
LENGTH: 1407 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: linear
TOPOLGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 334:
US-10-044-539-334

Query Match 100.0%; Score 5963; DB 14; Length 1407;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MPRAFCRAVSLIRSHYREVLPLATFVRRLGQGRVLYQGDPAFRLVAQCLVCPM 60
276 MPRAFCRAVSLIRSHYREVLPLATFVRRLGQGRVLYQGDPAFRLVAQCLVCPM 335
61 DAPPPAPSPFROVSCIKELIVAVLQRLCBGAKNTLAFGALLDQAGCPBAFTTSR 120
336 DAPPPAPSPFROVSCIKELIVAVLQRLCBGAKNTLAFGALLDQAGCPBAFTTSR 395
121 SYLPNTVTDLRSGAMGLLRVGDVLYHLARCALFVLVAPSCAYVCGPPLVQLGA 180
396 SYLPNTVTDLRSGAMGLLRVGDVLYHLARCALFVLVAPSCAYVCGPPLVQLGA 455
181 ATOARPPHAGPGRRLGGERAMNHSVREAGVPLGPAPGARRRGSSASRSILPFRPRR 240
456 ATOARPPHAGPGRRLGGERAMNHSVREAGVPLGPAPGARRRGSSASRSILPFRPRR 515
241 GAAPPEPRTPVGGSNVHAGRTGSPSDRGCVVSPAPAEATSLGALSGRHSPSVG 300
516 GAAPPEPRTPVGGSNVHAGRTGSPSDRGCVVSPAPAEATSLGALSGRHSPSVG 575
301 ROHHAGPSTSRPPRPMDPCPPVYAEIKHFLYSSGDKXQLRPSFLSLRPSLTGARL 360
576 ROHHAGPSTSRPPRPMDPCPPVYAEIKHFLYSSGDKXQLRPSFLSLRPSLTGARL 635
361 VETIFLGSRPWMGTPRRRLPRLQRYWQNRPLFLEILGNHAQCPYVLLKTHCPPLAAVT 420
636 VETIFLGSRPWMGTPRRRLPRLQRYWQNRPLFLEILGNHAQCPYVLLKTHCPPLAAVT 695
421 PAAGVCAREKPOGSVAAPBEEDTPRRLVQLRQHSPPQVYGFVACLRRLVPLMGSS 480
696 PAAGVCAREKPOGSVAAPBEEDTPRRLVQLRQHSPPQVYGFVACLRRLVPLMGSS 755
481 RHNERFRLNTKFKFISLGGAKLSLOELTWKMSVBDCAWLRRSPGVGCVPAEHRRLREI 540
756 RHNERFRLNTKFKFISLGGAKLSLOELTWKMSVBDCAWLRRSPGVGCVPAEHRRLREI 815


```

QY 541 LAKFJHMLMSYVYVVELLSFEVYETETQKRLFEYRBSWMSKIOSIGROHAKRVOJRE 600
Db 816 LAKFJHMLMSYVYVVELLSFEVYETETQKRLFEYRBSWMSKIOSIGROHAKRVOJRE 875
QY 601 LSEAEVRQREARPAALTSRLRFIEKPDGLRPIVNMDDYVGARTERREKRAERLTSRYKA 660
Db 876 LSEAEVRQREARPAALTSRLRFIEKPDGLRPIVNMDDYVGARTERREKRAERLTSRYKA 935
QY 661 LFSVINYERARPPGLLGASVLDJDIHNAKRFVULRYAODPPPELYEPKUDYTCAYPTI 720
Db 936 LFSVINYERARPPGLLGASVLDJDIHNAKRFVULRYAODPPPELYEPKUDYTCAYPTI 995
QY 721 PODRLTEVIASIIKEQNTYCVARVAVVOXAAHGHYRKAFKSHVSTLTLDQPYMRQFVAHL 780
Db 996 PODRLTEVIASIIKEQNTYCVARVAVVOXAAHGHYRKAFKSHVSTLTLDQPYMRQFVAHL 1055
QY 781 QETSFLRDAVYVEQSSSLNEASGLEDVFLRPMCHNAVRIRKSYVOCQIPQSGISTLT 840
Db 1056 QETSFLRDAVYVEQSSSLNEASGLEDVFLRPMCHNAVRIRKSYVOCQIPQSGISTLT 1115
QY 841 LCSLTCYGDMENTLFGAGIRPDGJLLRLVDDFLVTPHLTHAKTFLRTLVRGYPEYCVANL 900
Db 1116 LCSLTCYGDMENTLFGAGIRPDGJLLRLVDDFLVTPHLTHAKTFLRTLVRGYPEYCVANL 1175
QY 901 RKTVVNFPEDEALCGTAFVQNPAGHLPFPMCGILLDRTLEVOQSYSSYARTSRASVTF 960
Db 1176 RKTVVNFPEDEALCGTAFVQNPAGHLPFPMCGILLDRTLEVOQSYSSYARTSRASVTF 1235
QY 961 NRGFLAGNMRKLTGVLRLKXHSIFLDQVNSLQTCVNTYKILLDQVRFHACVOLDLP 102
Db 1236 NRGFLAGNMRKLTGVLRLKXHSIFLDQVNSLQTCVNTYKILLDQVRFHACVOLDLP 1295
QY 1021 FHOQVKNPTEFLRYSIDTASLCYSILKXAKNAGMSLGAKGAAGPLPSEAVOMLCHQAEFL 1080
Db 1296 FHOQVKNPTEFLRYSIDTASLCYSILKXAKNAGMSLGAKGAAGPLPSEAVOMLCHQAEFL 1355
QY 1081 KLTRRNVYVPLLGSLRTAOTLSKRLPCTITLAEAAANPALBEDFTIILD 1132
Db 1356 KLTRRNVYVPLLGSLRTAOTLSKRLPCTITLAEAAANPALBEDFTIILD 1407

RESULT 6
US-10-325-810-628
; Sequence 628, Application US/10325810
; Publication No. US20030204069A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Linguist, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/325,810
; FILING DATE: 20-Dec-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181

```

```

1 FILING DATE: 29-SEP-1997
2 APPLICATION NUMBER: US 08/724,643
3 FILING DATE: 01-OCT-1996
4 APPLICATION NUMBER: US 08/844,419
5 FILING DATE: 18-APR-1997
6 APPLICATION NUMBER: US 08/846,017
7 FILING DATE: 25-APR-1997
8 APPLICATION NUMBER: US 08/851,843
9 FILING DATE: 06-MAY-1997
10 APPLICATION NUMBER: US 08/854,050
11 FILING DATE: 09-MAY-1997
12 APPLICATION NUMBER: US 08/911,312
13 FILING DATE: 14-AUG-1997
14 APPLICATION NUMBER: US 08/912,951
15 FILING DATE: 14-AUG-1997
16 APPLICATION NUMBER: US 08/915,503
17 FILING DATE: 14-AUG-1997
18 APPLICATION NUMBER: WO PCT/US97/17885
19 FILING DATE: 01-OCT-1997
20 ATTORNEY/AGENT INFORMATION:
21 NAME: Aussenhus, Scott L.
22 REGISTRATION NUMBER: 42,271
23 REFERENCE/DOCKET NUMBER: 015389-002620US
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: (415) 576-0200
26 TELEFAX: (415) 576-0300
27 INFORMATION FOR SEQ ID NO: 628:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 1407 amino acids
30 TYPE: amino acid
31 STRADEDNESS: <Unknown>
32 MOLECULE TYPE: linear
33 TOPOLOGY: linear
34 FEATURE:
35 NAME/KEY: Protein
36 LOCATION: 1..1407
37 OTHER INFORMATION: /note="fusion protein composed of
38 enhanced green fluorescent protein
39 (EGFP) residues, residues encoded by the
40 5' untranslated region of hTnT mRNA and
41 hTnT protein sequence"
42 SEQUENCE DESCRIPTION: SEQ ID NO: 628:
43 US-10-325-810-628
44
45 Query Match 100.0%; Score 5963; DB 14; Length 1407;
46 Best Local Similarity 100.0%; Pctd. No. 0;
47 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
48
49 QY 1 MPRAAPGAVSLRSHRYEVLPLATFRRRLPGPGQWMLRQVGDPAAPAFALVAQCLVCVPM 60
50 DB 276 MPRAAPRCNVAASLRSHRYEVLPLATFRRRLPGPGQWMLRQVGDPAAPAFALVAQCLVCVPM 335
51 QY 61 DARPAPAPSEFROYSCLEKELVARVLORLCEGANKVLAFGFALLDGAAGGPEAFTTSVR 120
52 DB 336 DARPAPAPSEFROYSCLEKELVARVLORLCEGANKVLAFGFALLDGAAGGPEAFTTSVR 395
53 QY 121 SYLRNTYVDALRSGGAWLLIRRGDDVTVHLLARCAFLVVAAPCAVOYGGPPLYOIGA 180
54 DB 396 SYLRNTYVDALRSGGAWLLIRRGDDVTVHLLARCAFLVVAAPCAVOYGGPPLYOIGA 455
55 QY 181 ATOARPPPHAGSPRRRLGCERAMNHSVREAGVPLGLPAPGARRRGSGASRSLPLPKRPR 240
56 DB 456 ATOARPPPHAGSPRRRLGCERAMNHSVREAGVPLGLPAPGARRRGSGASRSLPLPKRPR 515
57 QY 241 GAAPPEPRTPYGGGWAHPGRTGSDRGFCVVSAPARAEATSLIEGLSGTRHSHPSVG 300
58 DB 516 GAAPPEPRTPYGGGWAHPGRTGSDRGFCVVSAPARAEATSLIEGLSGTRHSHPSVG 575
59 QY 301 RQHAAGPSTSRPRPMDTPCPFYAETKHTLYSSGDKELRPSFLTSLRPSLTGABRL 360
60 DB 576 RQHAAGPSTSRPRPMDTPCPFYAETKHTLYSSGDKELRPSFLTSLRPSLTGABRL 635
61 QY 361 VETIFLGSRPMPGTFRRLPLRQRYWQMRDLTELLGNHAQCPYGVLLKTHCPRLAAVT 420

```

```

Db 636 VETIFLGRPMWPGTFRRLPRLPQRYWQRPFLFELGHAOCFVGLLKHCHCPRAAVT 695
Qy 421 PAAGVARRKPOGSVAAPEDDTPDRLVQLROHSSPMQYGFACRLVPGMLGS 480
Db 696 PAAGVARRKPOGSVAAPEDDTPDRLVQLROHSSPMQYGFACRLVPGMLGS 755
Qy 481 RHNERFLNNTKFFISLGHAKLSLOELTWKNSVDCAMLRSSPGVCVPAAEHRLREI 540
Db 756 RHNERFLNNTKFFISLGHAKLSLOELTWKNSVDCAMLRSSPGVCVPAAEHRLREI 815
Qy 541 LKPELHMVSVVVELLSFVYVETTPQKRLFFYRPSVMSKLSIGIRHKLXVORE 600
Db 816 LKPELHMVSVVVELLSFVYVETTPQKRLFFYRPSVMSKLSIGIRHKLXVORE 875
Qy 601 LSEAEVQRREARPAALLTSRLRFIPKPDGLRPIVMDVVGARTFRREKRAERLTSRYKA 660
Db 876 LSEAEVQRREARPAALLTSRLRFIPKPDGLRPIVMDVVGARTFRREKRAERLTSRYKA 935
Qy 661 LRSVLNTEGARRRGLIGASVGLDIDHRAKMTFVLRVAAQDPPPLPYKVDVYATYTI 720
Db 936 LRSVLNTEGARRRGLIGASVGLDIDHRAKMTFVLRVAAQDPPPLPYKVDVYATYTI 995
Qy 721 POPRLTEVASTIKPQNTYCVRRYAVVYKAAHGHYKAFKSHVSTLTLDQPYMRQFVAHL 780
Db 996 POPRLTEVASTIKPQNTYCVRRYAVVYKAAHGHYKAFKSHVSTLTLDQPYMRQFVAHL 1055
Qy 781 QETSPILDAVVIQSSSLNEASSGLFDVFLRMCHAVRIRKGSVYQCGIPQSSILSTL 840
Db 1056 QETSPILDAVVIQSSSLNEASSGLFDVFLRMCHAVRIRKGSVYQCGIPQSSILSTL 1115
Qy 841 LCSLCYGDENKLPACIRRDGLLLRVDPFLVTPHLTAKTEFLTLVKGVEYECVAVNL 900
Db 1116 LCSLCYGDENKLPACIRRDGLLLRVDPFLVTPHLTAKTEFLTLVKGVEYECVAVNL 1175
Qy 901 RKTVPNPEVEDEALGTAIVQMPAHGLFPMWCGLLDRTLEVOQSYSSYARTSIRASYTF 960
Db 1176 RKTVPNPEVEDEALGTAIVQMPAHGLFPMWCGLLDRTLEVOQSYSSYARTSIRASYTF 1235
Qy 961 NRGFKAGRMRRKLPFVLRKCHSLFLDQVNSLQTVCNITKILLQAYRHAQVLDLP 1020
Db 1236 NRGFKAGRMRRKLPFVLRKCHSLFLDQVNSLQTVCNITKILLQAYRHAQVLDLP 1295
Qy 1021 FHQQVKNPTFFLRVSDTASLCYSILKAKNAGMSIGAKAGAPLPSEAVQWLCHQAFLL 1080
Db 1296 FHQQVKNPTFFLRVSDTASLCYSILKAKNAGMSIGAKAGAPLPSEAVQWLCHQAFLL 1355
Qy 1081 KLTRHRYTVYVPLIGSLRTAQTQSLRKLPGTTTLTALEAANPALPSDFKTIID 1132
Db 1356 KLTRHRYTVYVPLIGSLRTAQTQSLRKLPGTTTLTALEAANPALPSDFKTIID 1407

RESULT 7
US-10-877-124-628
Sequence 628, Application US/10877124
Publication No. US20040242529A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Linsner, Joachim
Nakamura, Toru
Chapman, Karen B.
Mortin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,124
FILING DATE: 24-Jun-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-Oct-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 35,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 628:
SEQUENCE CHARACTERISTICS:
LENGTH: 1407 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1407
OTHER INFORMATION: /note= "fusion protein composed of
enhanced green fluorescent protein
(Egfp) residues, residues encoded by the
5' untranslated region of hTERT mRNA and
hTERT protein sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 628:
US-10-877-124-628
Query Match 100.0%; Score 5963; DB 17; Length 1407;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCAVRSLIRSHRYREVLPLATFEVRLTSGQGRVTVQRGDPAFRALVAGCTVCPM 60
Db 276 MPRAPRCAVRSLIRSHRYREVLPLATFEVRLTSGQGRVTVQRGDPAFRALVAGCTVCPM 335
Qy 61 DARPAPAPSFROVSCIKELVAVRLQRLCERGAQVILAFGALLDGAAGGPEPAFTTSVR 120
Db 336 DARPAPAPSFROVSCIKELVAVRLQRLCERGAQVILAFGALLDGAAGGPEPAFTTSVR 395
Qy 121 SYLPTVTDLRSGGAGLLIRVGDVYLHLARCALPVTVAPSCAYQVCGPLVQLA 180
Db 396 SYLPTVTDLRSGGAGLLIRVGDVYLHLARCALPVTVAPSCAYQVCGPLVQLA 455

```

```

QY 181 ATOARPPPHASGPRRLGCEAWNHSYREAGVPLG:PAPGARRGGASASRLPLPKRPR 240
DB 456 ATOARPPPHASGPRRLGCEAWNHSYREAGVPLG:PAPARRGGASASRLPLPKRPR 515
QY 241 GAABEPRTFVGQGSWAHPGRTGSDRGFCVVSAPAPAEATSLGCAJSGTSHSPV 300
DB 516 GAABEPRTFVGQGSWAHPGRTGSDRGFCVVSAPAPAEATSLGCAJSGTSHSPV 575
QY 301 ROHAGGPPSTGPRPMDTGPCPYATKHFLLSSGKQLRPSFLSSLRPSLTGARL 360
DB 576 ROHAGGPPSTGPRPMDTGPCPYATKHFLLSSGKQLRPSFLSSLRPSLTGARL 635
QY 361 VETIFLGSRRPMDGTPRRLPLRQYQWMPLELLGNHACQPYGLLKTGCPRAAYT 420
DB 636 VETIFLGSRRPMDGTPRRLPLRQYQWMPLELLGNHACQPYGLLKTGCPRAAYT 695
QY 421 PAAGVCARXKQGSVAAPBEEDTDPRLVOLLROHSPWQVYGFVACLRRLVPLGMS 480
DB 696 PAAGVCARXKQGSVAAPBEEDTDPRLVOLLROHSPWQVYGFVACLRRLVPLGMS 755
QY 481 RHNRRLRLRTKRTISLGKAKLSLOELTWMSVDCAMLRSPGVGCPAPAEHRLREI 540
DB 756 RHNRRLRLRTKRTISLGKAKLSLOELTWMSVDCAMLRSPGVGCPAPAEHRLREI 815
QY 541 LAKEFLHMLSVYVELLSPEFYVETTFQKRLFFYRPSVMSKLSIGIRQHLKRVLE 600
DB 816 LAKEFLHMLSVYVELLSPEFYVETTFQKRLFFYRPSVMSKLSIGIRQHLKRVLE 875
QY 601 LSEAEVQHREARALLTSRLRFPRDGLRPIYNDYVVGARTFRREKAEHLTSRYVA 660
DB 876 LSEAEVQHREARALLTSRLRFPRDGLRPIYNDYVVGARTFRREKAEHLTSRYVA 935
QY 661 LFSVLANERARPGILGASVGLDDIRAWTFVLRYADPPELZYFVADVTAAYDI 720
DB 936 LFSVLANERARPGILGASVGLDDIRAWTFVLRYADPPELZYFVADVTAAYDI 995
QY 721 PODRLTEVIASTIPQNTYCYRRAVYQKAAHGVRAKAFKSHVSTLTDLPYKQFAHL 780
DB 996 PODRLTEVIASTIPQNTYCYRRAVYQKAAHGVRAKAFKSHVSTLTDLPYKQFAHL 1055
QY 781 QETSPLDVAVIEOSSSLNEASGLFDVFLRFPMCHHVRIRGKSYVCCQIPQGSILSTL 840
DB 1056 QETSPLDVAVIEOSSSLNEASGLFDVFLRFPMCHHVRIRGKSYVCCQIPQGSILSTL 1115
QY 841 LCSICYDMDENKLFAGIRDDGLRLVDDPLVTHLTHAKTFLRLVRGVPYEGCVNL 900
DB 1116 LCSICYDMDENKLFAGIRDDGLRLVDDPLVTHLTHAKTFLRLVRGVPYEGCVNL 1175
QY 901 RKTIVNFPVDEALGTAFAVQMPAHGLFPWCGILLDRTLLEVOGDSVARSIRASVTF 960
DB 1176 RKTIVNFPVDEALGTAFAVQMPAHGLFPWCGILLDRTLLEVOGDSVARSIRASVTF 1235
QY 961 NRGFKAGRNMRKLFVYLRLKCHSLFDLDQVNSIQVCTNIYKILLQAYRFAVYOLP 1020
DB 1236 NRGFKAGRNMRKLFVYLRLKCHSLFDLDQVNSIQVCTNIYKILLQAYRFAVYOLP 1295
QY 1021 FHQGVWKNPFFFLAVISDTSLCYSILKANAAGMSLAKAGAFLPBEAOWLCHOAFL 1080
DB 1296 FHQGVWKNPFFFLAVISDTSLCYSILKANAAGMSLAKAGAFLPBEAOWLCHOAFL 1355
QY 1081 KLFHRVTVYPLLSGLRTRAQTLRSKLPGLTLTLEAANPALPSPDKTLLD 1132
DB 1356 KLFHRVTVYPLLSGLRTRAQTLRSKLPGLTLTLEAANPALPSPDKTLLD 1407

```

```

RESULT 8
US-10-877-022-628
; Sequence 628; Application US/10877022
; Publication No. US20040247613A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;            Langner, Joachim
;            Nakamura, Toru

```

```

; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; APPLICATION DATA:
; FILING DATE: 24-Jun-2004
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-Apr-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-Apr-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-May-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-May-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-Aug-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-Aug-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-Aug-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-Oct-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-Oct-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 628:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1407 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1407
; OTHER INFORMATION: /note="fusion protein composed of
; enhanced green fluorescent protein
; (EGFP) residues, residues encoded by the
; 5 untranslated region of hTERT mRNA and
; hTERT protein sequence"
; SEQUENCE DESCRIPTION: SEQ ID NO: 628:
US-10-877-022-628

```

```

Query Match 100.0%; Score 5963; DB 17; Length 1407;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MPAPRCRAVRSILRSHYREVLPATFVRRLGPGQRLVQRGDPAPAFALVQCLVCVPM 60
DB 276 MPAPRCRAVRSILRSHYREVLPATFVRRLGPGQRLVQRGDPAPAFALVQCLVCVPM 335
QY 61 DAPPAPASFRQVSCLELVARVLOQLCEGAKVLAFFALDAGRGPEAFTTSVR 120
DB 336 DAPPAPASFRQVSCLELVARVLOQLCEGAKVLAFFALDAGRGPEAFTTSVR 395
QY 121 SYLNTVTDALRSGGAWGLLRVGDVVLHILARCALVLAAPCAVOCPEPLYQUGA 180
DB 396 SYLNTVTDALRSGGAWGLLRVGDVVLHILARCALVLAAPCAVOCPEPLYQUGA 455
QY 181 ATQAPPPHSGRRRLGGERAMNHSVREAGVPLGPAFGARRGGSASRLPLKRRR 240
DB 456 ATQAPPPHSGRRRLGGERAMNHSVREAGVPLGPAFGARRGGSASRLPLKRRR 515
QY 241 GAAPBEERTPVGGSWAHFQRTGPDRCFCVSPAPAEATSLGALSGTRHSHPSVG 300
DB 516 GAAPBEERTPVGGSWAHFQRTGPDRCFCVSPAPAEATSLGALSGTRHSHPSVG 575
QY 301 ROHHAGPSTSRPPRMDTCCPPVVAETGHLFYSQDKEQLRPSFLSLRSLTGARRL 360
DB 576 ROHHAGPSTSRPPRMDTCCPPVVAETGHLFYSQDKEQLRPSFLSLRSLTGARRL 635
QY 361 VETIFLGSRPMMGTERRRLPRLPQRYWQMRPLFLELGNHAQCPYVLLKTHCPRAAVT 420
DB 636 VETIFLGSRPMMGTERRRLPRLPQRYWQMRPLFLELGNHAQCPYVLLKTHCPRAAVT 695
QY 421 PAAGVCAAREKPOGSVAAPBEEDTDPRRLVOLLROHSSPMQYGFACRLRPLVPGMLGS 480
DB 696 PAAGVCAAREKPOGSVAAPBEEDTDPRRLVOLLROHSSPMQYGFACRLRPLVPGMLGS 755
QY 481 RHNERFRLNTKFFISLGHAKLSLOELTWKMSVBCALRRSPGVGCPAPAEHRLREI 540
DB 756 RHNERFRLNTKFFISLGHAKLSLOELTWKMSVBCALRRSPGVGCPAPAEHRLREI 815
QY 541 LAKFLHMLSVYVVELLRSEFFVYETTFQKNLFFYRPSVMSKLOSIGIRQHLKRYQURE 600
DB 816 LAKFLHMLSVYVVELLRSEFFVYETTFQKNLFFYRPSVMSKLOSIGIRQHLKRYQURE 875
QY 601 LSEAEVROGHEARPALTLSTRLPFKPDGLRPIVNMDDYVVGARTREKRAERLSRYKA 660
DB 876 LSEAEVROGHEARPALTLSTRLPFKPDGLRPIVNMDDYVVGARTREKRAERLSRYKA 935
QY 936 LFSVLNTERARBPGLIGASVGLGDDIHRAMRTFVLRAQDDPPELYKXVDVTGAYDTI 995
DB 661 LFSVLNTERARBPGLIGASVGLGDDIHRAMRTFVLRAQDDPPELYKXVDVTGAYDTI 720
QY 721 PODRLTEVIASTIKPQNTYCVRRYAVVQCAHGHVKAFFKSHVSTLTDLOPYMRQFVAHL 780
DB 996 PODRLTEVIASTIKPQNTYCVRRYAVVQCAHGHVKAFFKSHVSTLTDLOPYMRQFVAHL 1055
QY 781 QETSPLRDAVVIQESSLNEASSGLFVFLRPMCHAVAIRGKSVYOCGIPQGSILSTL 840
DB 1056 QETSPLRDAVVIQESSLNEASSGLFVFLRPMCHAVAIRGKSVYOCGIPQGSILSTL 1115
QY 841 LGSICVGDMENTLFAGIRRDGILLRLVDDFLVTEHLTHAKTFLATLYRGVPEYCVYVL 900
DB 1116 LGSICVGDMENTLFAGIRRDGILLRLVDDFLVTEHLTHAKTFLATLYRGVPEYCVYVL 1175
QY 901 RKTUVNFPVEDEALGGTAFVQMPAHGLFPGCGLLDTFTLEVOSSYASRTASATF 960
DB 1176 RKTUVNFPVEDEALGGTAFVQMPAHGLFPGCGLLDTFTLEVOSSYASRTASATF 1235
QY 961 NNGFKAQRNMRKLFQVLRKCHSLFLDIQVNSLOTVCTNIYKILLQAYRPHACVLOLP 1020
DB 1236 NNGFKAQRNMRKLFQVLRKCHSLFLDIQVNSLOTVCTNIYKILLQAYRPHACVLOLP 1295
QY 1021 FHOQVKNQTFPLRVISDPAISLCSYSLKXNAGMSLGAAGAAGPLPSEAVOMLCHQATL 1080
DB 1296 FHOQVKNQTFPLRVISDPAISLCSYSLKXNAGMSLGAAGAAGPLPSEAVOMLCHQATL 1355

QY 1081 KLTRHRTVYVPLGSLTJTAOTLSRKLPGTTLTALAAANPALPSDFKTLTD 1132
DB 1356 KLTRHRTVYVPLGSLTJTAOTLSRKLPGTTLTALAAANPALPSDFKTLTD 1407

RESULT 9
US-09-990-080-2
; Sequence 2, Application US/09990080
; Patent No. US20020102586A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 0.8/258c
; CURRENT APPLICATION NUMBER: US/09/990,080
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 09/052,864
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-080-2

Query Match 99.8%; Score 5952; DB 9; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSILRSHYREVLPATFVRRLGPGQRLVQRGDPAPAFALVQCLVCVPM 60
DB 1 MPAPRCRAVRSILRSHYREVLPATFVRRLGPGQRLVQRGDPAPAFALVQCLVCVPM 60
QY 61 DAPPAPASFRQVSCLELVARVLOQLCEGAKVLAFFALDAGRGPEAFTTSVR 120
DB 61 DAPPAPASFRQVSCLELVARVLOQLCEGAKVLAFFALDAGRGPEAFTTSVR 120
QY 121 SYLNTVTDALRSGGAWGLLRVGDVVLHILARCALVLAAPCAVOCPEPLYQUGA 180
DB 121 SYLNTVTDALRSGGAWGLLRVGDVVLHILARCALVLAAPCAVOCPEPLYQUGA 180
QY 181 ATQAPPPHSGRRRLGGERAMNHSVREAGVPLGPAFGARRGGSASRLPLKRRR 240
DB 181 ATQAPPPHSGRRRLGGERAMNHSVREAGVPLGPAFGARRGGSASRLPLKRRR 240
QY 241 GAAPBEERTPVGGSWAHFQRTGPDRCFCVSPAPAEATSLGALSGTRHSHPSVG 300
DB 241 GAAPBEERTPVGGSWAHFQRTGPDRCFCVSPAPAEATSLGALSGTRHSHPSVG 300
QY 301 ROHHAGPSTSRPPRMDTCCPPVVAETGHLFYSQDKEQLRPSFLSLRSLTGARRL 360
DB 301 ROHHAGPSTSRPPRMDTCCPPVVAETGHLFYSQDKEQLRPSFLSLRSLTGARRL 360
QY 361 VETIFLGSRPMMGTERRRLPRLPQRYWQMRPLFLELGNHAQCPYVLLKTHCPRAAVT 420
DB 361 VETIFLGSRPMMGTERRRLPRLPQRYWQMRPLFLELGNHAQCPYVLLKTHCPRAAVT 420
QY 421 PAAGVCAAREKPOGSVAAPBEEDTDPRRLVOLLROHSSPMQYGFACRLRPLVPGMLGS 480
DB 421 PAAGVCAAREKPOGSVAAPBEEDTDPRRLVOLLROHSSPMQYGFACRLRPLVPGMLGS 480
QY 481 RHNERFRLNTKFFISLGHAKLSLOELTWKMSVBCALRRSPGVGCPAPAEHRLREI 540
DB 481 RHNERFRLNTKFFISLGHAKLSLOELTWKMSVBCALRRSPGVGCPAPAEHRLREI 540
QY 541 LAKFLHMLSVYVVELLRSEFFVYETTFQKNLFFYRPSVMSKLOSIGIRQHLKRYQURE 600
DB 541 LAKFLHMLSVYVVELLRSEFFVYETTFQKNLFFYRPSVMSKLOSIGIRQHLKRYQURE 600
QY 601 LSEAEVROGHEARPALTLSTRLPFKPDGLRPIVNMDDYVVGARTREKRAERLSRYKA 660
DB 601 LSEAEVROGHEARPALTLSTRLPFKPDGLRPIVNMDDYVVGARTREKRAERLSRYKA 660

QY 661 LFSVLYNERARRPGLLGASVGLDDIHRAMRTFVLRYAODPPELTYFVKVDTGAYDTI 720
DB 661 LFSVLYNERARRPGLLGASVGLDDIHRAMRTFVLRYAODPPELTYFVKVDTGAYDTI 720
QY 721 PODRLTEVIASIIKQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPYMRQFVAHL 780
DB 721 PODRLTEVIASIIKQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPYMRQFVAHL 780
QY 781 QETSPLRDVAIVTEOSSSINBASGLFDVFLRPMCHAVIRIGKSVYOCQGIPOGSIISTL 840
DB 781 QETSPLRDVAIVTEOSSSINBASGLFDVFLRPMCHAVIRIGKSVYOCQGIPOGSIISTL 840
QY 841 LCSLCYGDMENTKLFAGIRRDGLLRLVDDFLVTPHILTHAKTFLRLTVRGVEYGCYVNL 900
DB 841 LCSLCYGDMENTKLFAGIRRDGLLRLVDDFLVTPHILTHAKTFLRLTVRGVEYGCYVNL 900
QY 901 RKTIVNFPVEDEALGTAFFVQMPAHGLFPMCGLLDTRILEVOSDYSSYARTSIRASLTF 960
DB 901 RKTIVNFPVEDEALGTAFFVQMPAHGLFPMCGLLDTRILEVOSDYSSYARTSIRASLTF 960
QY 961 NRGFKAGNRMRKLFVYLRKCHSLFLDQVNSIQVCTNIYKILLQAFRFAVYOLP 1020
DB 961 NRGFKAGNRMRKLFVYLRKCHSLFLDQVNSIQVCTNIYKILLQAFRFAVYOLP 1020
QY 1021 FHQOVWKNPFFFLRVIDSTASLCYSILKAKNAGMSLGAKGAGLPSEAVQWMLCHQAFLL 1080
DB 1021 FHQOVWKNPFFFLRVIDSTASLCYSILKAKNAGMSLGAKGAGLPSEAVQWMLCHQAFLL 1080
QY 1081 KLTRHRVTYVPLGSLRTAQQLSRKLPQTTLTLEAANPALPSPDKTILTD 1132
DB 1081 KLTRHRVTYVPLGSLRTAQQLSRKLPQTTLTLEAANPALPSPDKTILTD 1132

RESULT 10

US-09-749-728B-31
; Sequence 31, Application US/09749728B
; Patent No. US20020142457A1
; GENERAL INFORMATION:
; APPLICANT: Umezawa, Akihiro
; APPLICANT: Hata, Jun-ichi
; APPLICANT: Fukuda, Keiichi
; APPLICANT: Ogawa, Satoshi
; APPLICANT: Sakurada, Kazuhiro
; APPLICANT: Gojo, Satoshi
; APPLICANT: Yamada, Yoji
; TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDIOMY
; FILE REFERENCE: 06766-00043
; CURRENT APPLICATION NUMBER: US/09/749, 728B
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: H11-372826
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: PCT-JP00-01148
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: PCT-JP00-07741
; PRIOR FILING DATE: 2000-11-02
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver.2.0
; SEQ ID NO 31
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-749-728B-31

Query Match 99.8%; Score 5952; DB 9; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAAPCRAYSLRSHREVLPATFVRRLPGQGMWLVORGDPAARALVACLVCPV 60
DB 1 MPRAAPCRAYSLRSHREVLPATFVRRLPGQGMWLVORGDPAARALVACLVCPV 60
QY 61 DARPPPAAPSPFQVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120

DB 61 DARPPPAAPSPFQVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120
QY 121 SYLPNTVTDALFGSGAMGILLRVRGDDVYLHILARCALPVLVAPSCAYQVCGPPLYYOLCA 180
DB 121 SYLPNTVTDALFGSGAMGILLRVRGDDVYLHILARCALPVLVAPSCAYQVCGPPLYYOLCA 180
QY 181 ATOAAPPPASGRRRLICGERAMNHSVBAQVPLCLPAPGARRRGSGASRLPLPKRRR 240
DB 181 ATOAAPPPASGRRRLICGERAMNHSVBAQVPLCLPAPGARRRGSGASRLPLPKRRR 240
QY 241 GAAPPERTPVQGGMAHGRTRGSDGFCVSPAPPAEEXTSLEGALSGTRHSPVG 300
DB 241 GAAPPERTPVQGGMAHGRTRGSDGFCVSPAPPAEEXTSLEGALSGTRHSPVG 300
QY 301 RQHHAGPSTSRPPPMWTPCPBPVYAEIKHFLYSSGDKEQLRPSFLSLSPSLTGARRL 360
DB 301 RQHHAGPSTSRPPPMWTPCPBPVYAEIKHFLYSSGDKEQLRPSFLSLSPSLTGARRL 360
QY 361 VETIFLGSRRPMPGTPRRLPRLPQRYWQMRPLFLEILGNHAQCPYVLLKTHCPURLAAVT 420
DB 361 VETIFLGSRRPMPGTPRRLPRLPQRYWQMRPLFLEILGNHAQCPYVLLKTHCPURLAAVT 420
QY 421 PAAGVCAREKPOGSAVAEEDTDPRRLVOLLRQHSFMYQYGFRACLRLVPPGMLGS 480
DB 421 PAAGVCAREKPOGSAVAEEDTDPRRLVOLLRQHSFMYQYGFRACLRLVPPGMLGS 480
QY 481 RINERBRFLNTRKFFSLGHAFLSLOELTWKSVYDCAMLRSPVGCVAPEAHEHLREI 540
DB 481 RINERBRFLNTRKFFSLGHAFLSLOELTWKSVYDCAMLRSPVGCVAPEAHEHLREI 540
QY 541 IAKFLHMLMSYVVELLSFFVYETTFQXKRLFFYRPSVMSKIOSIGIRQHLKVOURE 600
DB 541 IAKFLHMLMSYVVELLSFFVYETTFQXKRLFFYRPSVMSKIOSIGIRQHLKVOURE 600
QY 601 LSEAEVROHREARPLILSRILFKPDGLRPIVMDVYVAGARTREKREARLISRYKA 660
DB 601 LSEAEVROHREARPLILSRILFKPDGLRPIVMDVYVAGARTREKREARLISRYKA 660
QY 661 LFSVLYNERARRPGLLGASVGLDDIHRAMRTFVLRYAODPPELTYFVKVDTGAYDTI 720
DB 661 LFSVLYNERARRPGLLGASVGLDDIHRAMRTFVLRYAODPPELTYFVKVDTGAYDTI 720
QY 721 PODRLTEVIASIIKQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPYMRQFVAHL 780
DB 721 PODRLTEVIASIIKQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPYMRQFVAHL 780
QY 781 QETSPLRDVAIVTEOSSSINBASGLFDVFLRPMCHAVIRIGKSVYOCQGIPOGSIISTL 840
DB 781 QETSPLRDVAIVTEOSSSINBASGLFDVFLRPMCHAVIRIGKSVYOCQGIPOGSIISTL 840
QY 841 LCSLCYGDMENTKLFAGIRRDGLLRLVDDFLVTPHILTHAKTFLRLTVRGVEYGCYVNL 900
DB 841 LCSLCYGDMENTKLFAGIRRDGLLRLVDDFLVTPHILTHAKTFLRLTVRGVEYGCYVNL 900
QY 901 RKTIVNFPVEDEALGTAFFVQMPAHGLFPMCGLLDTRILEVOSDYSSYARTSIRASLTF 960
DB 901 RKTIVNFPVEDEALGTAFFVQMPAHGLFPMCGLLDTRILEVOSDYSSYARTSIRASLTF 960
QY 961 NRGFKAGNRMRKLFVYLRKCHSLFLDQVNSIQVCTNIYKILLQAFRFAVYOLP 1020
DB 961 NRGFKAGNRMRKLFVYLRKCHSLFLDQVNSIQVCTNIYKILLQAFRFAVYOLP 1020
QY 1021 FHQOVWKNPFFFLRVIDSTASLCYSILKAKNAGMSLGAKGAGLPSEAVQWMLCHQAFLL 1080
DB 1021 FHQOVWKNPFFFLRVIDSTASLCYSILKAKNAGMSLGAKGAGLPSEAVQWMLCHQAFLL 1080
QY 1081 KLTRHRVTYVPLGSLRTAQQLSRKLPQTTLTLEAANPALPSPDKTILTD 1132
DB 1081 KLTRHRVTYVPLGSLRTAQQLSRKLPQTTLTLEAANPALPSPDKTILTD 1132

RESULT 11

US-09-843-676-225
Sequence 225, Application US/09843676
Patent No. US20020164786A1
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin H.
Andrews, William H.
TITLE OF INVENTION: No. US20020164786A1e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 535
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US/08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US/08/724,643
FILING DATE: 01-Oct-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 225:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 225:
US-09-843-676-225
Query Match 99.8%; Score 5952; DB 9; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MPAAPFCRAVRSILRSHYREVLPATFVRRLDPOGRLVQDGPAPFALVAQCVCVPM 60
DB 1 MPAAPFCRAVRSILRSHYREVLPATFVRRLDPOGRLVQDGPAPFALVAQCVCVPM 60
QY 61 DARPPAAASFROVSLCKELVARVLORLCERGAQVLAFFALDGAAGPPEATTSTVR 120
DB 61 DARPPAAASFROVSLCKELVARVLORLCERGAQVLAFFALDGAAGPPEATTSTVR 120
QY 121 SYLPNTVTDLRSGAGMLLRVGDVVLVLLARCALFVLAAPSCAVQVCGPPLYQIGA 180
DB 121 SYLPNTVTDLRSGAGMLLRVGDVVLVLLARCALFVLAAPSCAVQVCGPPLYQIGA 180
QY 181 ATGAPRPPHAGSRRLGCEBAMNHSVRAGVPLGIPAPGARRGSGASRSLPLKPRR 240
DB 181 ATGAPRPPHAGSRRLGCEBAMNHSVRAGVPLGIPAPGARRGSGASRSLPLKPRR 240

QY 241 GAAPERTVVGGSNAHPCRTGRPSDRGCVVSPAPPEBATSLEGALSGTRHSPSYG 300
DB 241 GAAPERTVVGGSNAHPCRTGRPSDRGCVVSPAPPEBATSLEGALSGTRHSPSYG 300
QY 301 ROHHAGPSTSRPPRPWDTPCPVVAETKHFVLSGSDXKQLRPSFLLSLRBSLTGARL 360
DB 301 ROHHAGPSTSRPPRPWDTPCPVVAETKHFVLSGSDXKQLRPSFLLSLRBSLTGARL 360
QY 361 VETIFLGRPMWPGTTRPLRLPQRYQWMPLELLELGNHACQCVVLKTHCPLEAAVT 420
DB 361 VETIFLGRPMWPGTTRPLRLPQRYQWMPLELLELGNHACQCVVLKTHCPLEAAVT 420
QY 421 PAAGVCAERKQPSVAAPPEEDTDPRLVQLLRQHSPPQVYGFVACLRVLPGLMGS 480
DB 421 PAAGVCAERKQPSVAAPPEEDTDPRLVQLLRQHSPPQVYGFVACLRVLPGLMGS 480
QY 481 RHNERRLRNTKKEFISLGRKAKLSIDELTWKMSVRCDAMLRSBGVCVPAEHRLEET 540
DB 481 RHNERRLRNTKKEFISLGRKAKLSIDELTWKMSVRCDAMLRSBGVCVPAEHRLEET 540
QY 541 LAKFLHMSVYVELLSFFVTEFTFOKNRLFYRPSWASKLQSIGIRHLKRVQLE 600
DB 541 LAKFLHMSVYVELLSFFVTEFTFOKNRLFYRPSWASKLQSIGIRHLKRVQLE 600
QY 601 LSAEVRQREARPAALITSLRPIPKPDGIRPVNMDYVGAFTFRERGAERLSRVYA 660
DB 601 LSAEVRQREARPAALITSLRPIPKPDGIRPVNMDYVGAFTFRERGAERLSRVYA 660
QY 661 LFSVLTNERARRPGLLGASVLAGDDIHRARTVLVRAODPPELYFKAVDVTGAYDTI 720
DB 661 LFSVLTNERARRPGLLGASVLAGDDIHRARTVLVRAODPPELYFKAVDVTGAYDTI 720
QY 721 PODRLTEVIASIIKPOVTYCVRRYAVVOXAAHGHVAKFKSHVSTLTDLOPYNRQFVAHL 780
DB 721 PODRLTEVIASIIKPOVTYCVRRYAVVOXAAHGHVAKFKSHVSTLTDLOPYNRQFVAHL 780
QY 781 QETSPLEDAVIVIOSSSLNASSGLDVPFRFCHAVNIRGSSVYOCGIGOGSLSTL 840
DB 781 QETSPLEDAVIVIOSSSLNASSGLDVPFRFCHAVNIRGSSVYOCGIGOGSLSTL 840
QY 841 LGSICVGDMEKFLFAGIRRDGLLRVDDPLVTPHLLTAKTFLRLTVGVEYGCVNL 900
DB 841 LGSICVGDMEKFLFAGIRRDGLLRVDDPLVTPHLLTAKTFLRLTVGVEYGCVNL 900
QY 901 RKTIVNFPVEDEALGTAFOVMAHGLFWCCGILDTLRLLEVQSDSSYAFSTIRASLT 960
DB 901 RKTIVNFPVEDEALGTAFOVMAHGLFWCCGILDTLRLLEVQSDSSYAFSTIRASLT 960
QY 961 NRGFKAGNNRKLFGVLRKCHSLFLDLQVNSLOTVCNIIYKILLQAVRFHACVQLP 1020
DB 961 NRGFKAGNNRKLFGVLRKCHSLFLDLQVNSLOTVCNIIYKILLQAVRFHACVQLP 1020
QY 1021 FHQVWKNPTFLRIVISDTASLCYSLKAKNAGMSIGAGAPLPSEAVQWLC HQAPLL 1080
DB 1021 FHQVWKNPTFLRIVISDTASLCYSLKAKNAGMSIGAGAPLPSEAVQWLC HQAPLL 1080
QY 1081 KLTRHRVTYVPLLSLRTAQTOLSRKLPGLTTLTALEAANPALPSPFKIILD 1132
DB 1081 KLTRHRVTYVPLLSLRTAQTOLSRKLPGLTTLTALEAANPALPSPFKIILD 1132
RESULT 12
US-09-953-052-2
Sequence 2, Application US/09953052
Patent No. US20020173476A1
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.

Andrews, William H.
 TITLE OF INVENTION: Antisense Compositions for Detecting and
 Inhibiting Telomerase Reverse Transcriptase
 NUMBER OF SEQUENCES: 72
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/953,052
 FILING DATE: 14-Sep-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/052,919
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/974,549
 FILING DATE: 19-NOV-1997
 APPLICATION NUMBER: US 08/974,584
 FILING DATE: 19-NOV-1997
 APPLICATION NUMBER: WO PCT/US97/17618
 FILING DATE: 01-OCT-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Parent, Annette S.
 REGISTRATION NUMBER: 42,058
 REFERENCE/DOCKET NUMBER: 015389-003600US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1132 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-953-052-2

Query Match 99.8%; Score 5952; DB 9; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVSLRSLRSHREVLPPLATFVRRLGPGWMLVQGDPAAPRALVAQCLVCVPM 60
 DB 1 MPAPRCRAVSLRSLRSHREVLPPLATFVRRLGPGWMLVQGDPAAPRALVAQCLVCVPM 60

QY 61 DARPAPAPSRQVSCUKELVAVRLQRLCERGANVLAFFGALLDARGGPPPAFTTSYR 120
 DB 61 DARPAPAPSRQVSCUKELVAVRLQRLCERGANVLAFFGALLDARGGPPPAFTTSYR 120

QY 121 SYLPNTVTDALRGSGAMGLLRVGDVTLVHLARCALFVLVAPSCAYQVGGPPLYQGA 180
 DB 121 SYLPNTVTDALRGSGAMGLLRVGDVTLVHLARCALFVLVAPSCAYQVGGPPLYQGA 180

QY 181 ATQAPPPHAGSGPRRLRCERAMNHSVYAGVPLGLPAPGARRRGSGASRLPLPKRPR 240
 DB 181 ATQAPPPHAGSGPRRLRCERAMNHSVYAGVPLGLPAPGARRRGSGASRLPLPKRPR 240

QY 241 GAAPPERTPVQGGSMAPRGTRGSDRGFCVVSAPARAEATSLIEGLSTGRSHBSVG 300
 DB 241 GAAPPERTPVQGGSMAPRGTRGSDRGFCVVSAPARAEATSLIEGLSTGRSHBSVG 300

QY 301 ROHAGPSTSRPPPMWDTCPPVYAEFKHFLYSSGDEQARPFLSLSPSLTGASRL 360
 DB 301 ROHAGPSTSRPPPMWDTCPPVYAEFKHFLYSSGDEQARPFLSLSPSLTGASRL 360

QY 361 VETIFLGSRPWMVPGTPRRLPRLPORVQMRPLFELLGNHAQCPYGVLLKTHCPRAAVT 420
 DB 361 VETIFLGSRPWMVPGTPRRLPRLPORVQMRPLFELLGNHAQCPYGVLLKTHCPRAAVT 420

QY 421 PAAGVCAREKPGGSVAAPBEEDTDPRLVOLLROHSSPMOYGFYACLRPLVPGGLMGS 480
 DB 421 PAAGVCAREKPGGSVAAPBEEDTDPRLVOLLROHSSPMOYGFYACLRPLVPGGLMGS 480

QY 481 RHNERRFLRNTKFFSLGKHAKLSLOELTWKMSVYDCAMLRSPGVGCVPAAEHRLBEI 540
 DB 481 RHNERRFLRNTKFFSLGKHAKLSLOELTWKMSVYDCAMLRSPGVGCVPAAEHRLBEI 540

QY 541 LAKFLHMTMSYVYVVLASFFVYVETTFQKRLFFYRSVSKOSICIRHAKRVQARE 600
 DB 541 LAKFLHMTMSYVYVVLASFFVYVETTFQKRLFFYRSVSKOSICIRHAKRVQARE 600

QY 601 LSEAERQHRERAPALITSRLFIKPDGLRPIVMQDVYARTFRERREKARLITSRYKA 660
 DB 601 LSEAERQHRERAPALITSRLFIKPDGLRPIVMQDVYARTFRERREKARLITSRYKA 660

QY 661 LFSVINYRPARRPGLLGASVTLGLDDIRAMRTFVLRAVAQPPPELVYKVDVGAAYTI 720
 DB 661 LFSVINYRPARRPGLLGASVTLGLDDIRAMRTFVLRAVAQPPPELVYKVDVGAAYTI 720

QY 721 PODRLTEVIASLIKQNTYCVRRYAVVQKAHGHYRKAFKSHVSTLIDLOPYMQFVAHL 780
 DB 721 PODRLTEVIASLIKQNTYCVRRYAVVQKAHGHYRKAFKSHVSTLIDLOPYMQFVAHL 780

QY 781 QETSPLRDAVYIEQSSSLNEASGGLFDFVLRPMCHAVRIRGKSYVQCGIPQGSILSTL 840
 DB 781 QETSPLRDAVYIEQSSSLNEASGGLFDFVLRPMCHAVRIRGKSYVQCGIPQGSILSTL 840

QY 841 LCSLCYGMENKLPFGIRRDGLLRLVNDPFLVPHLTHAKTFLRTVIRGPEGCYVNL 900
 DB 841 LCSLCYGMENKLPFGIRRDGLLRLVNDPFLVPHLTHAKTFLRTVIRGPEGCYVNL 900

QY 901 RKTIVNPFVEDEALGGLTAFVQMPAHGLFPMQGLLIDTTLTEVQSDYSYARTSIRASYTF 960
 DB 901 RKTIVNPFVEDEALGGLTAFVQMPAHGLFPMQGLLIDTTLTEVQSDYSYARTSIRASYTF 960

QY 961 NRGFAAGNMRKRLFGVRLKCHSLFDLOVNSLOTVNTYKILLLOAYRFAVCVLOLP 1020
 DB 961 NRGFAAGNMRKRLFGVRLKCHSLFDLOVNSLOTVNTYKILLLOAYRFAVCVLOLP 1020

QY 1021 FHQGVKXKPTFLRLVISTYASLCYSILAKKAGMSLGAKGAGPLPSBAVOMLCHQAFLL 1080
 DB 1021 FHQGVKXKPTFLRLVISTYASLCYSILAKKAGMSLGAKGAGPLPSBAVOMLCHQAFLL 1080

QY 1081 KLTRHRTVYVPLGSLRLTAQQLSRKLPGLTTLALEAANPALPSDFETIID 1132
 DB 1081 KLTRHRTVYVPLGSLRLTAQQLSRKLPGLTTLALEAANPALPSDFETIID 1132

RESULT 13
 US-09-788-110A-23
 ; Sequence 23, Application US/09788110A
 ; Publication No. US20040086518A1

```

; GENERAL INFORMATION:
; APPLICANT: Zanetti, Maurizio
; TITLE OF INVENTION: A Universal Vaccine and Method for Treating Cancer Employing
; TITLE OF INVENTION: Telomerase Reverse Transcriptase
; FILE REFERENCE: UCSD-07017
; CURRENT APPLICATION NUMBER: US/09/788,110A
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-110A-23

Query Match          99.8%; Score 5952; DB 11; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLSHREYVPLATFVRRLGPQGRVLQGRDPAFRLVAQCLVCVPM 60
DB 1 MPAPRCRAVRSLLSHREYVPLATFVRRLGPQGRVLQGRDPAFRLVAQCLVCVPM 60
QY 61 DAPPPAASPFQVSCLEKELVARVLQRLCERGAKNVIAFGFALLDGAAGPPEAFTTSVR 120
DB 61 DAPPPAASPFQVSCLEKELVARVLQRLCERGAKNVIAFGFALLDGAAGPPEAFTTSVR 120
QY 121 SYLNTVTDTALRSGAGMLLRVGDVVLHLLARCALFVLVASCAYQCGPPLYQGA 180
DB 121 SYLNTVTDTALRSGAGMLLRVGDVVLHLLARCALFVLVASCAYQCGPPLYQGA 180
QY 181 ATGAPPPASGRRRLGGERAMNSVREAGVPLGAPGARRGSSASRLPLPKRRR 240
DB 181 ATGAPPPASGRRRLGGERAMNSVREAGVPLGAPGARRGSSASRLPLPKRRR 240
QY 241 GAAPBERTPVQGSWAHPDRTGSDRGFCVVSAPPAEATSLGALSGTRHSHPSVG 300
DB 241 GAAPBERTPVQGSWAHPDRTGSDRGFCVVSAPPAEATSLGALSGTRHSHPSVG 300
QY 301 RQHHAGPSTSRPPRWDPCCPPVAAETGELVSSGDKQCLAPSLLSIRPSLGGARL 360
DB 301 RQHHAGPSTSRPPRWDPCCPPVAAETGELVSSGDKQCLAPSLLSIRPSLGGARL 360
QY 361 VETIFGSRPMWPGTFRLLPRLPORYQWRPLFLELLGNHACPPYVLLKTHCPRLAAVT 420
DB 361 VETIFGSRPMWPGTFRLLPRLPORYQWRPLFLELLGNHACPPYVLLKTHCPRLAAVT 420
QY 421 PAAGVCAAREKPOGSVAAPBEDTDRRLVQLRQSSPWQYGFVACLRRLVPPGLMGS 480
DB 421 PAAGVCAAREKPOGSVAAPBEDTDRRLVQLRQSSPWQYGFVACLRRLVPPGLMGS 480
QY 481 RHNERFLLNTKKFISLGAKLSLOELTWKMSVDCAWLRSPGVGCVPAAEHRLREI 540
DB 481 RHNERFLLNTKKFISLGAKLSLOELTWKMSVDCAWLRSPGVGCVPAAEHRLREI 540
QY 541 LAKFLHMLMSVYVELLSFFVYVETTFQXRLFFYRPSVMSKLSIGIRQHLKRVQURE 600
DB 541 LAKFLHMLMSVYVELLSFFVYVETTFQXRLFFYRPSVMSKLSIGIRQHLKRVQURE 600
QY 601 LSAEVRQREARPAALTSRLRFIPKPDGLRIYVMDVVGARTFRREARERLTSRYKA 660
DB 601 LSAEVRQREARPAALTSRLRFIPKPDGLRIYVMDVVGARTFRREARERLTSRYKA 660
QY 661 LFSVLYNEBARRRPGLIGASVLGDDIHRAMRTFVLRAQDPPEELVYKQDVDTAYDTI 720
DB 661 LFSVLYNEBARRRPGLIGASVLGDDIHRAMRTFVLRAQDPPEELVYKQDVDTAYDTI 720
QY 721 PODRLTEVASTIKPONTYCVRRYAVVQCAAHGHRKAFKSVSTLTLOPMRFVHL 780
DB 721 PODRLTEVASTIKPONTYCVRRYAVVQCAAHGHRKAFKSVSTLTLOPMRFVHL 780
QY 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRMCHHAVIRGKSYVQCGIPOGSLSTL 840

```

```

DB 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRMCHHAVIRGKSYVQCGIPOGSLSTL 840
QY 841 LCSLCYGDMMENKLFAGIRBDLLRLVDDPLVTPHLLTAKEFLRLTVGVEYGCVNL 900
DB 841 LCSLCYGDMMENKLFAGIRBDLLRLVDDPLVTPHLLTAKEFLRLTVGVEYGCVNL 900
QY 901 RKTYYNPFVDEALGGAFAFYQPARAGLFPWCGILLDTRTLEVQSDSSYARSIRASYTF 960
DB 901 RKTYYNPFVDEALGGAFAFYQPARAGLFPWCGILLDTRTLEVQSDSSYARSIRASYTF 960
QY 961 NRGFKAGNRRLKFGVLRKCHSLFLDLQVNSLQTVCTNITYKILLQAYRFAVCLQLP 1020
DB 961 NRGFKAGNRRLKFGVLRKCHSLFLDLQVNSLQTVCTNITYKILLQAYRFAVCLQLP 1020
QY 1021 FHOQVKNPFFLRVISTDASLCYSILKANKAGMSIGAKGAGPLPSEAVQWICHQAFLL 1080
DB 1021 FHOQVKNPFFLRVISTDASLCYSILKANKAGMSIGAKGAGPLPSEAVQWICHQAFLL 1080
QY 1081 KLTRHRTVYPLGSLRTAQTOLSRKLPQTTLTALBAANPALPSPDKTILD 1132
DB 1081 KLTRHRTVYPLGSLRTAQTOLSRKLPQTTLTALBAANPALPSPDKTILD 1132

RESULT 14
US-10-053-758-225
; Sequence 225, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cecch, Thomas R.
; Linguier, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030032075A1e1 Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015839-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 225:
; SEQUENCE CHARACTERISTICS:

```


LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 225:
US-10-053-758-225

Query Match 99.8%; Score 5952; DB 14; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVSLRSHRYREVLPATFVRRLGPOGMRVORGPAPAFALVAQCIVCPVM 60
DB 1 MPAPRCRAVSLRSHRYREVLPATFVRRLGPOGMRVORGPAPAFALVAQCIVCPVM 60
QY 61 DAPPPAPSPFQVSCIKELVARVLQRLCERGAKNVLAFGFALLDGARGGPEAFTTSVR 120
DB 61 DAPPPAPSPFQVSCIKELVARVLQRLCERGAKNVLAFGFALLDGARGGPEAFTTSVR 120
QY 121 SYLPTVTDLRSGGAMGILLRRVGDVYLHLLARCALFVLVAPSCAYQVCGSPLYQLGA 180
DB 121 SYLPTVTDLRSGGAMGILLRRVGDVYLHLLARCALFVLVAPSCAYQVCGSPLYQLGA 180
QY 181 ATQARPPHASPGRRLCERAMNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
DB 181 ATQARPPHASPGRRLCERAMNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
QY 241 GAAPPERTVVGQGSMAHPGRTGSPDRGCVVSPAPAEATSLGALSCTHSHPSVG 300
DB 241 GAAPPERTVVGQGSMAHPGRTGSPDRGCVVSPAPAEATSLGALSCTHSHPSVG 300
QY 301 ROHHAGPSTSRPRPMDTCPPIYAETKHFVLYSSGDKELRSFLLSLRPSLTGARRL 360
DB 301 ROHHAGPSTSRPRPMDTCPPIYAETKHFVLYSSGDKELRSFLLSLRPSLTGARRL 360
QY 361 VETIFLGSRRPMPGTGPRRLPLRPLQRYWQMRPLFLELLGNHACQPGVLLKTHCPRAAVT 420
DB 361 VETIFLGSRRPMPGTGPRRLPLRPLQRYWQMRPLFLELLGNHACQPGVLLKTHCPRAAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEDMDPRLYOLLRQHSPPQVGVFAACRLRPLPGLMS 480
DB 421 PAAGVCAREKPGQSVAAPEEDMDPRLYOLLRQHSPPQVGVFAACRLRPLPGLMS 480
QY 481 RHNERRLRNTKFIISLGHAKLSLOELTWKMSVDCAMLRSPGVGCYVPAAEHRLREEL 540
DB 481 RHNERRLRNTKFIISLGHAKLSLOELTWKMSVDCAMLRSPGVGCYVPAAEHRLREEL 540
QY 541 LAKEFLHLMVYVVELLSRFFYYTETTFQKORLFFRPSWSKLSQSLGIFQHLKRYQLSE 600
DB 541 LAKEFLHLMVYVVELLSRFFYYTETTFQKORLFFRPSWSKLSQSLGIFQHLKRYQLSE 600
QY 601 LSEAEVQHEARPAALLTSRLRFIPKPDGLPIYMDVYVGARTPREKKAEBLTGRVKA 660
DB 601 LSEAEVQHEARPAALLTSRLRFIPKPDGLPIYMDVYVGARTPREKKAEBLTGRVKA 660
QY 661 LFSVYNTERRARRPGLIGASVILGDDIHRAMRTFVLRAADPPPELYFVKVDVTGAYDTI 720
DB 661 LFSVYNTERRARRPGLIGASVILGDDIHRAMRTFVLRAADPPPELYFVKVDVTGAYDTI 720
QY 721 POBLRTVIAISIKPONTYCVRRYAVYQKAAHGVRAAFKSHVSTLTDLPYRKOVAAHL 780
DB 721 POBLRTVIAISIKPONTYCVRRYAVYQKAAHGVRAAFKSHVSTLTDLPYRKOVAAHL 780
QY 781 QETSPLRDAAVIEGSSSLNASSGLFDVFLRFMCNHAARIRGKSYVCCQGIPOGSLSTL 840
DB 781 QETSPLRDAAVIEGSSSLNASSGLFDVFLRFMCNHAARIRGKSYVCCQGIPOGSLSTL 840
QY 841 LCSTCYGDMENKLFAGIRPGGLLRVDDFLVTPHILTHAKTFLRTVIRVPEYGCVM 900
DB 841 LCSTCYGDMENKLFAGIRPGGLLRVDDFLVTPHILTHAKTFLRTVIRVPEYGCVM 900
QY 901 RKTYYNPFVEDEALGATFVQMPAHGLFPMCGLLDTRILEVQSDYSYARTSIRASVTF 960
DB 901 RKTYYNPFVEDEALGATFVQMPAHGLFPMCGLLDTRILEVQSDYSYARTSIRASVTF 960

DB 901 RKTYYNPFVEDEALGATFVQMPAHGLFPMCGLLDTRILEVQSDYSYARTSIRASVTF 960
QY 961 NRGFAGNMRRKLFVLRKLSFLDLQVNSLQVCTNITYKILLQAYEPHACVQLP 1020
DB 961 NRGFAGNMRRKLFVLRKLSFLDLQVNSLQVCTNITYKILLQAYEPHACVQLP 1020
QY 1021 FHQYWKNPTEFLRISPTASLCSYILKAKAGSLGAKGAPLSRAVQMLQHAFTL 1080
DB 1021 FHQYWKNPTEFLRISPTASLCSYILKAKAGSLGAKGAPLSRAVQMLQHAFTL 1080
QY 1081 KLTRHRYVYVLLGSLRTAQTLRSKLPGLTTLTALEAANALPSPDFKTIID 1132
DB 1081 KLTRHRYVYVLLGSLRTAQTLRSKLPGLTTLTALEAANALPSPDFKTIID 1132

RESULT 15
US-10-208-243-2
; Sequence 2, Application US/10208243
; Publication No. US20030044394A1
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
; APPLICANT: Genon Corporation
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
; FILE REFERENCE: 015389-003500PC
; CURRENT APPLICATION NUMBER: US/10/208,243
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US/09/675,321
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/112,006
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-208-243-2

Query Match 99.8%; Score 5952; DB 14; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVSLRSHRYREVLPATFVRRLGPOGMRVORGPAPAFALVAQCIVCPVM 60
DB 1 MPAPRCRAVSLRSHRYREVLPATFVRRLGPOGMRVORGPAPAFALVAQCIVCPVM 60
QY 61 DAPPPAPSPFQVSCIKELVARVLQRLCERGAKNVLAFGFALLDGARGGPEAFTTSVR 120
DB 61 DAPPPAPSPFQVSCIKELVARVLQRLCERGAKNVLAFGFALLDGARGGPEAFTTSVR 120
QY 121 SYLPTVTDLRSGGAMGILLRRVGDVYLHLLARCALFVLVAPSCAYQVCGSPLYQLGA 180
DB 121 SYLPTVTDLRSGGAMGILLRRVGDVYLHLLARCALFVLVAPSCAYQVCGSPLYQLGA 180
QY 181 ATQARPPHASPGRRLCERAMNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
DB 181 ATQARPPHASPGRRLCERAMNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
QY 241 GAAPPERTVVGQGSMAHPGRTGSPDRGCVVSPAPAEATSLGALSCTHSHPSVG 300
DB 241 GAAPPERTVVGQGSMAHPGRTGSPDRGCVVSPAPAEATSLGALSCTHSHPSVG 300
QY 301 ROHHAGPSTSRPRPMDTCPPIYAETKHFVLYSSGDKELRSFLLSLRPSLTGARRL 360
DB 301 ROHHAGPSTSRPRPMDTCPPIYAETKHFVLYSSGDKELRSFLLSLRPSLTGARRL 360
QY 361 VETIFLGSRRPMPGTGPRRLPLRPLQRYWQMRPLFLELLGNHACQPGVLLKTHCPRAAVT 420
DB 361 VETIFLGSRRPMPGTGPRRLPLRPLQRYWQMRPLFLELLGNHACQPGVLLKTHCPRAAVT 420

QY 421 PAAGVAREKPOGSVAAPBEEDTDPRLVQLRHSSPMQVGFVACLRRLVPPGLMGS 480
D 421 PAAGVAREKPOGSVAAPBEEDTDPRLVQLRHSSPMQVGFVACLRRLVPPGLMGS 480
QY 481 RHNERFLNRTKFFISLGHAKLSLOELTWKMSVDCAMLRSPGVGCYPAAEHLREI 540
D 481 RHNERFLNRTKFFISLGHAKLSLOELTWKMSVDCAMLRSPGVGCYPAAEHLREI 540
QY 541 LAKFLMLMSVYVELLSFFVYTTETTFQKNRLFYRPSWMSKOSIGRHLKRVQRE 600
D 541 LAKFLMLMSVYVELLSFFVYTTETTFQKNRLFYRPSWMSKOSIGRHLKRVQRE 600
QY 601 LSEAEVROHREARPAALITSLRRLPIPKDGLRPIVMDYVAGARTREKRAELTSRYKA 660
D 601 LSEAEVROHREARPAALITSLRRLPIPKDGLRPIVMDYVAGARTREKRAELTSRYKA 660
QY 661 LSVLMEAREARPGILGASVLDIHRAMRFVLRVAPADPEPLVYKVDVTAAYTI 720
D 661 LSVLMEAREARPGILGASVLDIHRAMRFVLRVAPADPEPLVYKVDVTAAYTI 720
QY 721 POBLTEVIAIIPQNTYCVRRYAVVCKAAHGHVKAFAKSHVSTLTLQPYMRQFVAHL 780
D 721 POBLTEVIAIIPQNTYCVRRYAVVCKAAHGHVKAFAKSHVSTLTLQPYMRQFVAHL 780
QY 781 QETSPLRDAVLEOSSLNEASSGLFDVFLRPMCHAVIRKGSYVQCGIPQSLSTL 840
D 781 QETSPLRDAVLEOSSLNEASSGLFDVFLRPMCHAVIRKGSYVQCGIPQSLSTL 840
QY 841 LSLCYGDMENKLFAGIRRDGLLRVDFLLVTEPHLTHAKTFLLTVRGVPEYCVVNL 900
D 841 LSLCYGDMENKLFAGIRRDGLLRVDFLLVTEPHLTHAKTFLLTVRGVPEYCVVNL 900
QY 901 RKTVMNFPVEDALGTAIVQMPAHGLFPGCGLLDTRILEVQSYSTASTASTF 960
D 901 RKTVMNFPVEDALGTAIVQMPAHGLFPGCGLLDTRILEVQSYSTASTASTF 960
QY 961 NGCFKAGRWKRKLFCVLRKCHSLFLDQVNSLQTVCTNLIKILLGAYFPHACVLDLP 1020
D 961 NGCFKAGRWKRKLFCVLRKCHSLFLDQVNSLQTVCTNLIKILLGAYFPHACVLDLP 1020
QY 1021 FHQOVKNDPFLRIVISDTASLCYSIILKAKNAGSLGAKGAPLPSAAYOMLCHQAFLL 1080
D 1021 FHQOVKNDPFLRIVISDTASLCYSIILKAKNAGSLGAKGAPLPSAAYOMLCHQAFLL 1080
QY 1081 KLTRHNVTVPLIGSLRTAQOLSRKLPSTLTALFAANPALPSDFTIID 1132
D 1081 KLTRHNVTVPLIGSLRTAQOLSRKLPSTLTALFAANPALPSDFTIID 1132

RESULT 16
US-10-054-295-225
Sequence 225, Application US/10054295
Publication No. US20030044953A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030044953A1e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-Oct-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 225:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 225:
US-10-054-295-225

Query Match 99.8%; Score 5952; DB 14; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSILRSHYREVLPLATFVRRLGPOGRLVORGDPAPFALVAQCLVCEVM 60
D 1 MPAPRCRAVRSILRSHYREVLPLATFVRRLGPOGRLVORGDPAPFALVAQCLVCEVM 60
QY 61 DAPPPAPESFRVYSLCKELVAVLORLCERAKNYLACGFALLDGRGPEAPFTTSVR 120
D 61 DAPPPAPESFRVYSLCKELVAVLORLCERAKNYLACGFALLDGRGPEAPFTTSVR 120
QY 121 SYLPNTVTDALRSGGAMGLLRVGDVVLHLARCALFVLVAPSCAYVCGPPLYOLGA 180
D 121 SYLPNTVTDALRSGGAMGLLRVGDVVLHLARCALFVLVAPSCAYVCGPPLYOLGA 180
QY 181 ATQAPPPHAGSPRRRLGCRAMNHSVREAGVPLGLPAGARRGGSASRLPLPKRRR 240
D 181 ATQAPPPHAGSPRRRLGCRAMNHSVREAGVPLGLPAGARRGGSASRLPLPKRRR 240
QY 241 GAAPPEPRTVGGGSAHAPGRTGPGSDRGFCVYSPAPPAEATSLGALSGTRHSPVSG 300
D 241 GAAPPEPRTVGGGSAHAPGRTGPGSDRGFCVYSPAPPAEATSLGALSGTRHSPVSG 300
QY 301 ROHAGPSTSRDPREMDTPCPVVAETHFLYSSGDKQLRPSFLSLRPSLTGARRL 360
D 301 ROHAGPSTSRDPREMDTPCPVVAETHFLYSSGDKQLRPSFLSLRPSLTGARRL 360
QY 361 VETITIGSRPMWPGTRRLPLPQRYWQMRPLFELLLGNHACOPGVILKTCPLRAAYT 420
D 361 VETITIGSRPMWPGTRRLPLPQRYWQMRPLFELLLGNHACOPGVILKTCPLRAAYT 420
QY 421 PAAGVAREKPOGSVAAPBEEDTDPRLVQLRHSSPMQVGFVACLRRLVPPGLMGS 480
D 421 PAAGVAREKPOGSVAAPBEEDTDPRLVQLRHSSPMQVGFVACLRRLVPPGLMGS 480
QY 481 RHNERFLNRTKFFISLGHAKLSLOELTWKMSVDCAMLRSPGVGCYPAAEHLREI 540
D 481 RHNERFLNRTKFFISLGHAKLSLOELTWKMSVDCAMLRSPGVGCYPAAEHLREI 540
QY 541 LAKFLMLMSVYVELLSFFVYTTETTFQKNRLFYRPSWMSKOSIGRHLKRVQRE 600
D 541 LAKFLMLMSVYVELLSFFVYTTETTFQKNRLFYRPSWMSKOSIGRHLKRVQRE 600

Tue Dec 21 15:43:31 2004

us-08-974-584c-118.rapb

Page 17

Dz	54	LAKLHMLMSVYVELLSRFYVETTFEQNRLEFFRKXVWSKLQSIGRHLKRYDRE	600
Qy	601	LSEAEVQHREARPAALLTSRLRFPKRGDLRPYMMDYVGARFPRREKARELTSYKA	660
Dz	601	LSEAEVQHREARPAALLTSRLRFPKRGDLRPYMMDYVGARFPRREKARELTSYKA	660
Qy	661	LFSVLANERARPBGLGASVLDGLDIDIRAMRTFVLRYAODPREPELVKADVGAADTI	720
Dz	661	LFSVLANERARPBGLGASVLDGLDIDIRAMRTFVLRYAODPREPELVKADVGAADTI	720
Qy	721	PODPLTEVIASIIKPONTYCYRRAVYQKANHGYKAFKXNVSTLDLOQYMOQFAHL	780
Dz	721	PODPLTEVIASIIKPONTYCYRRAVYQKANHGYKAFKXNVSTLDLOQYMOQFAHL	780
Qy	781	QETSPLLEDAVYEQSSSLNEASSGLFDVFLRPMCHNAVRIGKSYQCGIQSGISLTL	840
Dz	781	QETSPLLEDAVYEQSSSLNEASSGLFDVFLRPMCHNAVRIGKSYQCGIQSGISLTL	840
Qy	841	LCSLCYGDMENKLFAGIRDBDLLRLVDDFLYPLPHLTHACTFLRLYRGRPEYGCYVNL	900
Dz	841	LCSLCYGDMENKLFAGIRDBDLLRLVDDFLYPLPHLTHACTFLRLYRGRPEYGCYVNL	900
Qy	901	RKYVNEPVEDBEALGTAFFVQMPAHGFLPWCGLLDLTLEVOSSDYSAATSIRASYTF	960
Dz	901	RKYVNEPVEDBEALGTAFFVQMPAHGFLPWCGLLDLTLEVOSSDYSAATSIRASYTF	960
Qy	961	NRGSKAGNRMRKLFGLVRLKCHSLFDLYONSLOTYVTNLYKILLIQAYPEHACVLOLP	1020
Dz	961	NRGSKAGNRMRKLFGLVRLKCHSLFDLYONSLOTYVTNLYKILLIQAYPEHACVLOLP	1020
Qy	1021	FHQQVWKNKPTFLFLVISTDTSALCYSLIKAKVAGMSLGAAGAAGPLPSEAVOMLCHOAFL	1080
Dz	1021	FHQQVWKNKPTFLFLVISTDTSALCYSLIKAKVAGMSLGAAGAAGPLPSEAVOMLCHOAFL	1080
Qy	1081	KLTHRYVYVVLGSLRTAQTQSLKPLGTTLTALAAANPALPBDFTIIL	1132
Dz	1081	KLTHRYVYVVLGSLRTAQTQSLKPLGTTLTALAAANPALPBDFTIIL	1132

RESULT 17
 US-10-054-611-225
 Sequence 225: Application US/10054611
 Publication No. US20030059787A1
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 Linsner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin
 Andrews, William H.
 TITLE OF INVENTION: NO. US20030059787A1el Telomerase
 NUMBER OF SEQUENCES: 225
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/054,611
 FILING DATE: 18-Jan-2002
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/854,050
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/846,017

```

? FILING DATE: 25-APR-1997
? APPLICATION NUMBER: US 08/844,419
? FILING DATE: 18-APR-1997
? APPLICATION NUMBER: US 08/724,643
? FILING DATE: 01-OCT-1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Apple, Randolph T.
? REGISTRATION NUMBER: 36,429
? REFERENCE/DOCKET NUMBER: 015389-002930US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 576-0200
? TELEFAX: (415) 576-0300
? INFORMATION FOR SEQ ID NO: 225:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1132 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: Protein
? SEQUENCE DESCRIPTION: SEQ ID NO: 225:
US-10-054-611-225

Query Match          99.8%  Score 5952;  DB 14;  Length 1132;
Best Local Similarity 99.8%  Pred. No. 0;
Matches 1130;  Conservative 1;  Mismatches 1;  Indels 0;  Gaps 0.

```

Qy	1	MPYARPCRAVRSLLRSIHYREVLPLATFVRJRGPGQWRJVGQDPAAPFALYAQCCVCPW	60
Db	1	MPRAPRCRAVRSLLRSIHYREVLPLATFVRJRGPGQWRJVGQDPAAPFALYAQCCVCPW	60
Qy	61	DABPAPASPRFQVSCIKELVAVLQRCERGANVLAFGALLDGAERGEPAFTTSVR	120
Db	61	DABPAPASPRFQVSCIKELVAVLQRCERGANVLAFGALLDGAERGEPAFTTSVR	120
Qy	121	SYLPTYTDLARSGGANGLLRRGGDVVHLRLARCLFVLVABSCAYQVCGPPLYQGA	180
Db	121	SYLPTYTDLARSGGANGLLRRGGDVVHLRLARCLFVLVABSCAYQVCGPPLYQGA	180
Qy	181	ATQARPPHASGPPRRJGCEPAMHVSVEAGVPLGLPAPGARRGGSASRSLPLEKRRR	240
Db	181	ATQARPPHASGPPRRJGCEPAMHVSVEAGVPLGLPAPGARRGGSASRSLPLEKRRR	240
Qy	241	GAAPERTPRYGQSSMAHPRGTRGSDRGFCVSPAPARAEATSLBGLSGCRHSPBG	300
Db	241	GAAPERTPRYGQSSMAHPRGTRGSDRGFCVSPAPARAEATSLBGLSGCRHSPBG	300
Qy	301	RQNHAGPSTSRPRPMDTCCPYAETKXHLFYSGSDGEOLRPSFLSLSPSLGARSL	360
Db	301	RQNHAGPSTSRPRPMDTCCPYAETKXHLFYSGSDGEOLRPSFLSLSPSLGARSL	360
Qy	361	VETIFLGRPMMPGTPRRLLPRLPORYWOMRPLFELJGNHAQCPYGVILKTHCPRAAVT	420
Db	361	VETIFLGRPMMPGTPRRLLPRLPORYWOMRPLFELJGNHAQCPYGVILKTHCPRAAVT	420
Qy	421	PAQVYCARXQGSVAAPEBEDTPRRLVOLLQSSSMOYGYGFYRACLRPLPGLGMS	480
Db	421	PAQVYCARXQGSVAAPEBEDTPRRLVOLLQSSSMOYGYGFYRACLRPLPGLGMS	480
Qy	481	RHNERRPLRNTKKTISLQKHAKLISOELTWKSVYDCAMLRSPGVGCVPAAEHRLREBI	540
Db	481	RHNERRPLRNTKKTISLQKHAKLISOELTWKSVYDCAMLRSPGVGCVPAAEHRLREBI	540
Qy	541	LAKFLHMLMSYVYVELLSFFYVMTTQKRLPFYRSWSKOSIGIRQHLKRVOLRE	600
Db	541	LAKFLHMLMSYVYVELLSFFYVMTTQKRLPFYRSWSKOSIGIRQHLKRVOLRE	600
Qy	601	LSEAEVRQHREARPALTISRLEFIPKPDGLPPIVMNDYVVGARTPRREKAERLTSRYKA	660
Db	601	LSEAEVRQHREARPALTISRLEFIPKPDGLPPIVMNDYVVGARTPRREKAERLTSRYKA	660
Qy	661	LFSVLYNRRARPGLIGSVGLDDIHRAMTTFVLRYVAQOPPEPLFYKXVDYGAUDI	720
Db	661	LFSVLYNRRARPGLIGSVGLDDIHRAMTTFVLRYVAQOPPEPLFYKXVDYGAUDI	720

```

Qy 721 PQRRLTEVASTIKPONTYCVRRYAVVQKAAGHVAKAFKSHVSTLTDLPYMRQFVAHL 780
Db 721 PQRRLTEVASTIKPONTYCVRRYAVVQKAAGHVAKAFKSHVSTLTDLPYMRQFVAHL 780
Qy 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHAAVIRGKSYVOCGIGIPOGSIILSTL 840
Db 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHAAVIRGKSYVOCGIGIPOGSIILSTL 840
Qy 841 LCLSLCGDMENKLPAGIRRDGILLRLVDDPLVTPHLLTHAKTFLRLTVRGVEYGCYVNL 900
Db 841 LCLSLCGDMENKLPAGIRRDGILLRLVDDPLVTPHLLTHAKTFLRLTVRGVEYGCYVNL 900
Qy 901 RKTVMNFPVEDEALGTAFAVQMPAHGLFPMCGILLDTRTLEVOSSYSSYARSTIRASVTF 960
Db 901 RKTVMNFPVEDEALGTAFAVQMPAHGLFPMCGILLDTRTLEVOSSYSSYARSTIRASVTF 960
Qy 961 NRGFKAGRMNRRLFGVLRKCHSLFLDQVNSLQTVCTNIYKILLQAYRPHACVLOLP 1020
Db 961 NRGFKAGRMNRRLFGVLRKCHSLFLDQVNSLQTVCTNIYKILLQAYRPHACVLOLP 1020
Qy 1021 FHQVWKNPFFLRVISTDASLCYSTLKAKNAGMSLGAGGAGPLPSEAVQWLCQAFL 1080
Db 1021 FHQVWKNPFFLRVISTDASLCYSTLKAKNAGMSLGAGGAGPLPSEAVQWLCQAFL 1080
Qy 1081 KLTRHRVTYVPLIGSLRTAQTQLSRKLPGTTLTALAAANPALPSDFKTIID 1132
Db 1081 KLTRHRVTYVPLIGSLRTAQTQLSRKLPGTTLTALAAANPALPSDFKTIID 1132

RESULT 18
US-10-105-963-2
; Sequence 2, Application US/10105963
; Publication No. US20030068618A1
; GENERAL INFORMATION:
; APPLICANT: Genon Corporation
; APPLICANT: Deming, Chris
; APPLICANT: Clark, A. John
; TITLE OF INVENTION: J. Michael
; TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human
; TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection System
; FILE REFERENCE: 731/002
; CURRENT APPLICATION NUMBER: US/10/105,963
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/277,811
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-963-2

Query Match 99.8%; Score 5952; DB 14; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRRAPRCRAVRSILSHYREVLPLATFVRLGPQGMRLVORGDPAAPFALVAQCIVCPW 60
Db 1 MRRAPRCRAVRSILSHYREVLPLATFVRLGPQGMRLVORGDPAAPFALVAQCIVCPW 60
Qy 61 DARPPAAASFROVSCIKELVAVRQLCERCAKRVLAFGPALLDGAAGPPEAFITSVR 120
Db 61 DARPPAAASFROVSCIKELVAVRQLCERCAKRVLAFGPALLDGAAGPPEAFITSVR 120
Qy 121 SYLPNTVTDALRGSGAGWGLLRVRVDVVLVHLARCAFLVAVPSCAVQVGPPLVQGA 180
Db 121 SYLPNTVTDALRGSGAGWGLLRVRVDVVLVHLARCAFLVAVPSCAVQVGPPLVQGA 180
Qy 181 ATQAPPPPPASGPPRRRLGGERAMNHSVNBAGVPLCLPAPGARRRGSGASRLPLPKPRR 240
Db 181 ATQAPPPPPASGPPRRRLGGERAMNHSVNBAGVPLCLPAPGARRRGSGASRLPLPKPRR 240
Qy 240 ATQAPPPPPASGPPRRRLGGERAMNHSVNBAGVPLCLPAPGARRRGSGASRLPLPKPRR 240
Db 240 ATQAPPPPPASGPPRRRLGGERAMNHSVNBAGVPLCLPAPGARRRGSGASRLPLPKPRR 240

```

```

Qy 241 GAAPERTPVQGGSMHAPGRTGSPSDRGFCVVSPPAPAEATSLGALSGTRHSPVSG 300
Db 241 GAAPERTPVQGGSMHAPGRTGSPSDRGFCVVSPPAPAEATSLGALSGTRHSPVSG 300
Qy 301 ROHAGPSTSPRPPMDTCCPPVYAEETKHELSSGDKEDLRPSFLSSLRPSLTGARL 360
Db 301 ROHAGPSTSPRPPMDTCCPPVYAEETKHELSSGDKEDLRPSFLSSLRPSLTGARL 360
Qy 361 VETIFLGSRRPMPGTPLRLPLQRYWQMPFLLELLGNHAGCPYGVLLKTHCPLEAAVT 420
Db 361 VETIFLGSRRPMPGTPLRLPLQRYWQMPFLLELLGNHAGCPYGVLLKTHCPLEAAVT 420
Qy 421 PAAGVCAKREKQSSVAPPEEDTPRRVLVQLLEQSSPMQVYFVAPACLRRLVPELMS 480
Db 421 PAAGVCAKREKQSSVAPPEEDTPRRVLVQLLEQSSPMQVYFVAPACLRRLVPELMS 480
Qy 481 RHNERRLRNTKFFISIGKAKLSLOELTWKMSVRCAMLRSPGVCVPAAEHRLREEI 540
Db 481 RHNERRLRNTKFFISIGKAKLSLOELTWKMSVRCAMLRSPGVCVPAAEHRLREEI 540
Qy 541 LAKFLWMSVYVELLSFFYTETTFQONRLFFRPSVMSKLSIGTRHILKRYQLRE 600
Db 541 LAKFLWMSVYVELLSFFYTETTFQONRLFFRPSVMSKLSIGTRHILKRYQLRE 600
Qy 601 LSEAEVQOHEARAPALTSRLRFIPKPDGLRPIVNMDDYVAGARTPREKARSLTSRYKA 660
Db 601 LSEAEVQOHEARAPALTSRLRFIPKPDGLRPIVNMDDYVAGARTPREKARSLTSRYKA 660
Qy 661 LPSVLYNERARPPGLIGASVLAGDDIHRAIRFVLRADQPPPELYFVKVDTGAYDTI 720
Db 661 LPSVLYNERARPPGLIGASVLAGDDIHRAIRFVLRADQPPPELYFVKVDTGAYDTI 720
Qy 721 PQRRLTEVASTIKPONTYCVRRYAVVQKAAGHVAKAFKSHVSTLTDLPYMRQFVAHL 780
Db 721 PQRRLTEVASTIKPONTYCVRRYAVVQKAAGHVAKAFKSHVSTLTDLPYMRQFVAHL 780
Qy 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHAAVIRGKSYVOCGIGIPOGSIILSTL 840
Db 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHAAVIRGKSYVOCGIGIPOGSIILSTL 840
Qy 841 LCLSLCGDMENKLPAGIRRDGILLRLVDDPLVTPHLLTHAKTFLRLTVRGVEYGCYVNL 900
Db 841 LCLSLCGDMENKLPAGIRRDGILLRLVDDPLVTPHLLTHAKTFLRLTVRGVEYGCYVNL 900
Qy 901 RKTVMNFPVEDEALGTAFAVQMPAHGLFPMCGILLDTRTLEVOSSYSSYARSTIRASVTF 960
Db 901 RKTVMNFPVEDEALGTAFAVQMPAHGLFPMCGILLDTRTLEVOSSYSSYARSTIRASVTF 960
Qy 961 NRGFKAGRMNRRLFGVLRKCHSLFLDQVNSLQTVCTNIYKILLQAYRPHACVLOLP 1020
Db 961 NRGFKAGRMNRRLFGVLRKCHSLFLDQVNSLQTVCTNIYKILLQAYRPHACVLOLP 1020
Qy 1021 FHQVWKNPFFLRVISTDASLCYSTLKAKNAGMSLGAGGAGPLPSEAVQWLCQAFL 1080
Db 1021 FHQVWKNPFFLRVISTDASLCYSTLKAKNAGMSLGAGGAGPLPSEAVQWLCQAFL 1080
Qy 1081 KLTRHRVTYVPLIGSLRTAQTQLSRKLPGTTLTALAAANPALPSDFKTIID 1132
Db 1081 KLTRHRVTYVPLIGSLRTAQTQLSRKLPGTTLTALAAANPALPSDFKTIID 1132

RESULT 19
US-10-044-692-2
; Sequence 2, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Martin, Gregg B.
; APPLICANT: Harley, Calvin

```

Tue Dec 21 15:43:31 2004

us-08-974-584c-118.rapb

Page 19

Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692
FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REFERENCE/DOCKET NUMBER: 015389-002600US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-044-692-2
Query Match 99.8%; Score 5952; DB 14; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1133; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

301 ROHAGPESTSRPPRMDTPCPVYAETKHFLYSSGDEQURPSLSSLPSTLGARL 360
301 ROHAGPESTSRPPRMDTPCPVYAETKHFLYSSGDEQURPSLSSLPSTLGARL 360
361 VETITLGRPMWPGTFRRLPRLPORWOMRPLFELLGNHAQCPYGVLLKTHCPILAAVT 420
361 VETITLGRPMWPGTFRRLPRLPORWOMRPLFELLGNHAQCPYGVLLKTHCPILAAVT 420
421 PAGVCAREKPGQSVAAPEEDTDRRLVOLLROHSSPMOYGFYACTRLRLVPGMLGS 480
421 PAGVCAREKPGQSVAAPEEDTDRRLVOLLROHSSPMOYGFYACTRLRLVPGMLGS 480
481 RHNERRFLRNTKFKIISLGHAKLSLOELTWKMSYRDCAMLRSPGVGCPAAEHLREBEI 540
481 RHNERRFLRNTKFKIISLGHAKLSLOELTWKMSYRDCAMLRSPGVGCPAAEHLREBEI 540
541 LAKFLHMLMSYVYVLLASFFVYVTTTFOKNRLFFRPSVMSKLSIGIRHLKRVQJRE 600
541 LAKFLHMLMSYVYVLLASFFVYVTTTFOKNRLFFRPSVMSKLSIGIRHLKRVQJRE 600
601 LSEAEPHREARPPALTSRLRFLPKPDGLRPIVMMDYVGARTFRREKRAERLTSRYKA 660
601 LSEAEPHREARPPALTSRLRFLPKPDGLRPIVMMDYVGARTFRREKRAERLTSRYKA 660
661 LFSVUNYRARRPGLLGASVUGLDDIRAMRTFVLRYVAQDPPELRYVKVDVTGAYVTI 720
661 LFSVUNYRARRPGLLGASVUGLDDIRAMRTFVLRYVAQDPPELRYVKVDVTGAYVTI 720
721 PODRLTEVIASIKPONTYCYRVAVVOKAHGHVXKFKSHVSTLTLOPYMROFVAHL 780
721 PODRLTEVIASIKPONTYCYRVAVVOKAHGHVXKFKSHVSTLTLOPYMROFVAHL 780
781 QETSPDLDAVYIEQSSSLENASSGLFDVFLRFMCHAVRIRKSYVVOCGIPQSSILSTL 840
781 QETSPDLDAVYIEQSSSLENASSGLFDVFLRFMCHAVRIRKSYVVOCGIPQSSILSTL 840
841 LCSLCYGMENKLPFGIRRDGLRLVDDFLVPHLTHAKTFRLTVRGVPEGVNVL 900
841 LCSLCYGMENKLPFGIRRDGLRLVDDFLVPHLTHAKTFRLTVRGVPEGVNVL 900
901 RKTIVNFEVEDEALGTAIVQMPAHGLFPMCGLLDTRTLEVOSSYARTSIRASYTF 960
901 RKTIVNFEVEDEALGTAIVQMPAHGLFPMCGLLDTRTLEVOSSYARTSIRASYTF 960
961 NRGFGAGNMRKLFVGRILKCHSLFDLOVNSIQVCTNLYKILLQAYRFAHCYQLP 1020
961 NRGFGAGNMRKLFVGRILKCHSLFDLOVNSIQVCTNLYKILLQAYRFAHCYQLP 1020
1021 FHQGVWKNPTFFLRVISTASLCYSILKAKNAGMSLGKAGAGLPSEAVOMLCHQAFIL 1080
1021 FHQGVWKNPTFFLRVISTASLCYSILKAKNAGMSLGKAGAGLPSEAVOMLCHQAFIL 1080
1081 KLTRHRTVYVPLIGSLRTAQOLSRKLPGLTTLTALBAANDALPSDEFTIIL 1132
1081 KLTRHRTVYVPLIGSLRTAQOLSRKLPGLTTLTALBAANDALPSDEFTIIL 1132
RESULT 20
US-10-044-539-2
Sequence 2, Application US/10044539
Publication No. US20030100093A1
GENERAL INFORMATION:
Applicant: Cech, Thomas R.
Inventor: Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/044,539
 FILING DATE: 11-Jan-2002
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/912,951
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002600US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1132 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-044-539-2

Query Match 99.8%; Score 5952; DB 14; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLTSLSHYREVLPATFVRLGPQGRRLVQSGDPAPAPALVAQCIVCPM 60
 DB 1 MPAPRCRAVRSLTSLSHYREVLPATFVRLGPQGRRLVQSGDPAPAPALVAQCIVCPM 60

QY 61 DARPPAPASFRQVSCLEKELVARVLOQLCERGAKNVLAFFGALLDAGRGPEAFTTSVR 120
 DB 61 DARPPAPASFRQVSCLEKELVARVLOQLCERGAKNVLAFFGALLDAGRGPEAFTTSVR 120

QY 121 STLPNTVDTALRGSGAGWGLLRVGDVYVHLAFCALFVIVAPSCAVQVCGPPIYQGA 180
 DB 121 STLPNTVDTALRGSGAGWGLLRVGDVYVHLAFCALFVIVAPSCAVQVCGPPIYQGA 180

QY 181 ATQARPPASGRRRLGGERAMNHSVREAGVPLGLPAGARRGSGASRSLPLKRRR 240
 DB 181 ATQARPPASGRRRLGGERAMNHSVREAGVPLGLPAGARRGSGASRSLPLKRRR 240

QY 241 GAAPFERPPVQGSVAHPGRTGSDRGFCVVSAPAPAEETSLSEGLSGRRHSHSVG 300
 DB 241 GAAPFERPPVQGSVAHPGRTGSDRGFCVVSAPAPAEETSLSEGLSGRRHSHSVG 300

QY 301 RQHHAGPSTSPRRPMDTFCPPVYAEYGFLYSSGDEKQLRPSFLSLSRSLTGARRL 360
 DB 301 RQHHAGPSTSPRRPMDTFCPPVYAEYGFLYSSGDEKQLRPSFLSLSRSLTGARRL 360

QY 361 VETIFGSRPMWPGTFRRLPLPQRYWQMRPLFLELGNHACPYGLVILKTHCPRAAVT 420

DB 361 VETIFGSRPMWPGTFRRLPLPQRYWQMRPLFLELGNHACPYGLVILKTHCPRAAVT 420

QY 421 PAAGVCAKEKPOGSVAAPBEEDTPRRLYOLLROSSSPVOYGVFARACRLVPGKMS 480
 DB 421 PAAGVCAKEKPOGSVAAPBEEDTPRRLYOLLROSSSPVOYGVFARACRLVPGKMS 480

QY 481 RHNERFPLRTKFKISLGAKKLSDLELTKMSVRCALRRSPGVGCPAAEHRLREBI 540
 DB 481 RHNERFPLRTKFKISLGAKKLSDLELTKMSVRCALRRSPGVGCPAAEHRLREBI 540

QY 541 LAFELHMSVYVELLRSEFPYETTFQGNRLFPRBSVMSKLSIGIRQLKRYQLRE 600
 DB 541 LAFELHMSVYVELLRSEFPYETTFQGNRLFPRBSVMSKLSIGIRQLKRYQLRE 600

QY 601 LSEAEVROHEARPAULTSRIRFIPKPDGRPIVMNDYVGAARTPREARERLTSRYKA 660
 DB 601 LSEAEVROHEARPAULTSRIRFIPKPDGRPIVMNDYVGAARTPREARERLTSRYKA 660

QY 661 LPSVLNERARBRPGLIGASVTLGDDIHRAMRTFVLRQAODPPPELYFVKVDVTGAYDTI 720
 DB 661 LPSVLNERARBRPGLIGASVTLGDDIHRAMRTFVLRQAODPPPELYFVKVDVTGAYDTI 720

QY 721 PQRLTEVIASTIKPQNTYCVRRYAVQKAHGVKAKFSVSTLTDQPYMRQPVHL 780
 DB 721 PQRLTEVIASTIKPQNTYCVRRYAVQKAHGVKAKFSVSTLTDQPYMRQPVHL 780

QY 781 QETSPLRDAVLEQSSSLNEASSGLDVEFLRFMCHNAVIRKSYVQCGIIPQGSILSTL 840
 DB 781 QETSPLRDAVLEQSSSLNEASSGLDVEFLRFMCHNAVIRKSYVQCGIIPQGSILSTL 840

QY 841 LGLCLGDMENKLPAGIRRDGLLRVYDPLVLTPLTHAKFLRLVNGVEYGVNVL 900
 DB 841 LGLCLGDMENKLPAGIRRDGLLRVYDPLVLTPLTHAKFLRLVNGVEYGVNVL 900

QY 901 RKTIVNFPVDEALGTAFAVQMPAGLFPKCGILLDTRELVQSDSYARSISASVTF 960
 DB 901 RKTIVNFPVDEALGTAFAVQMPAGLFPKCGILLDTRELVQSDSYARSISASVTF 960

QY 961 NRGFKAQRNRRLFGVLRIRKCHSLFLDIQVNSLQTCVNIKILLQAYRHACTYQLP 1020
 DB 961 NRGFKAQRNRRLFGVLRIRKCHSLFLDIQVNSLQTCVNIKILLQAYRHACTYQLP 1020

QY 1021 FHOQWKNPFELFRVSDTASLCYSTLKXKNAGMSLGAKGAGLPSEAVQMLCHQAFLL 1080
 DB 1021 FHOQWKNPFELFRVSDTASLCYSTLKXKNAGMSLGAKGAGLPSEAVQMLCHQAFLL 1080

QY 1081 KLTRHRVTVPLGLSLRTAQQLSRKLPQTTLTALBAANPALPSDKTILL 1132
 DB 1081 KLTRHRVTVPLGLSLRTAQQLSRKLPQTTLTALBAANPALPSDKTILL 1132

RESULT 21
 US-10-295-681-57
 Sequence 57, Application US/10295681
 Publication No. US20030166270A1
 GENERAL INFORMATION:
 APPLICANT: E. Premkumar Reddy
 APPLICANT: Sushil G. Rane
 APPLICANT: Richard V. Metcus
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REVERSIBLY
 INDUCING CONTINUAL GROWTH IN NORMAL CELLS
 FILE REFERENCE: 6056-307
 CURRENT APPLICATION NUMBER: US/10/295,681
 PRIOR FILING DATE: 2002-11-15
 PRIOR APPLICATION NUMBER: US 60/334,760
 NUMBER OF SEQ ID NOS: 69
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 57
 LENGTH: 1132
 TYPE: PRT
 ORGANISM: Homo sapiens

Tue Dec 21 15:43:31 2004

us-08-974-584c-118.rapb

Page 21

US-10-295-681-57

Query Match 99.8%; Score 5952; DB 14; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVSLRSHYREVLPLATFVRRLGPOGMRLVORGPAPAFPAIWAQCLVCM 60
DB 1 MPAPRCRAVSLRSHYREVLPLATFVRRLGPOGMRLVORGPAPAFPAIWAQCLVCM 60
QY 61 DAPPPAPSPROVSCIKELVAVLQCLCERGAKNVLAFGFALLDAGRGPPAFTTSVR 120
DB 61 DAPPPAPSPROVSCIKELVAVLQCLCERGAKNVLAFGFALLDAGRGPPAFTTSVR 120
QY 121 SYLPNTVTDALRSGAMGLLRVGDVLAHLARCALFLVAPSCAYQCGPPLTQLGA 180
DB 121 SYLPNTVTDALRSGAMGLLRVGDVLAHLARCALFLVAPSCAYQCGPPLTQLGA 180
QY 181 ATQARPPHAGSPRRRLGGERAMNHSYREAGVPLGJAPGARRRGASAKSLPLPRPRR 240
DB 181 ATQARPPHAGSPRRRLGGERAMNHSYREAGVPLGJAPGARRRGASAKSLPLPRPRR 240
QY 241 GAAPPERTVGGGSMHPRTRGSPDRGFCVSPAPAPAEATSLGALSGTHSHPSVG 300
DB 241 GAAPPERTVGGGSMHPRTRGSPDRGFCVSPAPAPAEATSLGALSGTHSHPSVG 300
QY 301 ROHAGPSTSRPPRPMDTCPPEVYATKHFILYSSGKEQLRPSFLSLRPSLTGARL 360
DB 301 ROHAGPSTSRPPRPMDTCPPEVYATKHFILYSSGKEQLRPSFLSLRPSLTGARL 360
QY 361 VERIFLCSRPWMPGTPRRLPLRQRYWQMPLELIGNHACCPYVLLKXHCPLRAVT 420
DB 361 VERIFLCSRPWMPGTPRRLPLRQRYWQMPLELIGNHACCPYVLLKXHCPLRAVT 420
QY 421 PAAGVCAKREKQSSVAAPEEDTDPRLVOLLROHSPMOVGFVACLRPLVPLKMS 480
DB 421 PAAGVCAKREKQSSVAAPEEDTDPRLVOLLROHSPMOVGFVACLRPLVPLKMS 480
QY 481 RHNERRFLRNTKKEFISLGHAKLSLOELTWKMSVRDCAWLRSPGVCPAAEHLREBI 540
DB 481 RHNERRFLRNTKKEFISLGHAKLSLOELTWKMSVRDCAWLRSPGVCPAAEHLREBI 540
QY 541 LAPELHMKSVYVELLSRFFVYETTFQCNRLFFRPSVWSKLSIGIRQHLKRYQLE 600
DB 541 LAPELHMKSVYVELLSRFFVYETTFQCNRLFFRPSVWSKLSIGIRQHLKRYQLE 600
QY 601 LSAEAYROHREARPALTSRLRFPKPDGLRPIVNMDDVVGARTFRERKAEELTSRYA 660
DB 601 LSAEAYROHREARPALTSRLRFPKPDGLRPIVNMDDVVGARTFRERKAEELTSRYA 660
QY 661 LBSVLYVERARRRGLIGASVLSJDDIHRAMRTFVLRADPPPELYFYKVDYTGAYDI 720
DB 661 LBSVLYVERARRRGLIGASVLSJDDIHRAMRTFVLRADPPPELYFYKVDYTGAYDI 720
QY 721 POURLTEVIAISIKPONTYCVRRYAVVOKAAGHVAKAFKSHVSTLTDOPYMRQVAVL 780
DB 721 POURLTEVIAISIKPONTYCVRRYAVVOKAAGHVAKAFKSHVSTLTDOPYMRQVAVL 780
QY 781 QETSPLRDVAVIIOSSSLNEASSGLFDVFLREMGCHAVIRKGSYVOCGIGISTLSTL 840
DB 781 QETSPLRDVAVIIOSSSLNEASSGLFDVFLREMGCHAVIRKGSYVOCGIGISTLSTL 840
QY 841 LGSICVGDWENKLFAGIRBDGLLRVVDPLVTPHLTAKTFLRLVAVGVEYGVAVL 900
DB 841 LGSICVGDWENKLFAGIRBDGLLRVVDPLVTPHLTAKTFLRLVAVGVEYGVAVL 900
QY 901 RKTIVNFPVEDALGTAFAVQMPAHGLFPWCGILLDTRILEVQSDVSARSISIRASYTF 960
DB 901 RKTIVNFPVEDALGTAFAVQMPAHGLFPWCGILLDTRILEVQSDVSARSISIRASYTF 960
QY 961 NRGFKAGRRNRRLFGVLRKCHSLPLDQVNSLQTVCTNIYKILLQAYRFAVCVLP 1020
DB 961 NRGFKAGRRNRRLFGVLRKCHSLPLDQVNSLQTVCTNIYKILLQAYRFAVCVLP 1020

QY 1021 FHQVWKNPTFFLRISTASLCYSILKAKNAGSLGAKGAGPLPSAVOMLCHOAFL 1080
DB 1021 FHQVWKNPTFFLRISTASLCYSILKAKNAGSLGAKGAGPLPSAVOMLCHOAFL 1080
QY 1081 KLRHRVTVPLGSLRTAQOTLSRKLPGTTLTALMAANPALPSDFKTIID 1132
DB 1081 KLRHRVTVPLGSLRTAQOTLSRKLPGTTLTALMAANPALPSDFKTIID 1132

RESULT 22
US-10-325-810-2
Sequence 2, Application US/10325810
Publication No. US20030204069A1
GENERAL INFORMATION:
APPLICANT: Czech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-Oct-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Aussenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-325-810-2

Query Match 99.8%; Score 5952; DB 14; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPBARCRAVRSLSHRYEVLPLATFVRRLGQGMRLVORGDPAFRALVAQCLVCPW 60
DB 1 MPBARCRAVRSLSHRYEVLPLATFVRRLGQGMRLVORGDPAFRALVAQCLVCPW 60

QY 61 DARPPPAABSFQVSCLELVARVQLRCEGAKNVLAFGFALLDGAAGPPEAFTTSVR 120
DB 61 DARPPPAABSFQVSCLELVARVQLRCEGAKNVLAFGFALLDGAAGPPEAFTTSVR 120

QY 121 SYLPNTVTDALRSGAMGILLRRVGDVLYHLARCALFVLVAPSCAYVCGPPLYQIGA 180
DB 121 SYLPNTVTDALRSGAMGILLRRVGDVLYHLARCALFVLVAPSCAYVCGPPLYQIGA 180

QY 181 ATQARPPPHASGRRRLGGERAMNHSVREAGVPLGPAAGARRGGSASRSLLPKRPRR 240
DB 181 ATQARPPPHASGRRRLGGERAMNHSVREAGVPLGPAAGARRGGSASRSLLPKRPRR 240

QY 241 GAAPBERPRTVQGSMAHPRTRGSDRGFCVVSAPARAEATSTLEGALSTRHSHPSVG 300
DB 241 GAAPBERPRTVQGSMAHPRTRGSDRGFCVVSAPARAEATSTLEGALSTRHSHPSVG 300

QY 301 ROHHAGPSTSRPPRWDTPCPVVAETKHPFLYSSGDKEQLRPSLLSLRPSLTGARL 360
DB 301 ROHHAGPSTSRPPRWDTPCPVVAETKHPFLYSSGDKEQLRPSLLSLRPSLTGARL 360

QY 361 VETIFLGSRRPMMGTPRRRLPRLPQRYWQMRPLFLELLGNHAOCPPYVLLKTHCPRAAVT 420
DB 361 VETIFLGSRRPMMGTPRRRLPRLPQRYWQMRPLFLELLGNHAOCPPYVLLKTHCPRAAVT 420

QY 421 PAAGVAREKPGQSVAAPEEDTDPRRLVQLRQHSFPQVYGFARACLRRLVPPGLWGS 480
DB 421 PAAGVAREKPGQSVAAPEEDTDPRRLVQLRQHSFPQVYGFARACLRRLVPPGLWGS 480

QY 481 RNHERFLLNTKFTSLGKHALSLQELTWKMSVDCAMLRSPGVCVPAEHRRLREI 540
DB 481 RNHERFLLNTKFTSLGKHALSLQELTWKMSVDCAMLRSPGVCVPAEHRRLREI 540

QY 541 LAKFLHMLSVYVVELLRSFFVYETTTQKNLFFYRPSVSKOSIGIRHLKRVQRE 600
DB 541 LAKFLHMLSVYVVELLRSFFVYETTTQKNLFFYRPSVSKOSIGIRHLKRVQRE 600

QY 601 LSEAEVROHREARPALITSRLRFIPKPDGLRPIVMMDYVVGARTPREKREARLTSRYKA 660
DB 601 LSEAEVROHREARPALITSRLRFIPKPDGLRPIVMMDYVVGARTPREKREARLTSRYKA 660

QY 661 LRSVLYNERARRPGLIGASVGLDIDIRAMRTFVRYAODPPPELYVYKVDYGAFTI 720
DB 661 LRSVLYNERARRPGLIGASVGLDIDIRAMRTFVRYAODPPPELYVYKVDYGAFTI 720

QY 721 PODRLLEVIASTIKPONTYCVARVAVOQAAHGHYRKAFKSHVSTLTLDQPMRQFVAHL 780
DB 721 PODRLLEVIASTIKPONTYCVARVAVOQAAHGHYRKAFKSHVSTLTLDQPMRQFVAHL 780

QY 781 QETSPLRDAVITBOSSSLNEASSGLFDVFLRPMCHAVIRKSKSVYQCGIPQGSILSTL 840
DB 781 QETSPLRDAVITBOSSSLNEASSGLFDVFLRPMCHAVIRKSKSVYQCGIPQGSILSTL 840

QY 841 LSLCYGDMENKLFAGIRRDGLLRLVDPFLVTPHLTAKTFLTLVARGVEYCVNLT 900
DB 841 LSLCYGDMENKLFAGIRRDGLLRLVDPFLVTPHLTAKTFLTLVARGVEYCVNLT 900

QY 901 RKTVVNFVEEDALGGTAFCVQPAHGLFPWCGLLDTRTLEVOSSYVARSITSASTF 960
DB 901 RKTVVNFVEEDALGGTAFCVQPAHGLFPWCGLLDTRTLEVOSSYVARSITSASTF 960

QY 961 NRGFKAGRMRRKLFGLVKCHSLFLDLQVNSLQTCVNICNIXIILLQAYRHAQVLDLP 1020
DB 961 NRGFKAGRMRRKLFGLVKCHSLFLDLQVNSLQTCVNICNIXIILLQAYRHAQVLDLP 1020

RESULT 23
US-10-388-578-2
Sequence 2, Application US/10388578
Publication No. US20030224411A1
GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Stanton, Lawrence
APPLICANT: Ralph, Brandeberger
APPLICANT: Joseph, Gold D.
APPLICANT: John, Irving
APPLICANT: Mandalam, Ramkumar
APPLICANT: Mok, Michael
APPLICANT: Shelton, Dawne
TITLE OF INVENTION: Genes that are Up- or Down-Regulated During Differentiation of Human Embryonic Stem Cells
FILE REFERENCE: 135/001
CURRENT APPLICATION NUMBER: US/10/388,578
CURRENT FILING DATE: 2003-03-13
NUMBER OF SEQ ID NOS: 139
SOFTWARE: Custom
SEQ ID NO 2
LENGTH: 1132
TYPE: PRT
ORGANISM: Homo sapiens
US-10-388-578-2

Query Match 99.8%; Score 5952; DB 14; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPBARCRAVRSLSHRYEVLPLATFVRRLGQGMRLVORGDPAFRALVAQCLVCPW 60
DB 1 MPBARCRAVRSLSHRYEVLPLATFVRRLGQGMRLVORGDPAFRALVAQCLVCPW 60

QY 61 DARPPPAABSFQVSCLELVARVQLRCEGAKNVLAFGFALLDGAAGPPEAFTTSVR 120
DB 61 DARPPPAABSFQVSCLELVARVQLRCEGAKNVLAFGFALLDGAAGPPEAFTTSVR 120

QY 121 SYLPNTVTDALRSGAMGILLRRVGDVLYHLARCALFVLVAPSCAYVCGPPLYQIGA 180
DB 121 SYLPNTVTDALRSGAMGILLRRVGDVLYHLARCALFVLVAPSCAYVCGPPLYQIGA 180

QY 181 ATQARPPPHASGRRRLGGERAMNHSVREAGVPLGPAAGARRGGSASRSLLPKRPRR 240
DB 181 ATQARPPPHASGRRRLGGERAMNHSVREAGVPLGPAAGARRGGSASRSLLPKRPRR 240

QY 241 GAAPBERPRTVQGSMAHPRTRGSDRGFCVVSAPARAEATSTLEGALSTRHSHPSVG 300
DB 241 GAAPBERPRTVQGSMAHPRTRGSDRGFCVVSAPARAEATSTLEGALSTRHSHPSVG 300

QY 301 ROHHAGPSTSRPPRWDTPCPVVAETKHPFLYSSGDKEQLRPSLLSLRPSLTGARL 360
DB 301 ROHHAGPSTSRPPRWDTPCPVVAETKHPFLYSSGDKEQLRPSLLSLRPSLTGARL 360

QY 361 VETIFLGSRRPMMGTPRRRLPRLPQRYWQMRPLFLELLGNHAOCPPYVLLKTHCPRAAVT 420
DB 361 VETIFLGSRRPMMGTPRRRLPRLPQRYWQMRPLFLELLGNHAOCPPYVLLKTHCPRAAVT 420

QY 421 PAAGVAREKPGQSVAAPEEDTDPRRLVQLRQHSFPQVYGFARACLRRLVPPGLWGS 480
DB 421 PAAGVAREKPGQSVAAPEEDTDPRRLVQLRQHSFPQVYGFARACLRRLVPPGLWGS 480

QY 481 RHNRERFLRNTKFKISLGGKNAKLSLOELTWKMSVRDCAMLRSPGVGCVPAEHRRLREI 540
 Db 481 RHNRERFLRNTKFKISLGGKNAKLSLOELTWKMSVRDCAMLRSPGVGCVPAEHRRLREI 540
 QY 541 LAKFLHMLMSYVVELLSRFYVETTFQKNRLEFFYPSPWSKLSQISGIRQHLKRVQJRE 600
 Db 541 LAKFLHMLMSYVVELLSRFYVETTFQKNRLEFFYPSPWSKLSQISGIRQHLKRVQJRE 600
 QY 601 LSEAEVRQHRERARPPGLLTSRLRFIPKPDGLRPIVMMQVVGARTFRREKRAEELTSVKA 660
 Db 601 LSEAEVRQHRERARPPGLLTSRLRFIPKPDGLRPIVMMQVVGARTFRREKRAEELTSVKA 660
 QY 661 LFSVLNTERARPPGLLTSRLRFIPKPDGLRPIVMMQVVGARTFRREKRAEELTSVKA 720
 Db 661 LFSVLNTERARPPGLLTSRLRFIPKPDGLRPIVMMQVVGARTFRREKRAEELTSVKA 720
 QY 721 PODRLTEVIASITIKPQNTYCVRYAVVOXAAHGHVRAKFKSHVSTLTDLPYMRQFVAHL 780
 Db 721 PODRLTEVIASITIKPQNTYCVRYAVVOXAAHGHVRAKFKSHVSTLTDLPYMRQFVAHL 780
 QY 781 QETSPLRDVAVIEQSSSLNEASGSLFDVFLRPMCHAVRIRGKSYVQCGIPQGSILSTL 840
 Db 781 QETSPLRDVAVIEQSSSLNEASGSLFDVFLRPMCHAVRIRGKSYVQCGIPQGSILSTL 840
 QY 841 LCSLCYGDMEKTKFAGIRRDGILLRLVDDFLVTPHILTHAKTFLRLTVRGVPEYGCYNL 900
 Db 841 LCSLCYGDMEKTKFAGIRRDGILLRLVDDFLVTPHILTHAKTFLRLTVRGVPEYGCYNL 900
 QY 901 RKTIVNPFVEDEALGTAFAVQMPAHGLFPWCGLLDRTLEVOSSDYARSIRASYTF 960
 Db 901 RKTIVNPFVEDEALGTAFAVQMPAHGLFPWCGLLDRTLEVOSSDYARSIRASYTF 960
 QY 961 NRGFKAQNNMRKLFGLVRLKCHSLFLDLQVNSIQTYCTNIYKILLQAVRFHACVQLP 1020
 Db 961 NRGFKAQNNMRKLFGLVRLKCHSLFLDLQVNSIQTYCTNIYKILLQAVRFHACVQLP 1020
 QY 1021 FHQGVWKNPTFFFLVISPSTASLCSILKAKNAGMSLGAAGAPLPSEAVQMLCHQAFIL 1080
 Db 1021 FHQGVWKNPTFFFLVISPSTASLCSILKAKNAGMSLGAAGAPLPSEAVQMLCHQAFIL 1080
 QY 1081 KTRHRVTVVPLIGSLRTAQTLRSKLPGTTLTALERANPALPSDFKITLD 1132
 Db 1081 KTRHRVTVVPLIGSLRTAQTLRSKLPGTTLTALERANPALPSDFKITLD 1132

RESULT 24
 US-10-602-441-2
 ; Sequence 2, Application US/10602441
 ; Publication No. US20040106128A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Geron Corporation
 ; APPLICANT: Majumdar, Anish Sen
 ; APPLICANT: Ferber, Iris
 ; APPLICANT: Frolkis, Maria
 ; APPLICANT: Wang, Zhuo
 ; TITLE OF INVENTION: Cancer Vaccines Containing Xenogeneic Epitopes of Telomerase Reve
 ; FILE REFERENCE: 086/002
 ; CURRENT APPLICATION NUMBER: US/10/602,441
 ; PRIOR FILING DATE: 2003-06-24
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 1132
 ; TYPE: PRN
 ; ORGANISM: Homo sapiens
 US-10-602-441-2
 Query Match 99.8%; Score 5952; DB 16; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;

Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MPRAPRCRAVRSLASHYREVPLATFVRRLGPOGMRLVORDDPAAPFALVQCIVCVPM 60
 Db 1 MPRAPRCRAVRSLASHYREVPLATFVRRLGPOGMRLVORDDPAAPFALVQCIVCVPM 60
 QY 61 DARPPPAASFRQVSLKELVARVQLRCEBGAKNVLAFGALLDGAAGGPEAFTTSVR 120
 Db 61 DARPPPAASFRQVSLKELVARVQLRCEBGAKNVLAFGALLDGAAGGPEAFTTSVR 120
 QY 121 SYLPMNTVDALRGSGAMGILLRVEDDVLVHLAALFVLVAPSCAYOVGPRYQJGA 180
 Db 121 SYLPMNTVDALRGSGAMGILLRVEDDVLVHLAALFVLVAPSCAYOVGPRYQJGA 180
 QY 181 ATQARPPPHASGPRRLGGERAMNHSVREAGVPLGLPAPGARRRSGSASRLPLPKPRR 240
 Db 181 ATQARPPPHASGPRRLGGERAMNHSVREAGVPLGLPAPGARRRSGSASRLPLPKPRR 240
 QY 241 GAAPPEERTPVQCGSWAPRGTRGSDRGFCVSPAPRAEATSLFGLSGTRHSHSVG 300
 Db 241 GAAPPEERTPVQCGSWAPRGTRGSDRGFCVSPAPRAEATSLFGLSGTRHSHSVG 300
 QY 301 RQHHAGPSTSRPPRMDTPCPVYAEKHFLLYSAGDEKQRLPSFLSLSPSLGARRL 360
 Db 301 RQHHAGPSTSRPPRMDTPCPVYAEKHFLLYSAGDEKQRLPSFLSLSPSLGARRL 360
 QY 361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFELIGNHAQCPYGVLLKTHCPRLAAVT 420
 Db 361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFELIGNHAQCPYGVLLKTHCPRLAAVT 420
 QY 421 PAAGVCAERKPOGSAAPBEEDTPRRLVOLLROHSSWQYGFACRLRLVPPGLMS 480
 Db 421 PAAGVCAERKPOGSAAPBEEDTPRRLVOLLROHSSWQYGFACRLRLVPPGLMS 480
 QY 481 RHNRERFLRNTKFKISLGGKNAKLSLOELTWKMSVRDCAMLRSPGVGCVPAEHRRLREI 540
 Db 481 RHNRERFLRNTKFKISLGGKNAKLSLOELTWKMSVRDCAMLRSPGVGCVPAEHRRLREI 540
 QY 541 LAKFLHMLMSYVVELLSRFYVETTFQKNRLEFFYPSPWSKLSQISGIRQHLKRVQJRE 600
 Db 541 LAKFLHMLMSYVVELLSRFYVETTFQKNRLEFFYPSPWSKLSQISGIRQHLKRVQJRE 600
 QY 601 LSEAEVRQHRERARPPGLLTSRLRFIPKPDGLRPIVMMQVVGARTFRREKRAEELTSVKA 660
 Db 601 LSEAEVRQHRERARPPGLLTSRLRFIPKPDGLRPIVMMQVVGARTFRREKRAEELTSVKA 660
 QY 661 LFSVLNTERARPPGLLTSRLRFIPKPDGLRPIVMMQVVGARTFRREKRAEELTSVKA 720
 Db 661 LFSVLNTERARPPGLLTSRLRFIPKPDGLRPIVMMQVVGARTFRREKRAEELTSVKA 720
 QY 721 PODRLTEVIASITIKPQNTYCVRYAVVOXAAHGHVRAKFKSHVSTLTDLPYMRQFVAHL 780
 Db 721 PODRLTEVIASITIKPQNTYCVRYAVVOXAAHGHVRAKFKSHVSTLTDLPYMRQFVAHL 780
 QY 781 QETSPLRDVAVIEQSSSLNEASGSLFDVFLRPMCHAVRIRGKSYVQCGIPQGSILSTL 840
 Db 781 QETSPLRDVAVIEQSSSLNEASGSLFDVFLRPMCHAVRIRGKSYVQCGIPQGSILSTL 840
 QY 841 LCSLCYGDMEKTKFAGIRRDGILLRLVDDFLVTPHILTHAKTFLRLTVRGVPEYGCYNL 900
 Db 841 LCSLCYGDMEKTKFAGIRRDGILLRLVDDFLVTPHILTHAKTFLRLTVRGVPEYGCYNL 900
 QY 901 RKTIVNPFVEDEALGTAFAVQMPAHGLFPWCGLLDRTLEVOSSDYARSIRASYTF 960
 Db 901 RKTIVNPFVEDEALGTAFAVQMPAHGLFPWCGLLDRTLEVOSSDYARSIRASYTF 960
 QY 961 NRGFKAQNNMRKLFGLVRLKCHSLFLDLQVNSIQTYCTNIYKILLQAVRFHACVQLP 1020
 Db 961 NRGFKAQNNMRKLFGLVRLKCHSLFLDLQVNSIQTYCTNIYKILLQAVRFHACVQLP 1020
 QY 1021 FHQGVWKNPTFFFLVISPSTASLCSILKAKNAGMSLGAAGAPLPSEAVQMLCHQAFIL 1080
 Db 1021 FHQGVWKNPTFFFLVISPSTASLCSILKAKNAGMSLGAAGAPLPSEAVQMLCHQAFIL 1080

```

QY      1081 KLTRHRVTYVPLGSLRTAQTOLSRKLPQTTLTALAAANPALPSDFKTIID 1132
DB      1081 KLTRHRVTYVPLGSLRTAQTOLSRKLPQTTLTALAAANPALPSDFKTIID 1132

RESULT 25
US-10-389-431-2
; Sequence 2, Application US/10389431
; Publication No. US20040180347A1
GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Stanton, Lawrence
; APPLICANT: Ralph, Brandenberger
; APPLICANT: Joseph, Gold D.
; APPLICANT: John, Irving
; APPLICANT: Mandalam, Ramkumar
; APPLICANT: Mok, Michael
; TITLE OF INVENTION: A Marker System for Preparing and Characterizing High-Quality Hum
; FILE REFERENCE: 135/002
; CURRENT APPLICATION NUMBER: US/10/389,431
; CURRENT FILING DATE: 2003-03-13
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-389-431-2

Query Match      99.8%; Score 5952; DB 16; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1      1 MRRAPRCRAVRSILRSYREVLPLATFVRRLGPGMRVLQVRGDPAPAFALVAQCIVCPM 60
DB      1      1 MRRAPRCRAVRSILRSYREVLPLATFVRRLGPGMRVLQVRGDPAPAFALVAQCIVCPM 60

QY      61      DARRPPAAASFQVSTLKEIVARVLOLCEGAKVLAFFGLDGAAGPREAFTTVR 120
DB      61      DARRPPAAASFQVSTLKEIVARVLOLCEGAKVLAFFGLDGAAGPREAFTTVR 120

QY      121     SYLNTVTALRGSGAGMLLRRVGDVVLHLLARCAFLVLAAPSACAYQVCGPPLYLQGA 180
DB      121     SYLNTVTALRGSGAGMLLRRVGDVVLHLLARCAFLVLAAPSACAYQVCGPPLYLQGA 180

QY      181     ATGARPPEPHASGRRRLGGERAMNHSVREAGVPLGIPAGARRRGSASRSLLPKRRR 240
DB      181     ATGARPPEPHASGRRRLGGERAMNHSVREAGVPLGIPAGARRRGSASRSLLPKRRR 240

QY      241     GAAPPEERTPVGGGSAHAGRTGSPDRGFCVSPARPAEATSLGALSGTRHSHPSVG 300
DB      241     GAAPPEERTPVGGGSAHAGRTGSPDRGFCVSPARPAEATSLGALSGTRHSHPSVG 300

QY      301     RQHHAAPSGTSRRPMDTPCPVVAETKHFLLYSSGDKQLRPSFLLSLRPSLTGAARL 360
DB      301     RQHHAAPSGTSRRPMDTPCPVVAETKHFLLYSSGDKQLRPSFLLSLRPSLTGAARL 360

QY      361     VETIFIGSRPWWGTGRRRLPLPORYWQWRPLFLELGNHACPPGVLLKTCPLRAAVT 420
DB      361     VETIFIGSRPWWGTGRRRLPLPORYWQWRPLFLELGNHACPPGVLLKTCPLRAAVT 420

QY      421     PAAGVCAAREKPOGSAVAPEEDTDPRLVOLLROHSSPWQVGYFVACLRRLVPPGLMGS 480
DB      421     PAAGVCAAREKPOGSAVAPEEDTDPRLVOLLROHSSPWQVGYFVACLRRLVPPGLMGS 480

QY      481     RHHERFPLNTKFKFISLGHAKLSLOELTWKSVYDCAWLRRSPGVGCVPAHEHLEIREI 540
DB      481     RHHERFPLNTKFKFISLGHAKLSLOELTWKSVYDCAWLRRSPGVGCVPAHEHLEIREI 540

QY      541     LAKFLHMLSVYVVELLSFFVYTTTFQKRLFFYRPSVMSKIOSIGIRQLKXVQURE 600
DB      541     LAKFLHMLSVYVVELLSFFVYTTTFQKRLFFYRPSVMSKIOSIGIRQLKXVQURE 600

```

```

DB      541     LAKFLHMLSVYVVELLSFFVYTTTFQKRLFFYRPSVMSKIOSIGIRQLKXVQURE 600
QY      601     LSEAEVROHREAPALLTSRLREIPEKPDGLRPIVMNDVYVAGATRRERKARLTSRYKA 660
DB      601     LSEAEVROHREAPALLTSRLREIPEKPDGLRPIVMNDVYVAGATRRERKARLTSRYKA 660

QY      661     LFSVLYNEPARRRPGILGASVLAGUDITHRAMRTFVLRVRAQDPPPELYFKVQVTVGYDTI 720
DB      661     LFSVLYNEPARRRPGILGASVLAGUDITHRAMRTFVLRVRAQDPPPELYFKVQVTVGYDTI 720

QY      721     PQDLTEVIASIKPONTYCVRRYAVVQKAAHGVKAFKSHVSTLTDLOPYMRQFVAHL 780
DB      721     PQDLTEVIASIKPONTYCVRRYAVVQKAAHGVKAFKSHVSTLTDLOPYMRQFVAHL 780

QY      781     QETSPLRDAAVITQSSSLNPAASGLPDVLRPMCHAAVLRKKSYYQCCGIGQSTLSLT 840
DB      781     QETSPLRDAAVITQSSSLNPAASGLPDVLRPMCHAAVLRKKSYYQCCGIGQSTLSLT 840

QY      841     LGSICGDMENKLPAGIRRDGLLRVDPFLVTPHLTAKTFLTLVNGVEBEGCVNL 900
DB      841     LGSICGDMENKLPAGIRRDGLLRVDPFLVTPHLTAKTFLTLVNGVEBEGCVNL 900

QY      901     RKTIVNFPVEDEALGTAFAVQMPAHGLPWCGLLDTRTLBYQSDYSYARTSIRASTVF 960
DB      901     RKTIVNFPVEDEALGTAFAVQMPAHGLPWCGLLDTRTLBYQSDYSYARTSIRASTVF 960

QY      961     NRGFKAGNRMRKLPGLRLKCHSLPLDLOVNSLQTCVNTIKILLQAYRFAVCYLQHP 1020
DB      961     NRGFKAGNRMRKLPGLRLKCHSLPLDLOVNSLQTCVNTIKILLQAYRFAVCYLQHP 1020

QY      1021     FHQWKNPPTFLRVISDTASLCYSILKAKNAGMSIGAGAAAPLSEAVQWLCHQAPIL 1080
DB      1021     FHQWKNPPTFLRVISDTASLCYSILKAKNAGMSIGAGAAAPLSEAVQWLCHQAPIL 1080

QY      1081     KLTRHRVTYVPLGSLRTAQTOLSRKLPQTTLTALAAANPALPSDFKTIID 1132
DB      1081     KLTRHRVTYVPLGSLRTAQTOLSRKLPQTTLTALAAANPALPSDFKTIID 1132

RESULT 26
US-10-877-124-2
; Sequence 2, Application US/10877124
; Publication No. US20040242529A1
GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Hartley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,124
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549

```

FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: WO PCT/US97/17618
 FILING DATE: 01-OCT-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002610US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1132 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-877-124-2

Query Match 99.8%; Score 5952; DB 17; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAAPCAVSLRSYREVLPLATFVRRLGPGQMWLVORGPAPAFALVAQVLCVPM 60
 DB 1 MPRAAPCAVSLRSYREVLPLATFVRRLGPGQMWLVORGPAPAFALVAQVLCVPM 60

QY 61 DAPPPAPSPFQVSCLEKELVAVYLQRCERGANVIAFGFALIDGARGGPEAFTTSVR 120
 DB 61 DAPPPAPSPFQVSCLEKELVAVYLQRCERGANVIAFGFALIDGARGGPEAFTTSVR 120

QY 121 SYLNTVTDALRGSGAGMLLRVGGDVLVHLARCALFVLVAPSCAYQVCGPPLVQLGA 180
 DB 121 SYLNTVTDALRGSGAGMLLRVGGDVLVHLARCALFVLVAPSCAYQVCGPPLVQLGA 180

QY 181 ATOARPPPHAGSPRRRLGCEPAMNHSYREAGVPLGLPAPGARRRGSSASLPLPKPRR 240
 DB 181 ATOARPPPHAGSPRRRLGCEPAMNHSYREAGVPLGLPAPGARRRGSSASLPLPKPRR 240

QY 241 GAAPERTPTVQGSMAHPGTRGSPDRGFCVSPAPPAEATSLSEALSGTRSHSVG 300
 DB 241 GAAPERTPTVQGSMAHPGTRGSPDRGFCVSPAPPAEATSLSEALSGTRSHSVG 300

QY 301 ROHAGPSTSRPRPMDTCCPPYVATKHFLLVSSGDKQLRPSFLLSLRPSLTGARRL 360
 DB 301 ROHAGPSTSRPRPMDTCCPPYVATKHFLLVSSGDKQLRPSFLLSLRPSLTGARRL 360

QY 361 VETIFLGRPMWPGTPRLPRLPQRYWQMRPLFELLGNHAQCYGYLTKHCHPLRAAVT 420
 DB 361 VETIFLGRPMWPGTPRLPRLPQRYWQMRPLFELLGNHAQCYGYLTKHCHPLRAAVT 420

QY 421 PAAGCAEKQGSVAAPSEEDTPRRLVOLLROHSSPMQYGFVRACTRLVPPGWMG 480
 DB 421 PAAGCAEKQGSVAAPSEEDTPRRLVOLLROHSSPMQYGFVRACTRLVPPGWMG 480

QY 481 RHNERFLNRTKFTSLGKHAKLSTQELTWKSVYDCAMLRSPGVGCVPAEHRLEETI 540
 DB 481 RHNERFLNRTKFTSLGKHAKLSTQELTWKSVYDCAMLRSPGVGCVPAEHRLEETI 540

QY 481 RHNERFLNRTKFTSLGKHAKLSTQELTWKSVYDCAMLRSPGVGCVPAEHRLEETI 540
 DB 481 RHNERFLNRTKFTSLGKHAKLSTQELTWKSVYDCAMLRSPGVGCVPAEHRLEETI 540

QY 541 LAKFHTMMSYVVVLLSFFVYETTTQKRLFFRYRSVWSKOSTIRQHLKRVQURE 600
 DB 541 LAKFHTMMSYVVVLLSFFVYETTTQKRLFFRYRSVWSKOSTIRQHLKRVQURE 600

QY 601 LSEAEVQHREARPPALITSRLRFIPKPDGLRPIVMQDVYVAGARTREKAERLTSRYKA 660
 DB 601 LSEAEVQHREARPPALITSRLRFIPKPDGLRPIVMQDVYVAGARTREKAERLTSRYKA 660

QY 661 LFSVINYERARPPGLGASVGLDDIHPAMTFVLVFAADPPPELVYKVDVTCAYDTI 720
 DB 661 LFSVINYERARPPGLGASVGLDDIHPAMTFVLVFAADPPPELVYKVDVTCAYDTI 720

QY 721 PODRLTEVIASTIKRQNTYCVRYAVVOKAAGHVRKAFKSHVSTLTLOPYMROFVAHL 780
 DB 721 PODRLTEVIASTIKRQNTYCVRYAVVOKAAGHVRKAFKSHVSTLTLOPYMROFVAHL 780

QY 781 OETSPURDAVVIQSSSUNBASGLFDVFLRPMCHAVRIRGKSYVQCGIIPQGSISTL 840
 DB 781 OETSPURDAVVIQSSSUNBASGLFDVFLRPMCHAVRIRGKSYVQCGIIPQGSISTL 840

QY 841 LLSLCYGMENKLFAGIRRDGILLRLVDDPLVPLTHAKTEFLTLVAGVBEYGVVNL 900
 DB 841 LLSLCYGMENKLFAGIRRDGILLRLVDDPLVPLTHAKTEFLTLVAGVBEYGVVNL 900

QY 901 RKTIVNFPVEDALGTAFCVQMPAHGLFPWCGILDTRELEVQSDYSSYARTISASVTF 960
 DB 901 RKTIVNFPVEDALGTAFCVQMPAHGLFPWCGILDTRELEVQSDYSSYARTISASVTF 960

QY 961 NRGFTAGNRMRKLFQVRLKCHSLFDLQVNSLOTVCNTIYKILLQAFRFAVQLP 1020
 DB 961 NRGFTAGNRMRKLFQVRLKCHSLFDLQVNSLOTVCNTIYKILLQAFRFAVQLP 1020

QY 1021 FHQVWKNFTFPLRISIDTASLCYSLKAKHAGSLGAKGAAPLPSAVQMLCHQATLL 1080
 DB 1021 FHQVWKNFTFPLRISIDTASLCYSLKAKHAGSLGAKGAAPLPSAVQMLCHQATLL 1080

QY 1081 KLTRRRTVPLLGSLRTAQTLRSKLPDTTLTLEAANPALPSDFXTIID 1132
 DB 1081 KLTRRRTVPLLGSLRTAQTLRSKLPDTTLTLEAANPALPSDFXTIID 1132

RESULT 27
 US-10-877-022-2
 ; Sequence 2, Application US//10877022
 ; Publication No. US20040247613A1
 GENERAL INFORMATION:
 APPLICANT: Cecch, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin B.
 Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/877,022
 FILING DATE: 24-Jun-2004
 CLASSIFICATION: <Unknown>

```

PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-Oct-1997
APPLICATION NUMBER: WO PCT/US97/17685
FILING DATE: 01-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-877-022-2

Query Match      99.8%; Score 5952; DB 17; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLSLRSHYREVLPATFVRRLGPOGRVLVQRGDPAPAFRLVAQCVCVPM 60
DB 1 MPAPRCRAVRSLSLRSHYREVLPATFVRRLGPOGRVLVQRGDPAPAFRLVAQCVCVPM 60
QY 61 DARPPAPASFRQVSCIKELVARVLQRLCERGAKNVLAFGFALLDGAAGPPEAFTTSVR 120
DB 61 DARPPAPASFRQVSCIKELVARVLQRLCERGAKNVLAFGFALLDGAAGPPEAFTTSVR 120
QY 121 STLPNTVTALRSGSGWGLLLRRVGDVTVHLLACALFVLYABSCAYQVCGPPLYQUGA 180
DB 121 STLPNTVTALRSGSGWGLLLRRVGDVTVHLLACALFVLYABSCAYQVCGPPLYQUGA 180
QY 181 ATQARPPAPASGRRRLGGERAMNHSVRAGVPLGLPAPGARRRGSGASRSLLPKRRR 240
DB 181 ATQARPPAPASGRRRLGGERAMNHSVRAGVPLGLPAPGARRRGSGASRSLLPKRRR 240
QY 241 GAAPBEERTPVQCGVAHPGRTGSDRGFCVVASPARPAEATSLGALSGTRHSHSVG 300
DB 241 GAAPBEERTPVQCGVAHPGRTGSDRGFCVVASPARPAEATSLGALSGTRHSHSVG 300
QY 301 RQHHAGPSTSPRRPMDTPCPVYAETGFLYSSGDKKOLRPSFLSLSLPSLTGARL 360
DB 301 RQHHAGPSTSPRRPMDTPCPVYAETGFLYSSGDKKOLRPSFLSLSLPSLTGARL 360
QY 361 VETIFLGSRRPMGTPRRLRLPQRYWQRPFLLELGNHACQPYVILLKTHCPRAAVT 420
DB 361 VETIFLGSRRPMGTPRRLRLPQRYWQRPFLLELGNHACQPYVILLKTHCPRAAVT 420
QY 421 PAAGVAREKPGQSVAAPEEDTDPRRLVQLLRQSSPMQVYGFRACLRLVPPGLMGS 480
DB 421 PAAGVAREKPGQSVAAPEEDTDPRRLVQLLRQSSPMQVYGFRACLRLVPPGLMGS 480

```

```

DB 421 PAAGVAREKPGQSVAAPEEDTDPRRLVQLLRQSSPMQVYGFRACLRLVPPGLMGS 480
QY 481 RHNRRLRLNTKTFISLGRKAKLSLOELTWKMSVRCCAMLRBPQVCVPAARLRREI 540
DB 481 RHNRRLRLNTKTFISLGRKAKLSLOELTWKMSVRCCAMLRBPQVCVPAARLRREI 540
QY 541 LAKELHMLSVYVELLSFFVTEFTFCQNRLEFPRSPWSKLOSIGIRHILKRYOLRE 600
DB 541 LAKELHMLSVYVELLSFFVTEFTFCQNRLEFPRSPWSKLOSIGIRHILKRYOLRE 600
QY 601 LSEAEVTOHRBARPALITSLRLPIPKPDGRPLVNMNDYVVGATTPREKRAEPLTSRVKA 660
DB 601 LSEAEVTOHRBARPALITSLRLPIPKPDGRPLVNMNDYVVGATTPREKRAEPLTSRVKA 660
QY 661 LFSVLANERARRPGLIGASVLDGDDIHRARTVLRADQPPPELYPFKVDVTGAYDTI 720
DB 661 LFSVLANERARRPGLIGASVLDGDDIHRARTVLRADQPPPELYPFKVDVTGAYDTI 720
QY 721 PODRLTEVIASIIKPOVTYCVRRYAVVQKAAGHVKAFFKSHVSTLTDQPYWRQFVAHL 780
DB 721 PODRLTEVIASIIKPOVTYCVRRYAVVQKAAGHVKAFFKSHVSTLTDQPYWRQFVAHL 780
QY 781 QETSPLBDVAVIEOSSSLNEASSGLPDVPLRFPMCHAVLRGKSVYQCGIPQGSILSTL 840
DB 781 QETSPLBDVAVIEOSSSLNEASSGLPDVPLRFPMCHAVLRGKSVYQCGIPQGSILSTL 840
QY 841 LCSLCYGDMEKMLFAGIRRDGLLRVDDPLVTPHLYAKTFLRLTVRGVEYGCVMU 900
DB 841 LCSLCYGDMEKMLFAGIRRDGLLRVDDPLVTPHLYAKTFLRLTVRGVEYGCVMU 900
QY 901 RKTVMNFPVDEALGGAFAVQPAHGLFPWCGLLDTRILEVQSDVSSAARISIRSLTF 960
DB 901 RKTVMNFPVDEALGGAFAVQPAHGLFPWCGLLDTRILEVQSDVSSAARISIRSLTF 960
QY 961 NRQFKAGRNRRKLFGLVRLKCHSLFLDLQVNSLQTVCTNINYYKILLQAYRFFACVLOLP 1020
DB 961 NRQFKAGRNRRKLFGLVRLKCHSLFLDLQVNSLQTVCTNINYYKILLQAYRFFACVLOLP 1020
QY 1021 FHOQVMKNPFFFLRVISDTRSLCYSTILKAKNAGMSIGAGAGCPLESEAVOMLCHOAFL 1080
DB 1021 FHOQVMKNPFFFLRVISDTRSLCYSTILKAKNAGMSIGAGAGCPLESEAVOMLCHOAFL 1080
QY 1081 KLTRHRATVYPLGLSRLTAQOTLSRLPGTTLTALBAANPALPSDFKTIID 1132
DB 1081 KLTRHRATVYPLGLSRLTAQOTLSRLPGTTLTALBAANPALPSDFKTIID 1132

RESULT 28
US-10-044-692-323
Sequence 323, Application US/10044692
Publication No. US2003096344A1
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
            Lingner, Joachim
            Nakamura, Toru
            Chapman, Karen B.
            Morin, Gregg B.
            Harley, Calvin
            Andrews, William H.
TITLE OF INVENTION: HUMAN TELOWERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/044,692
  FILING DATE: 11-Jan-2002
  CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/912,951
  FILING DATE: <unknown>
  APPLICATION NUMBER: US 08/854,050
  FILING DATE: 09-MAY-1997
  APPLICATION NUMBER: US 08/851,843
  FILING DATE: 06-MAY-1997
  APPLICATION NUMBER: US 08/846,017
  FILING DATE: 25-APR-1997
  APPLICATION NUMBER: US 08/844,419
  FILING DATE: 18-APR-1997
  APPLICATION NUMBER: US 08/724,643
  FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
  NAME: Apple, Randolph T.
  REGISTRATION NUMBER: 36,429
  REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 576-0200
  TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 323:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 1154 amino acids
    TYPE: amino acid
    STRANDEDNESS: <unknown>
    TOPOLOGY: linear
    MOLECULE TYPE: protein
    SEQUENCE DESCRIPTION: SEQ ID NO: 323:
US-10-044-692-323

Query Match      99.8%; Score 5952; DB 14; Length 1154;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Db 461 RHNERRFLNRTKKFISLGGAKLSIQELTWKSVYDCAWLRSPGVCPAAEHRRLREI 540
QY 541 LAKFLHMLMSYVYVLLRSFFYYTETTFQXNRLEFFRYRBSVMSKLSIGIRQHLKRVQJRE 600
Db 541 LAKFLHMLMSYVYVLLRSFFYYTETTFQXNRLEFFRYRBSVMSKLSIGIRQHLKRVQJRE 600
QY 601 LSEAVERQHRERAPALLTSRLRFIPKPDGLPIVMMDVYVAGARFRERKRELRITSRYKA 660
Db 601 LSEAVERQHRERAPALLTSRLRFIPKPDGLPIVMMDVYVAGARFRERKRELRITSRYKA 660
QY 661 LFSVLYNERARAPGLIGASVGLDIDIRAWRTFVLRYVAQDPPELYEVKVDYGAAYDTI 720
Db 661 LFSVLYNERARAPGLIGASVGLDIDIRAWRTFVLRYVAQDPPELYEVKVDYGAAYDTI 720
QY 721 PDRLTEVIASIIKQNTYCYRRAVYVOKAAHGHVRAFKSHVSTLTDLQYMKQFVAHL 780
Db 721 PDRLTEVIASIIKQNTYCYRRAVYVOKAAHGHVRAFKSHVSTLTDLQYMKQFVAHL 780
QY 781 QETSPLRDAVYIEQSSSLNEASSGLFDVFLRFMCHHAVIRIGKSYVCCQGIPOGSIISTL 840
Db 781 QETSPLRDAVYIEQSSSLNEASSGLFDVFLRFMCHHAVIRIGKSYVCCQGIPOGSIISTL 840
QY 841 LCSLCYGMENKLPAGIRRDGILLRLVDFLLVTPHLLTHAKTFLTLVRYGVPEYCVVNL 900
Db 841 LCSLCYGMENKLPAGIRRDGILLRLVDFLLVTPHLLTHAKTFLTLVRYGVPEYCVVNL 900
QY 901 RKTIVNPFVEDBALGGTAFVQWPAHGLFPMCGILLDRTLEVSQSSYATRSIVASTVF 960
Db 901 RKTIVNPFVEDBALGGTAFVQWPAHGLFPMCGILLDRTLEVSQSSYATRSIVASTVF 960
QY 961 NRGFVAGNNMRKLPGLVRLXCHSLFLDLOVNSIQTVCTNIYKILLGAYFHAACVQLP 1020
Db 961 NRGFVAGNNMRKLPGLVRLXCHSLFLDLOVNSIQTVCTNIYKILLGAYFHAACVQLP 1020
QY 1021 FHOQVWKQPTFFLRVISTASICYSILKAKNAGMSLGAKGAAGPSPSAVQMLCHQAFLL 1080
Db 1021 FHOQVWKQPTFFLRVISTASICYSILKAKNAGMSLGAKGAAGPSPSAVQMLCHQAFLL 1080
QY 1081 KLTRRRTVYVPLGSLRTAQOTLSRKLPGTTLTALAANPALPSDFETIILD 1132
Db 1081 KLTRRRTVYVPLGSLRTAQOTLSRKLPGTTLTALAANPALPSDFETIILD 1132

RESULT 29
US-10-044-539-323
; Sequence 323, Application US/10044539
; Publication No. US20030100093A1
GENERAL INFORMATION:
  APPLICANT: Cecch, Thomas R.
              Lingner, Joachim
              Nakamura, Toru
              Chapman, Karen B.
              Morin, Gregg B.
              Hatley, Calvin
              Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Townsend and Townsend and Crew LLP
  STREET: Two Embarcadero Center, 8th floor
  CITY: San Francisco
  STATE: California
  COUNTRY: United States of America
  ZIP: 94111
COMPUTER READABLE FORM:
  MEDIUM TYPE: floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/044,539
  FILING DATE: 11-Jan-2002

```



```

? FILING DATE: 01-OCT-1996
? APPLICATION NUMBER: US 08/844,419
? FILING DATE: 18-APR-1997
? APPLICATION NUMBER: US 08/846,017
? FILING DATE: 25-APR-1997
? APPLICATION NUMBER: US 08/851,843
? FILING DATE: 06-MAY-1997
? APPLICATION NUMBER: US 08/854,050
? FILING DATE: 09-MAY-1997
? APPLICATION NUMBER: US 08/911,312
? FILING DATE: 14-AUG-1997
? APPLICATION NUMBER: US 08/912,951
? FILING DATE: 14-AUG-1997
? APPLICATION NUMBER: US 08/915,503
? FILING DATE: 14-AUG-1997
? APPLICATION NUMBER: WO PCT/US97/17885
? FILING DATE: 01-OCT-1997
? ATTORNEY/AGENT INFORMATION:
? NAME: Ausenhus, Scott L.
? REGISTRATION NUMBER: 42,271
? REFERENCE/DOCKET NUMBER: 015389-002620US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 576-0200
? TELEFAX: (415) 576-0300
? INFORMATION FOR SEQ ID NO: 611:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1154 amino acids
? TYPE: amino acid
? STRANDEDNESS: <Unknown>
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? FEATURE:
? NAME/KEY: Protein
? LOCATION: 1..1154
? OTHER INFORMATION: /note= "fusion protein composed of hTfT
? Myc epitope and His6 tag"
? SEQUENCE DESCRIPTION: SEQ ID NO: 611:
US-10-325-810-611

Query Match 99.8%; Score 5952; DB 14; Length 1154;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

? DB 421 PAAGVCAAEKQGSVAAPBEEDTDPRRLVQLLRHSSWQYGVFRAQLRLVPGJLMS 480
? DB 481 RHNERFLRNTKKFSLGKHAKLSTOELTWMSVRDCAMLRSPGVGCVPAAEHRLREI 540
? DB 481 RHNERFLRNTKKFSLGKHAKLSTOELTWMSVRDCAMLRSPGVGCVPAAEHRLREI 540
? DB 541 LAKFLHMLMSYVVELLRSPFYVETTFQXNRLEFPYRPSVMSKLQSIGIRQLKRVQJRE 600
? DB 541 LAKFLHMLMSYVVELLRSPFYVETTFQXNRLEFPYRPSVMSKLQSIGIRQLKRVQJRE 600
? DB 601 LSEAVRQHRERAPRLTLRSRFTPKPGCLRPITNMDVVGAAEFREKRERLTSRKA 660
? DB 601 LSEAVRQHRERAPRLTLRSRFTPKPGCLRPITNMDVVGAAEFREKRERLTSRKA 660
? DB 661 LFSVLYNERARPPGLGASVLGLDDIRHAWRTFYLRYAADPPPELYFVKVDVTGAYDTI 720
? DB 661 LFSVLYNERARPPGLGASVLGLDDIRHAWRTFYLRYAADPPPELYFVKVDVTGAYDTI 720
? DB 721 PDDLTLVIASTIKRQNTYCYRRAVAVVOKAAHGVKAFKSHVSTLTLDLQPYMQFVAHL 780
? DB 721 PDDLTLVIASTIKRQNTYCYRRAVAVVOKAAHGVKAFKSHVSTLTLDLQPYMQFVAHL 780
? DB 781 QETSLPDAVYIEQSSSINEASSGLFDVFLRFMCCHAVRIRGKASYOCQGIPOGSIISLTL 840
? DB 781 QETSLPDAVYIEQSSSINEASSGLFDVFLRFMCCHAVRIRGKASYOCQGIPOGSIISLTL 840
? DB 841 LCSLCYGMENKLPAGIRRDGLRLVDDFLVPLTHAKTFLRLTVRGVPEYGCYNL 900
? DB 841 LCSLCYGMENKLPAGIRRDGLRLVDDFLVPLTHAKTFLRLTVRGVPEYGCYNL 900
? DB 901 RKTIVNFEVDEALGGTAFVQMPAHGLFPWCGILLDPRTLEVOSSYASTSRASVTF 960
? DB 901 RKTIVNFEVDEALGGTAFVQMPAHGLFPWCGILLDPRTLEVOSSYASTSRASVTF 960
? DB 961 NRGFXAGNMERKLFVGLRLKCHSLFDLDQVNSIQVCTNIIKILLQAYEFHACVQLP 1020
? DB 961 NRGFXAGNMERKLFVGLRLKCHSLFDLDQVNSIQVCTNIIKILLQAYEFHACVQLP 1020
? DB 1021 FHQQVKNKPTFFLRISTASTASLCYSILKAKNAGSLGKGAAGPLPSAVWMLGQAVLL 1080
? DB 1021 FHQQVKNKPTFFLRISTASTASLCYSILKAKNAGSLGKGAAGPLPSAVWMLGQAVLL 1080
? DB 1081 KLTRHRTVYVPLGSLRTAQTOLSRKLPGTTLTLEAANPALPSDFETIIL 1132
? DB 1081 KLTRHRTVYVPLGSLRTAQTOLSRKLPGTTLTLEAANPALPSDFETIIL 1132

RESULT 31
US-10-877-124-611
; Sequence 611, Application US/10877124
; Publication No. US20040242529A1
GENERAL INFORMATION:
APPLICANT: Czech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Hartley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,124
FILING DATE: 24-Jun-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-Oct-1997
APPLICATION NUMBER: WO PCT/US97/17865
FILING DATE: 01-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 611:
SEQUENCE CHARACTERISTICS:
LENGTH: 1154 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1154
OTHER INFORMATION: /note= "fusion protein composed of hTERT
protein sequence, vector sequences, the
Myc epitope and His6 tag"
SEQUENCE DESCRIPTION: SEQ ID NO: 611:
US-10-877-124-611
Query Match 99.8%; Score 5952; DB 17; Length 1154;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRAPRCRAVRSLSHREVLPLATFVRRLGPOGWRVLVQGDPAFAFALVAQCLVCVPM 60
DB 1 MRAPRCRAVRSLSHREVLPLATFVRRLGPOGWRVLVQGDPAFAFALVAQCLVCVPM 60
QY 61 DARPPAPAFROVSCIKELVARVLQRCERGAKNVLAFFGALLDGAAGPPEAFTTSVR 120
DB 61 DARPPAPAFROVSCIKELVARVLQRCERGAKNVLAFFGALLDGAAGPPEAFTTSVR 120
QY 121 STLPNTVTDALGSGAGWGLLRVVDVVLHLLACALFVLYABSCAYQVGPPIYOLGA 180
DB 121 STLPNTVTDALGSGAGWGLLRVVDVVLHLLACALFVLYABSCAYQVGPPIYOLGA 180
QY 181 ATQAPPPHASPBRRLGGERAMNSVREAGVPLGLPAPGARRRGSGASRSLP.PKRRR 240
DB 181 ATQAPPPHASPBRRLGGERAMNSVREAGVPLGLPAPGARRRGSGASRSLP.PKRRR 240
QY 241 GAAPPERTPVGGQSWAHPGRTGSGDRGFCVSPAPAEATSLGALSSTRHSBVG 300
DB 241 GAAPPERTPVGGQSWAHPGRTGSGDRGFCVSPAPAEATSLGALSSTRHSBVG 300

```

```

DB 241 GAAPPERTPVGGQSWAHPGRTGSGDRGFCVSPAPAEATSLGALSSTRHSBVG 300
QY 301 RQHAGBPSTSRPPRPMDTPCPVVAETKHPLYSSGDKQLRPSFLISSRLPSLTGARPL 360
DB 301 RQHAGBPSTSRPPRPMDTPCPVVAETKHPLYSSGDKQLRPSFLISSRLPSLTGARPL 360
QY 361 VETIFIGSRPMPGTPRRLPLRQRYWQMRPLFELILGHNAQCPGVLTKTCPRAAYT 420
DB 361 VETIFIGSRPMPGTPRRLPLRQRYWQMRPLFELILGHNAQCPGVLTKTCPRAAYT 420
QY 421 PAAGVAREXPQGSVAAPBEDTDPRLVOLLROHSSPMQVYGFVACLRRLVPPGLWS 480
DB 421 PAAGVAREXPQGSVAAPBEDTDPRLVOLLROHSSPMQVYGFVACLRRLVPPGLWS 480
QY 481 RHNERPFLRNTKFFISLGHAKLSLOELTWKMSVRCALRRSPGVCPAAEHRLRETI 540
DB 481 RHNERPFLRNTKFFISLGHAKLSLOELTWKMSVRCALRRSPGVCPAAEHRLRETI 540
QY 541 LAPELWMSVYVVELLRSPFYVTEFPQNRLEFPREPMSKLOSIGIRHLKRYLRE 600
DB 541 LAPELWMSVYVVELLRSPFYVTEFPQNRLEFPREPMSKLOSIGIRHLKRYLRE 600
QY 601 LSEAVERQREARPAALLTSRLRPIPKPDGLRPIVMNDYVVGARTRRERGAARLSRYVA 660
DB 601 LSEAVERQREARPAALLTSRLRPIPKPDGLRPIVMNDYVVGARTRRERGAARLSRYVA 660
QY 661 LFSVLNVERARPRGLGASVLAGDDIHRAMRTFVLRAQDPPELFFKVDVTGAYDTI 720
DB 661 LFSVLNVERARPRGLGASVLAGDDIHRAMRTFVLRAQDPPELFFKVDVTGAYDTI 720
QY 721 PQRLTEVIASIIKPNNTYCVRRYAVVQKAHGVAKAFKSVSTLTDLQPYMRQFVAL 780
DB 721 PQRLTEVIASIIKPNNTYCVRRYAVVQKAHGVAKAFKSVSTLTDLQPYMRQFVAL 780
QY 781 QETSPLRDVAVLEOSSLSNEASSGLFDVLRPMCHAAVIRKSYVQCGIGQSLSTL 840
DB 781 QETSPLRDVAVLEOSSLSNEASSGLFDVLRPMCHAAVIRKSYVQCGIGQSLSTL 840
QY 841 LGSLEYGMENKLFAGIRRDGLLRVDDPLVTPHLTHAKTFLRLVAGVEYGVNL 900
DB 841 LGSLEYGMENKLFAGIRRDGLLRVDDPLVTPHLTHAKTFLRLVAGVEYGVNL 900
QY 901 RKTIVNFPVEDELGGTAFAVQMPAHGLFPWCGLLDTRLLEVOSSYASRSTIASVTF 960
DB 901 RKTIVNFPVEDELGGTAFAVQMPAHGLFPWCGLLDTRLLEVOSSYASRSTIASVTF 960
QY 961 NRGFKAGRMNRKLFVLRKCHSLFLDQVNSLQTCVCTNIYKILLQAFRFACVLQLP 1020
DB 961 NRGFKAGRMNRKLFVLRKCHSLFLDQVNSLQTCVCTNIYKILLQAFRFACVLQLP 1020
QY 1021 FHOQWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAGGAAGPLPSEAVQMLCHQAFLL 1080
DB 1021 FHOQWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAGGAAGPLPSEAVQMLCHQAFLL 1080
QY 1081 KLTRHRVTYVPLIGSLRTAQTOLSRKLPQTTLTALAANPALPSPDKTILD 1132
DB 1081 KLTRHRVTYVPLIGSLRTAQTOLSRKLPQTTLTALAANPALPSPDKTILD 1132

```

RESULT 32
 US-10-877-022-611
 ; Sequence 611, Application US/10877022
 ; Publication No. US20040247613A1
 ; GENERAL INFORMATION:
 APPLICANT: Cecch, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin B.
 Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/877,022
 FILING DATE: 24-Jun-2004
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/432,503
 FILING DATE: 02-Nov-1999
 APPLICATION NUMBER: 08/974,549
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-Apr-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-Apr-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-May-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-May-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: WO PCT/US97/17618
 FILING DATE: 01-Oct-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-Oct-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002610US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 611:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1154 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..1154
 OTHER INFORMATION: /note= "fusion protein composed of hTERT
 protein sequence, vector sequences, the
 Myc epitope and His6 tag"
 SEQUENCE DESCRIPTION: SEQ ID NO: 611:

US-10-877-022-611

Query Match 99.8%; Score 5952; DB 17; Length 1154;

Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPRAAPCAVSLRSHREVLPATFVRRLPGQWRLVQSGPAPAFALVAQCLVCPW 60
 Db 1 MPRAAPCAVSLRSHREVLPATFVRRLPGQWRLVQSGPAPAFALVAQCLVCPW 60
 Qy 61 DARPPAPASFRQVSCLELVARVLQRLCERGANVLAFGALLDGAAGGPPEAFITTSVR 120
 Db 61 DARPPAPASFRQVSCLELVARVLQRLCERGANVLAFGALLDGAAGGPPEAFITTSVR 120

Qy 121 SYLPTVTDALRSGANGLLRRVGDVVLHLLARCLFVLVAAPSCAYQVCGPFLYQLGA 180
 Db 121 SYLPTVTDALRSGANGLLRRVGDVVLHLLARCLFVLVAAPSCAYQVCGPFLYQLGA 180
 Qy 181 ATOARPPPHASGPPRRRLGCEPAMNHSVREAGVPGLPAPGARRRGSSASRLPLPKRPR 240
 Db 181 ATOARPPPHASGPPRRRLGCEPAMNHSVREAGVPGLPAPGARRRGSSASRLPLPKRPR 240
 Qy 241 GAAPPEPTPVQGSMAHPGRTGSDRGFCVSPAPAPAEATSLLEGALSGTRSHSVG 300
 Db 241 GAAPPEPTPVQGSMAHPGRTGSDRGFCVSPAPAPAEATSLLEGALSGTRSHSVG 300
 Qy 301 RQHAGPSTSRPPRPMDTCCPVYAEIKHFLYSSGDKQLRPSFLLSLRPSLTGARL 360
 Db 301 RQHAGPSTSRPPRPMDTCCPVYAEIKHFLYSSGDKQLRPSFLLSLRPSLTGARL 360
 Qy 361 VETIFLGSRPWMPGTFRRLPRLPQRYQMRPLFELLGNHACQCYVLKTHCGELRAVT 420
 Db 361 VETIFLGSRPWMPGTFRRLPRLPQRYQMRPLFELLGNHACQCYVLKTHCGELRAVT 420
 Qy 421 PAAGVCAKEPQGSVAAPSEEDTPRRLYQLRQSSPWQYGFVPAQLRPLVPGJLMS 480
 Db 421 PAAGVCAKEPQGSVAAPSEEDTPRRLYQLRQSSPWQYGFVPAQLRPLVPGJLMS 480
 Qy 481 RHNERPLRNTKKFISLGKHAKLISLQETWMSVVDCAMLERSGVCVPAEHLREBI 540
 Db 481 RHNERPLRNTKKFISLGKHAKLISLQETWMSVVDCAMLERSGVCVPAEHLREBI 540
 Qy 541 LAKPLHMLMSVYVELLSFPFYVETTPQKNRLFYRPSVMSKXOSIGIRQHLKRVQRE 600
 Db 541 LAKPLHMLMSVYVELLSFPFYVETTPQKNRLFYRPSVMSKXOSIGIRQHLKRVQRE 600
 Qy 601 LSEAEVRQREARPALTSRLRFIPKPDGLRPIVMNDVVGARFPRRKRERLTSRYKA 660
 Db 601 LSEAEVRQREARPALTSRLRFIPKPDGLRPIVMNDVVGARFPRRKRERLTSRYKA 660
 Qy 661 LFSVTNVRARRPGLLGASVGLDIDHRAKRTFALRFAQDPPELFLVKKVDVGAIVTI 720
 Db 661 LFSVTNVRARRPGLLGASVGLDIDHRAKRTFALRFAQDPPELFLVKKVDVGAIVTI 720
 Qy 721 PODRLTEVIASIIKQNTYCVRYAVVQKAAGHVRKAFKSHVSTLTDLPYMRQFVAL 780
 Db 721 PODRLTEVIASIIKQNTYCVRYAVVQKAAGHVRKAFKSHVSTLTDLPYMRQFVAL 780
 Qy 781 QETSPLRDAVITEGSSINEMASGLFDVFLRPMCHAVRIRIGKSVVQCGIFQGSILSTL 840
 Db 781 QETSPLRDAVITEGSSINEMASGLFDVFLRPMCHAVRIRIGKSVVQCGIFQGSILSTL 840
 Qy 841 LCSLCYGMENKLPFAGIRRDGLRLVDDFLVPHLTHAKTFRLTVRGVEYCVNVL 900
 Db 841 LCSLCYGMENKLPFAGIRRDGLRLVDDFLVPHLTHAKTFRLTVRGVEYCVNVL 900
 Qy 901 RKTIVNFPVEDALGTAFFVQMPAHGLFPWCGLLDITRTEVQSSYSYARSISASLTF 960
 Db 901 RKTIVNFPVEDALGTAFFVQMPAHGLFPWCGLLDITRTEVQSSYSYARSISASLTF 960
 Qy 961 NNGFKAGRMWRKLGAVRIRKCHSLFDLDQVNSLQTCVNTYKILLDAYRHACVLDLP 1020
 Db 961 NNGFKAGRMWRKLGAVRIRKCHSLFDLDQVNSLQTCVNTYKILLDAYRHACVLDLP 1020
 Qy 1021 FHOQVWKNTFFLRVISTDASLCVSIILKAKNAGMSLGAKGAAGPLPSBAVQMLCHQAFDL 1080
 Db 1021 FHOQVWKNTFFLRVISTDASLCVSIILKAKNAGMSLGAKGAAGPLPSBAVQMLCHQAFDL 1080
 Qy 1081 KLTRHRVTVVPLLSLRTAQTQLSRKLPETTLTALEAANPALPSDFKTIID 1132
 Db 1081 KLTRHRVTVVPLLSLRTAQTQLSRKLPETTLTALEAANPALPSDFKTIID 1132

RESULT 33
 US-10-044-692-325
 ; Sequence 325, Application US/10044692

Publication No. US20030096344A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Mortin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692
FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 325:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 325:
US-10-044-692-325
Query Match 99.8%; Score 5952; DB 14; Length 1189;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

181 ATQARPPPHASGPRRRIGCERAMNHSVREAGVPLGAPAGARRRGSASRSLPLPKRPR 240
238 ATQARPPPHASGPRRRIGCERAMNHSVREAGVPLGAPAGARRRGSASRSLPLPKRPR 297
241 GAAPERPTVGQSMAPARTGSPRGCVSPAPAEASLGLSGTSHSPVC 300
298 GAAPERPTVGQSMAPARTGSPRGCVSPAPAEASLGLSGTSHSPVC 357
301 ROHAGPSTSRPPRPDPCPPVATKAFILYSSGDKEDLRSPFLSLRSLTGARRL 360
358 ROHAGPSTSRPPRPDPCPPVATKAFILYSSGDKEDLRSPFLSLRSLTGARRL 417
361 VETIFLGRPMWMTGTPRRLPLPQRYWQRPPLFELLLGNHAQCPYVLLKTHQZPLAAYT 420
418 VETIFLGRPMWMTGTPRRLPLPQRYWQRPPLFELLLGNHAQCPYVLLKTHQZPLAAYT 477
421 PAAGVCAERKPGQSVAAPEEEDTPRRLVOLLRQHSPPQVYGFVACLRRLVPLGMS 480
478 PAAGVCAERKPGQSVAAPEEEDTPRRLVOLLRQHSPPQVYGFVACLRRLVPLGMS 537
481 RHNERRFLRNTKFTISLGHAKLSLOELTKQSVRDCAWLRSRGVCVPAAEHRIREI 540
538 RHNERRFLRNTKFTISLGHAKLSLOELTKQSVRDCAWLRSRGVCVPAAEHRIREI 597
541 LAKEFLHMSVYVVELRSPFYVTEETTPQKNRLFEPYRSPWSKLSIGIRHLKRYQLRE 600
598 LAKEFLHMSVYVVELRSPFYVTEETTPQKNRLFEPYRSPWSKLSIGIRHLKRYQLRE 657
601 LSAEAYRQREARPAALTSRLRPIPKPDGLRPIVNDYVVGARTPRERKARLTSRYKA 660
658 LSAEAYRQREARPAALTSRLRPIPKPDGLRPIVNDYVVGARTPRERKARLTSRYKA 717
661 LFSVLNTERARRPGLGASVLDGDDIHRAMRFVLRVADDPPELYPFKVVNTGAYDTI 720
718 LFSVLNTERARRPGLGASVLDGDDIHRAMRFVLRVADDPPELYPFKVVNTGAYDTI 777
721 PODRLTEVASIIPKQNTYCVARYAVQQAAGHAKAFKSHVSTLTDLOPYMRQFVAHL 780
778 PODRLTEVASIIPKQNTYCVARYAVQQAAGHAKAFKSHVSTLTDLOPYMRQFVAHL 837
781 QETSPLRDVAVIEQSSSLNEASGLFVDVLRMCHNAVIRKSYVCCGIFQGSILSTL 840
838 QETSPLRDVAVIEQSSSLNEASGLFVDVLRMCHNAVIRKSYVCCGIFQGSILSTL 897
841 LCSLCGDMENKLFAGIRRDGILLRLVDDFLVTLTAKEFLTLVNGVREYCVNVL 900
898 LCSLCGDMENKLFAGIRRDGILLRLVDDFLVTLTAKEFLTLVNGVREYCVNVL 957
901 RKTIVNFPVEDEALGSTAVQMPANGLPWCGLLIDRTLVEQSDYSYARTSIRASVTF 960
958 RKTIVNFPVEDEALGSTAVQMPANGLPWCGLLIDRTLVEQSDYSYARTSIRASVTF 1017
961 NRGFKAGRMRRKLFGLRLKCHSLFLDQVNSLQVCTNIIKILLQAVRPHACVQLP 1020
1018 NRGFKAGRMRRKLFGLRLKCHSLFLDQVNSLQVCTNIIKILLQAVRPHACVQLP 1077
1021 FHQQWKNPTFFLRVISTDASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAEFL 1080
1078 FHQQWKNPTFFLRVISTDASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAEFL 1137
1081 KLTRHRVTVYVPLIGSLRTAQTLQSLKRLGTTTLTALEAANPALPBDFTIIL 1132
1138 KLTRHRVTVYVPLIGSLRTAQTLQSLKRLGTTTLTALEAANPALPBDFTIIL 1189

RESULT 34
US-10-044-539-325
Sequence 325, Application US/10044539
Publication No. US20030100093A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim

Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin
 Andrews, William H.
 TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
 THERAPEUTIC METHODS
 NUMBER OF SEQUENCES: 335
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/044,539
 FILING DATE: 11-Jan-2002
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/912,951
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002600US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 325:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1189 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 325:
 US-10-044-539-325
 Query Match 99.8%; Score 5952; DB 14; Length 1189;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

241 GAAPPERTPVGGQSWAHGRTGRGSDRGCVVSPARPAEATSLGALSGTRHSPSVG 300
 258 GAAPPERTPVGGQSWAHGRTGRGSDRGCVVSPARPAEATSLGALSGTRHSPSVG 357
 301 ROHHAGPSTSRPRPMDTPCPVYAEIKHFLYSSGDKEQLRPSFLLSLRPSLTGARRL 360
 358 ROHHAGPSTSRPRPMDTPCPVYAEIKHFLYSSGDKEQLRPSFLLSLRPSLTGARRL 417
 421 VETITLGRPMWPGTFRLLRPLRPQRYOMRLEFELLGNHACQCYGVLLKTHCCLRAVT 420
 478 PAAGVCAEKPOGSAAPAEEDTPRRLYVOLLRQHSFPMQYGVFVACRLRVLPGMG 480
 481 RHNERPLRNTKFTSLGKHAKLQSLQETWMSYRDCAMLRSPGVGCVPAEHLRBEI 540
 538 RHNERPLRNTKFTSLGKHAKLQSLQETWMSYRDCAMLRSPGVGCVPAEHLRBEI 597
 541 LAKELHWMISVYVELLSFFVYETTFQKRLFFYRPSVMSKLSIGIRQLKRVOLRE 600
 558 LAKELHWMISVYVELLSFFVYETTFQKRLFFYRPSVMSKLSIGIRQLKRVOLRE 657
 601 LSEAEVRQREARPALTSRLRFTPKPDGLRPIVMDVVGARTFRREKAERLTSRYKA 660
 658 LSEAEVRQREARPALTSRLRFTPKPDGLRPIVMDVVGARTFRREKAERLTSRYKA 717
 661 LFSVINYRARRPGLIGSVGLDIDIRAKMTFVLKRAQOPPELYVVKVDYGVAYDTI 720
 718 LFSVINYRARRPGLIGSVGLDIDIRAKMTFVLKRAQOPPELYVVKVDYGVAYDTI 777
 721 PODRLTEVIASLIKPNQTYCVRRYAVVQKAHGVKAKFHSVSTLIDQPYMKQFVAHL 780
 778 PODRLTEVIASLIKPNQTYCVRRYAVVQKAHGVKAKFHSVSTLIDQPYMKQFVAHL 837
 781 QETSPLRAVYIEGSSSINEASSGLFDVFLRPMCHAVRIRKSVYCCGIPQSSIIISTL 840
 838 QETSPLRAVYIEGSSSINEASSGLFDVFLRPMCHAVRIRKSVYCCGIPQSSIIISTL 897
 841 LQSLCYGMENKLPFGIRRDGILLRVDPFLVPHLHAKTFLTLVRGVEGCVNVL 900
 898 LQSLCYGMENKLPFGIRRDGILLRVDPFLVPHLHAKTFLTLVRGVEGCVNVL 957
 901 RKTIVNFEVEDEALGGTAFVQMPAHGLPFWCGLLDTRTLEVSQDSSYARTSIRASVTF 960
 958 RKTIVNFEVEDEALGGTAFVQMPAHGLPFWCGLLDTRTLEVSQDSSYARTSIRASVTF 1017
 961 NGGFAGNNRRKLPFGVRLKCHSLFDLQVNSIQTVCTNIYKILLDAFHFACVLDLP 1020
 1018 NGGFAGNNRRKLPFGVRLKCHSLFDLQVNSIQTVCTNIYKILLDAFHFACVLDLP 1077
 1021 FHOQWKNPTFFLRVISTDASLCYSILKAKNAGMSLGAKGAGPLPSBAVOMLCHQAEFL 1080
 1078 FHOQWKNPTFFLRVISTDASLCYSILKAKNAGMSLGAKGAGPLPSBAVOMLCHQAEFL 1137
 1081 KLTRHRVTYVPLIGSLRFAQQLSRKLPGLTITALEAANPALPSDFETIID 1132
 1138 KLTRHRVTYVPLIGSLRFAQQLSRKLPGLTITALEAANPALPSDFETIID 1189

RESULT 35
 US-10-325-810-613
 ; Sequence 613, Application US/10325810
 ; Publication No. US20030204069A1
 ; GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 Linguet, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin B.

```

? Andrews, William H.
? TITLE OF INVENTION: Human Telomerase Catalytic Subunit
? NUMBER OF SEQUENCES: 613
? CORRESPONDENCE ADDRESS:
? ADDRESSER: Townsend and Townsend and Crew LLP
? CITY: San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94111-3834
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
?
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/10/325,810
? FILING DATE: 20-Dec-2002
? CLASSIFICATION: <Unknown>
?
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/09/402,181
? FILING DATE: 29-Sep-1997
? APPLICATION NUMBER: US 08/724,643
? FILING DATE: 01-Oct-1996
? APPLICATION NUMBER: US 08/844,419
? FILING DATE: 18-Apr-1997
? APPLICATION NUMBER: US 08/846,017
? FILING DATE: 25-Apr-1997
? APPLICATION NUMBER: US 08/851,843
? FILING DATE: 06-May-1997
? APPLICATION NUMBER: US 08/854,050
? FILING DATE: 09-May-1997
? APPLICATION NUMBER: US 08/911,312
? FILING DATE: 14-Aug-1997
? APPLICATION NUMBER: US 08/912,951
? FILING DATE: 14-Aug-1997
? APPLICATION NUMBER: US 08/915,503
? FILING DATE: 14-Aug-1997
? APPLICATION NUMBER: WO PCT/US97/117885
? FILING DATE: 01-Oct-1997
?
? ATTORNEY/AGENT INFORMATION:
? NAME: Ausemus, Scott L.
? REGISTRATION NUMBER: 42,271
? REFERENCE/DOCKET NUMBER: 015389-002620US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 576-0200
? TELEFAX: (415) 576-0300
?
? INFORMATION FOR SEQ ID NO: 613:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1189 amino acids
? TYPE: amino acid
? STRANDEDNESS: <Unknown>
? TOPOLOGY: linear
? MOLECULE TYPE: protein
?
? NAME/KEY: Protein
? LOCATION: 1..1189
? OTHER INFORMATION: /note= "fusion protein composed of
? melittin signal sequence and full length
? hTERT protein"
?
? SEQUENCE DESCRIPTION: SEQ ID NO: 613:
?
? US-10-325-810-613
?
? Query Match 99.8%; Score 5952; DB 14; Length 1189;
? Best Local Similarity 99.8%; Pred. No. 0;
? Matches 110; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
?
? QY 1 MPRARCAVRSLLSHREVPLATFVRRLGPGCMRLVORGDDPAFAALVAQCLVCPW 60
? DB 58 MPRARCAVRSLLSHREVPLATFVRRLGPGCMRLVORGDDPAFAALVAQCLVCPW 117
?
? QY 61 DARPPAAPSPROVSCIKELVARVLQRLCERGAKNVLAFGALLDGAAGGPPPAFTTSVR 120

```

```

? DB 118 DARPPAAPSPROVSCIKELVARVLQRLCERGAKNVLAFGALLDGAAGGPPPAFTTSVR 177
? QY 121 SYLPTNTVDALRSGAGMLLRVGGDVLVHLARCALFLVAPSCAYQCGPLVQLG 180
? DB 178 SYLPTNTVDALRSGAGMLLRVGGDVLVHLARCALFLVAPSCAYQCGPLVQLG 237
? QY 181 ATOARPPHAGSPRRRLGCERAMNHSREAGVPLGAPARRRGSASRLPLPRPR 240
? DB 238 ATOARPPHAGSPRRRLGCERAMNHSREAGVPLGAPARRRGSASRLPLPRPR 297
? QY 241 GAAPPERTVGGGSMNHPGRTGPSDRGCVVSPAPAEATSLGALSGTSHSPSG 300
? DB 298 GAAPPERTVGGGSMNHPGRTGPSDRGCVVSPAPAEATSLGALSGTSHSPSG 357
? QY 301 ROHHAGPSTSRPPRPMDTCCPVVAETKFLVSSGDKQLRBSFLLSRLPSLTGARLT 360
? DB 358 ROHHAGPSTSRPPRPMDTCCPVVAETKFLVSSGDKQLRBSFLLSRLPSLTGARLT 417
? QY 361 VETIFLGSRRPMWGTPLRLPRLPQRYWQKPLLELLGNHAQCPVVLKTHCPLEAAVT 420
? DB 418 VETIFLGSRRPMWGTPLRLPRLPQRYWQKPLLELLGNHAQCPVVLKTHCPLEAAVT 477
? QY 421 PAAGVCAREKPGQSVAPAEEDTDPRLVQLRQSSPMQVGYFVACLRRLVPPGLMS 480
? DB 478 PAAGVCAREKPGQSVAPAEEDTDPRLVQLRQSSPMQVGYFVACLRRLVPPGLMS 537
? QY 481 RHNERRLRNTKXFLISLGRKAKSLQELTWKMSVRDCAMLRSPGYCVPAAEHRLREI 540
? DB 538 RHNERRLRNTKXFLISLGRKAKSLQELTWKMSVRDCAMLRSPGYCVPAAEHRLREI 597
? QY 541 LAKEFLHMSVYVVELLRSPFYETTFQKNRLFRRPVMWSLQSIGRQLKRYQLRE 600
? DB 598 LAKEFLHMSVYVVELLRSPFYETTFQKNRLFRRKVMWSLQSIGRQLKRYQLRE 657
? QY 601 LSAEAVRQHEARPAALLTSRLRFLPKPDGLRPIVMNDVYVAGARTPREREARLTISRYKA 660
? DB 658 LSAEAVRQHEARPAALLTSRLRFLPKPDGLRPIVMNDVYVAGARTPREREARLTISRYKA 717
? QY 661 LFSVLNVERARRRGLGASVGLGDDIHRAMRTFVLRYRQADPEPLRYFKVQVTAQYDTI 720
? DB 718 LFSVLNVERARRRGLGASVGLGDDIHRAMRTFVLRYRQADPEPLRYFKVQVTAQYDTI 777
? QY 721 PODRLTEVIASIIKPNQTYCVRRYAVVQKAHGHVAKAFKSHVSTLTDLPYMRQFAHL 780
? DB 778 PODRLTEVIASIIKPNQTYCVRRYAVVQKAHGHVAKAFKSHVSTLTDLPYMRQFAHL 837
? QY 781 QETSPLRDAVITFOSSSLNEASSGLFDVFLRMCHAVIRKSYVQCGIFQGSILSTL 840
? DB 838 QETSPLRDAVITFOSSSLNEASSGLFDVFLRMCHAVIRKSYVQCGIFQGSILSTL 897
? QY 841 LGSILCYGDMENKLFAGIRRDGLLRVDDPFLVTPHLLTAKFTLTLVAGVEYGCYNL 900
? DB 898 LGSILCYGDMENKLFAGIRRDGLLRVDDPFLVTPHLLTAKFTLTLVAGVEYGCYNL 957
? QY 901 RKTVNVFPVEDEALGGTAIVQMPAHGLFPWCGLLDTRILEVQSDYSYARTSISASVTF 960
? DB 958 RKTVNVFPVEDEALGGTAIVQMPAHGLFPWCGLLDTRILEVQSDYSYARTSISASVTF 1017
? QY 961 NRGFKAGRMNRRLLFGVLRKLKCHSLPLDQVNSLQTCVNIYKILLOAYRHACVLOLP 1020
? DB 1018 NRGFKAGRMNRRLLFGVLRKLKCHSLPLDQVNSLQTCVNIYKILLOAYRHACVLOLP 1077
? QY 1081 KLTRHRVTYVPLIGSLRTAQTOLSRLLPCTTLTALAAANPRLPSDFKTIID 1132
? DB 1138 KLTRHRVTYVPLIGSLRTAQTOLSRLLPCTTLTALAAANPRLPSDFKTIID 1189

```

RESULT 36
US-10-877-124-613

Sequence 613, Application US/10877.124
Publication No. US2004024529A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
City: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,124
FILING DATE: 24-Jun-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1998
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-Oct-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 613:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1189
OTHER INFORMATION: /note="fusion protein composed of
telitin signal sequence and full length
hTERT protein"
SEQUENCE DESCRIPTION: SEQ ID NO: 613:
US-10-877-124-613

Query Match 99.8%; Score 5952; DB 17; Length 1189;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	MPRAPRCRAVSLIRSHREVLPATFYRLIGPGMRLVGRDPAARALVAQCLVCVPM	60
DB	58	MPRAPRCRAVSLIRSHREVLPATFYRLIGPGMRLVGRDPAARALVAQCLVCVPM	117
QY	61	DARPPAPSPROYSCLEKELVARVLQRCERGANVLAFAFGALDGAAGSPPEAFTTSVR	120
DB	118	DARPPAPSPROYSCLEKELVARVLQRCERGANVLAFAFGALDGAAGSPPEAFTTSVR	177
QY	121	SYLPNTVTDLRGSGAMGLLRVYDVLVHLLARCALFVLVAPSCAYVCGPPLVQLGA	180
DB	178	SYLPNTVTDLRGSGAMGLLRVYDVLVHLLARCALFVLVAPSCAYVCGPPLVQLGA	237
QY	181	ATQAPPPHAGSPRRRLGCEBAMNHSVEAGVPLGLPAGARRRGSASRLPLPKPRR	240
DB	238	ATQAPPPHAGSPRRRLGCEBAMNHSVEAGVPLGLPAGARRRGSASRLPLPKPRR	297
QY	241	GAAPPERTPVQGGSWAHPRGRTRGSDRGFCVSPAPPAEATSLEGALSGTRSHPSVG	300
DB	298	GAAPPERTPVQGGSWAHPRGRTRGSDRGFCVSPAPPAEATSLEGALSGTRSHPSVG	357
QY	301	ROHAGPSTSRPPRPWDTPCPVYAEKHTFLYSSGDEQRLPSTLSLRPSLTGARRL	360
DB	358	ROHAGPSTSRPPRPWDTPCPVYAEKHTFLYSSGDEQRLPSTLSLRPSLTGARRL	417
QY	361	VETITLGRPMWPGTFRRLPLRQRYWQMRPLFELIGNHACCPGYLLKTHCPLEAAVT	420
DB	418	VETITLGRPMWPGTFRRLPLRQRYWQMRPLFELIGNHACCPGYLLKTHCPLEAAVT	477
QY	421	PAAGVCAEEKPGQSVAAPEEDTDPRRLVOLLRQHSWQYGYGYACLRLLVPPGLMS	480
DB	478	PAAGVCAEEKPGQSVAAPEEDTDPRRLVOLLRQHSWQYGYGYACLRLLVPPGLMS	537
QY	481	RNERRFLRNKKFSLGKHAKLSTQELTWKMSVYDCMLRSPVGCVPAAERHLSREI	540
DB	538	RNERRFLRNKKFSLGKHAKLSTQELTWKMSVYDCMLRSPVGCVPAAERHLSREI	597
QY	541	LAKFLHMLMSYVVLRSFFVYETTFQKNRLFYRPSWSKLSQISIRQHLKRVQURE	600
DB	598	LAKFLHMLMSYVVLRSFFVYETTFQKNRLFYRPSWSKLSQISIRQHLKRVQURE	657
QY	601	ISEAEVRQREARPPALTSRLFLPKPDGLRPIVMDVVGARTTRRREKAERLTSRYKA	660
DB	658	ISEAEVRQREARPPALTSRLFLPKPDGLRPIVMDVVGARTTRRREKAERLTSRYKA	717
QY	661	LFSVLYNESARAPGLIGASVGLDDIHRAMRTFVLRAADPPPELVYKVYDVTGAYDTI	720
DB	718	LFSVLYNESARAPGLIGASVGLDDIHRAMRTFVLRAADPPPELVYKVYDVTGAYDTI	777
QY	721	PODRLLEVIASITKQNTYCVARYAVVQAAAGHYRKAFKSHVSTLTDLQPMRPFVHL	780
DB	778	PODRLLEVIASITKQNTYCVARYAVVQAAAGHYRKAFKSHVSTLTDLQPMRPFVHL	837
QY	781	QETSPLRDAVVEQSSSLNEASGAFDYFLRMCCHAVRIRGKSYYVQCGIPQGSILSTL	840
DB	838	QETSPLRDAVVEQSSSLNEASGAFDYFLRMCCHAVRIRGKSYYVQCGIPQGSILSTL	897
QY	841	LCSLCYGDMENKLPAGIRRDGLLRLVDDFLVTLTHAKTFLRTLVGYVEYCVVNL	900
DB	898	LCSLCYGDMENKLPAGIRRDGLLRLVDDFLVTLTHAKTFLRTLVGYVEYCVVNL	957
QY	901	RKTVNPPEVEDALGTAFCVGMARGLPVMCGLLDRTLEVQSSYSSARSTISATYF	960
DB	958	RKTVNPPEVEDALGTAFCVGMARGLPVMCGLLDRTLEVQSSYSSARSTISATYF	1017
QY	961	NRGFYAGRMRRKLGVLRLKCHSLFDLQVNSLQVCTNIYKILLQAYRFHACVQLP	1020
DB	1018	NRGFYAGRMRRKLGVLRLKCHSLFDLQVNSLQVCTNIYKILLQAYRFHACVQLP	1077

QY 1021 FHQWKNPFPFRLRVISDTASLCYSTLKAKNAGMSIGAKGAGPLPSEAVQWLCQAFLL 1080
Db 1078 FHQWKNPFPFRLRVISDTASLCYSTLKAKNAGMSIGAKGAGPLPSEAVQWLCQAFLL 1137
QY 1081 KLRHRTVTVPLGLSLRTAQTQSRKLPSTTLTALAAANPALPSDFKTIID 1132
Db 1138 KLRHRTVTVPLGLSLRTAQTQSRKLPSTTLTALAAANPALPSDFKTIID 1189

RESULT 37

US-10-877-022-613
Sequence 613, Application US/10877022
Publication No. US2004024763A1
GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/877,022

FILING DATE: 24-Jun-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/432,503

FILING DATE: 02-Nov-1999

APPLICATION NUMBER: 08/974,549

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-Apr-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-Apr-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-May-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-May-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: WO PCT/US97/11618

FILING DATE: 01-Oct-1997

APPLICATION NUMBER: WO PCT/US97/117885

FILING DATE: 01-Oct-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 613:

SEQUENCE CHARACTERISTICS:

LENGTH: 1189 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1189
OTHER INFORMATION: /note= "fusion protein composed of
melittin signal sequence and full length
hTERT protein"
SEQUENCE DESCRIPTION: SEQ ID NO: 613:
US-10-877-022-613

Query Match 99.8%; Score 5953; DB 17; Length 1189;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLRSHYREVLPLATFVERLGFQGRVLYVQGDPAAPALVAQCLVCPM 60
Db MPAPRCRAVRSLLRSHYREVLPLATFVERLGFQGRVLYVQGDPAAPALVAQCLVCPM 117
QY 61 DAPPPAPSPFQVSCIKELVAVLQRLCEBKAQNTLAGFALLDQARGGPEAFTTSVR 120
Db DAPPPAPSPFQVSCIKELVAVLQRLCEBKAQNTLAGFALLDQARGGPEAFTTSVR 177
QY 118 DAPPPAPSPFQVSCIKELVAVLQRLCEBKAQNTLAGFALLDQARGGPEAFTTSVR 177
Db DAPPPAPSPFQVSCIKELVAVLQRLCEBKAQNTLAGFALLDQARGGPEAFTTSVR 237
QY 121 SYLPTVTDALRSGAMGLLRVGDVVLHLARCALFVLVAPSCAYVCCPEYQLGA 180
Db SYLPTVTDALRSGAMGLLRVGDVVLHLARCALFVLVAPSCAYVCCPEYQLGA 237
QY 181 ATOARPPHAGSPRRRLGCBRAHNSVRAQVPLGLPAGARRGGSASRLPLPRPRR 240
Db ATOARPPHAGSPRRRLGCBRAHNSVRAQVPLGLPAGARRGGSASRLPLPRPRR 297
QY 238 ATOARPPHAGSPRRRLGCBRAHNSVRAQVPLGLPAGARRGGSASRLPLPRPRR 297
Db ATOARPPHAGSPRRRLGCBRAHNSVRAQVPLGLPAGARRGGSASRLPLPRPRR 300
QY 241 GAAPPEERTVGGGSAHNGRTGPDGFCVSPAPRAEETSLEGALSGTRHSPVG 300
Db GAAPPEERTVGGGSAHNGRTGPDGFCVSPAPRAEETSLEGALSGTRHSPVG 357
QY 298 GAAPPEERTVGGGSAHNGRTGPDGFCVSPAPRAEETSLEGALSGTRHSPVG 357
Db GAAPPEERTVGGGSAHNGRTGPDGFCVSPAPRAEETSLEGALSGTRHSPVG 360
QY 301 RQHAGPSTSRPPRMDTPCPVYAEYKHPYSSGDKQLPSPILLSRLSTGARRL 360
Db RQHAGPSTSRPPRMDTPCPVYAEYKHPYSSGDKQLPSPILLSRLSTGARRL 417
QY 358 RQHAGPSTSRPPRMDTPCPVYAEYKHPYSSGDKQLPSPILLSRLSTGARRL 417
Db RQHAGPSTSRPPRMDTPCPVYAEYKHPYSSGDKQLPSPILLSRLSTGARRL 420
QY 361 VETIFIGSRPMPGTPRRLLPQRYWQMRPLFELIGHAACPPGVLLKTCPLRAAT 420
Db VETIFIGSRPMPGTPRRLLPQRYWQMRPLFELIGHAACPPGVLLKTCPLRAAT 477
QY 418 VETIFIGSRPMPGTPRRLLPQRYWQMRPLFELIGHAACPPGVLLKTCPLRAAT 477
Db VETIFIGSRPMPGTPRRLLPQRYWQMRPLFELIGHAACPPGVLLKTCPLRAAT 537
QY 421 PAAGVAREKPOGSAVAPEEDTDPRRLVQLRQSSPQVGYFVACRLRLVPPGLMS 480
Db PAAGVAREKPOGSAVAPEEDTDPRRLVQLRQSSPQVGYFVACRLRLVPPGLMS 537
QY 478 PAAGVAREKPOGSAVAPEEDTDPRRLVQLRQSSPQVGYFVACRLRLVPPGLMS 537
Db PAAGVAREKPOGSAVAPEEDTDPRRLVQLRQSSPQVGYFVACRLRLVPPGLMS 540
QY 481 RHNERFPLNTKFKFISLGAKLSLOELTWKMSVSDCAMLRSRPGVCVPAEHRLEBI 540
Db RHNERFPLNTKFKFISLGAKLSLOELTWKMSVSDCAMLRSRPGVCVPAEHRLEBI 597
QY 538 RHNERFPLNTKFKFISLGAKLSLOELTWKMSVSDCAMLRSRPGVCVPAEHRLEBI 597
Db RHNERFPLNTKFKFISLGAKLSLOELTWKMSVSDCAMLRSRPGVCVPAEHRLEBI 600
QY 541 LAKFLHMLSVYVEELRSFFVTEFPQKSLFFYRPSWKSLSIGRQLKXVQLE 600
Db LAKFLHMLSVYVEELRSFFVTEFPQKSLFFYRPSWKSLSIGRQLKXVQLE 657
QY 598 LAKFLHMLSVYVEELRSFFVTEFPQKSLFFYRPSWKSLSIGRQLKXVQLE 657
Db LAKFLHMLSVYVEELRSFFVTEFPQKSLFFYRPSWKSLSIGRQLKXVQLE 660
QY 601 LSAEVRQREARAPALITSLRLPIPKPDGLRPIVANDVYVAGARTRRERARLTSRYKA 660
Db LSAEVRQREARAPALITSLRLPIPKPDGLRPIVANDVYVAGARTRRERARLTSRYKA 717
QY 658 LSAEVRQREARAPALITSLRLPIPKPDGLRPIVANDVYVAGARTRRERARLTSRYKA 717
Db LSAEVRQREARAPALITSLRLPIPKPDGLRPIVANDVYVAGARTRRERARLTSRYKA 720
QY 661 LFSVLNVEPARPGLIGASVGLGDDIHRAMRFVLRVRAODPPELYFYKVDVTAGYTI 720
Db LFSVLNVEPARPGLIGASVGLGDDIHRAMRFVLRVRAODPPELYFYKVDVTAGYTI 777
QY 718 LFSVLNVEPARPGLIGASVGLGDDIHRAMRFVLRVRAODPPELYFYKVDVTAGYTI 777
Db LFSVLNVEPARPGLIGASVGLGDDIHRAMRFVLRVRAODPPELYFYKVDVTAGYTI 780
QY 721 PQDRLEVTASIIKPNTYCVRRYAVVQKAHGHVKAQKSHVSTLTDLPYRQFVAHL 780
Db PQDRLEVTASIIKPNTYCVRRYAVVQKAHGHVKAQKSHVSTLTDLPYRQFVAHL 837
QY 778 PQDRLEVTASIIKPNTYCVRRYAVVQKAHGHVKAQKSHVSTLTDLPYRQFVAHL 837
Db PQDRLEVTASIIKPNTYCVRRYAVVQKAHGHVKAQKSHVSTLTDLPYRQFVAHL 840
QY 781 QETSPLRDAVVLEQSSSLNEASSGLFDVLRMCHAVIRKSVYVQCGLPQSSILSTL 840
Db QETSPLRDAVVLEQSSSLNEASSGLFDVLRMCHAVIRKSVYVQCGLPQSSILSTL 897
QY 838 QETSPLRDAVVLEQSSSLNEASSGLFDVLRMCHAVIRKSVYVQCGLPQSSILSTL 897
Db QETSPLRDAVVLEQSSSLNEASSGLFDVLRMCHAVIRKSVYVQCGLPQSSILSTL 900
QY 841 LQSLCYGDMENKLFAGIRRDGLLRVDDFLVLTBHLTHAKFTLTVRGVEXGVVNL 900
Db LQSLCYGDMENKLFAGIRRDGLLRVDDFLVLTBHLTHAKFTLTVRGVEXGVVNL

```

Db      898 LCSLCYGDMEKLFAGIRRDGILLRLVDDFLVTLPHLTHAKTFLRLTVGVEYCVNL 957
Qy      901 RKTIVNPFVDEALGTAFAVQMPAHGIFPWCGLLIDTRILEVQSDVSARTSIRASYTF 960
Db      958 RKTIVNPFVDEALGTAFAVQMPAHGIFPWCGLLIDTRILEVQSDVSARTSIRASYTF 1017
Qy      961 NRGFKAGNRNRKLFVLRKCHSLFLDLQVNSLQVCTNIYKILLLOAYRFHACVLOLP 1020
Db      1018 NRGFKAGNRNRKLFVLRKCHSLFLDLQVNSLQVCTNIYKILLLOAYRFHACVLOLP 1077
Qy      1021 FHQGVKNPFFELRVISDTSLCYSILKAKAGNSLGAAGAPLSEAVQWLCQAFL 1080
Db      1078 FHQGVKNPFFELRVISDTSLCYSILKAKAGNSLGAAGAPLSEAVQWLCQAFL 1137
Qy      1081 KLTRHRTVYVPLGSLRTAQTOLSRKLGTTLTALAAANPALPSDEKTL 1132
Db      1138 KLTRHRTVYVPLGSLRTAQTOLSRKLGTTLTALAAANPALPSDEKTL 1189

```

```

RESULT 38
US-10-044-692-324
Sequence 324, Application US/10044692
Publication No. US20030096344A1
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692
FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-Oct-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 324:
SEQUENCE CHARACTERISTICS:

```

```

;
; LENGTH: 1200 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 324:
US-10-044-692-324

Query Match          99.8%; Score 5952; DB 14; Length 1200;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MPRAPRCAYVSLNSHREVLPLATFVRRLGPGQMRVVGDDPAFAFALVAQCIVCPW 60
Db      69 MPRAPRCAYVSLNSHREVLPLATFVRRLGPGQMRVVGDDPAFAFALVAQCIVCPW 128
Qy      61 DARPPPAAPSFQVSCLELVARVLQRLCERGAQVLAFGFALDGAAGPPEAFTTSVR 120
Db      129 DARPPPAAPSFQVSCLELVARVLQRLCERGAQVLAFGFALDGAAGPPEAFTTSVR 188
Qy      121 SYLPNTVTDALRGSGAMGILLRRVGDVYLVAHLARCALFVLA8CAVQVCGPPLYQGA 180
Db      189 SYLPNTVTDALRGSGAMGILLRRVGDVYLVAHLARCALFVLA8CAVQVCGPPLYQGA 248
Qy      181 ATOARPPPHASGRRRLGGERAMNSVREAGVPLGLPAPGARRRGGSASRSLPLKPRR 240
Db      249 ATOARPPPHASGRRRLGGERAMNSVREAGVPLGLPAPGARRRGGSASRSLPLKPRR 308
Qy      241 GAAPERTPVQGSMAHPRGRTGSDRGFCVSPAPPAEATSLLEGALSGTRSHSPVG 300
Db      309 GAAPERTPVQGSMAHPRGRTGSDRGFCVSPAPPAEATSLLEGALSGTRSHSPVG 368
Qy      301 RQHHAGPSTSPRPMPWTCPCPVVAETKHFYSSGDKEQLRPSLLSLRSLTGARL 360
Db      369 RQHHAGPSTSPRPMPWTCPCPVVAETKHFYSSGDKEQLRPSLLSLRSLTGARL 428
Qy      361 VETIFGSRPMWPGRRRLPLPQRYWQMRPFLLELGNHACCPGVLLKTHCPRLAAVT 420
Db      429 VETIFGSRPMWPGRRRLPLPQRYWQMRPFLLELGNHACCPGVLLKTHCPRLAAVT 488
Qy      421 PAAGVCAAREKPOGSAAPBEDTDPRRLVOLIRQSSWQYGFPAACLRRLVPPGLNGS 480
Db      489 PAAGVCAAREKPOGSAAPBEDTDPRRLVOLIRQSSWQYGFPAACLRRLVPPGLNGS 548
Qy      481 RHNERRPLNRTKFFSLGHAHLSTLOELTWKMSVDCAMLRSPVGCVPAAEHRLREI 540
Db      549 RHNERRPLNRTKFFSLGHAHLSTLOELTWKMSVDCAMLRSPVGCVPAAEHRLREI 608
Qy      541 LAKFLHMLSVYVVELLSFFVYETTFQKELFFYRDSWSKLSIGIRQLKVKQJRE 600
Db      609 LAKFLHMLSVYVVELLSFFVYETTFQKELFFYRDSWSKLSIGIRQLKVKQJRE 668
Qy      601 LSEAEVRQREARPALITSRLRFIRKPGCLPIVAMDVVGARTRRKBAERLRSYKA 660
Db      669 LSEAEVRQREARPALITSRLRFIRKPGCLPIVAMDVVGARTRRKBAERLRSYKA 728
Qy      661 LFSVLNTERARRPGLLGASVGLDIDHRAVRTFVLRAQDPEPLLYFYKVDVTGAYDTI 720
Db      729 LFSVLNTERARRPGLLGASVGLDIDHRAVRTFVLRAQDPEPLLYFYKVDVTGAYDTI 788
Qy      721 PODRLTEVYASIIKQONTYCVRRYAVVOQAAGHAKFAKSVSTLTDLPQMRQFVAHL 780
Db      789 PODRLTEVYASIIKQONTYCVRRYAVVOQAAGHAKFAKSVSTLTDLPQMRQFVAHL 848
Qy      781 QETSPLRDAVVEQSSSLNEASSGLFDVFLRMCHAAVIRKSVYQCGIQQSILSTL 840
Db      849 QETSPLRDAVVEQSSSLNEASSGLFDVFLRMCHAAVIRKSVYQCGIQQSILSTL 908
Qy      841 LCSLCYGDMEKLFAGIRRDGILLRLVDDFLVTLPHLTHAKTFLRLTVGVEYCVNL 900
Db      909 LCSLCYGDMEKLFAGIRRDGILLRLVDDFLVTLPHLTHAKTFLRLTVGVEYCVNL 968
Qy      901 RKTIVNPFVDEALGTAFAVQMPAHGIFPWCGLLIDTRILEVQSDVSARTSIRASYTF 960

```

Db 969 RKTIVNFPVEDALGTAIVQMPAHGLPFWCGLLDTRILEVQSDYSYARISASLT 1028
 QY 961 NRGFKAGRMRRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
 Db 1029 NRGFKAGRMRRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1088
 QY 1021 FHQVWKNFTFLFRLVSDTASLCYSILKKNAGMS:GAGGAGPLPSEVWQLCHQATLL 1080
 Db 1089 FHQVWKNFTFLFRLVSDTASLCYSILKKNAGMS:GAGGAGPLPSEVWQLCHQATLL 1148
 QY 1081 KLTNRHVTVPFLGSLRTAQTQSLRKLPGTTLTALAAANPALPSDFKTLID 1132
 Db 1149 KLTNRHVTVPFLGSLRTAQTQSLRKLPGTTLTALAAANPALPSDFKTLID 1200

RESULT 39
 US-10-044-539-324
 Sequence 324, Application US/10044539
 Publication No. US20030100093A1
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin
 Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
 THERAPEUTIC METHODS
 NUMBER OF SEQUENCES: 335
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/044,539
 FILING DATE: 11-Jan-2002
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/912,951
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-May-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-May-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-Apr-1997
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-Apr-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-Oct-1996

ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002600US

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 324:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1200 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear

MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 324:
 US-10-044-539-324

Query Match 99.8%; Score 5952; DB 14; Length 1200;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSILRSRYREVLPLATFVRRLRGQGKRLVORGPPAFRALVAOCLVGVW 60
 Db 69 MPRAPRCRAVRSILRSRYREVLPLATFVRRLRGQGKRLVORGPPAFRALVAOCLVGVW 128
 QY 61 DAPPAPAPSPFROVSCIKELVAVRQLCRGAKNYLAFGLDLAGGAPPAFTTSR 120
 Db 129 DAPPAPAPSPFROVSCIKELVAVRQLCRGAKNYLAFGLDLAGGAPPAFTTSR 188
 QY 121 SYLNTVTDALRGSGAWGLLIRVGDVLYHLIARCALFVLVAPSCAYVCGPPLYQLCA 180
 Db 189 SYLNTVTDALRGSGAWGLLIRVGDVLYHLIARCALFVLVAPSCAYVCGPPLYQLCA 248
 QY 181 ATQARPPHAGSPRRRLGCRANHSVREAGVPLGPAFGARRGGASASRLPLPRPRR 240
 Db 249 ATQARPPHAGSPRRRLGCRANHSVREAGVPLGPAFGARRGGASASRLPLPRPRR 308
 QY 241 GAAPBEPRTFVGQSWAHPGRTGSPSDRGFCVVSPPAPAEATSLGALSGRHSHSVG 300
 Db 309 GAAPBEPRTFVGQSWAHPGRTGSPSDRGFCVVSPPAPAEATSLGALSGRHSHSVG 368
 QY 301 RQHHAGPSTSRPRRMDPCRPVYAEKHFILYSSGDKCOLPSFLSLRSLSGTARL 360
 Db 369 RQHHAGPSTSRPRRMDPCRPVYAEKHFILYSSGDKCOLPSFLSLRSLSGTARL 428
 QY 361 VETIFLGSRPWPGTFRRLPLRQRYWQMRPLFLELIGNHAOCPYGVLLKTRCPJRAVT 420
 Db 429 VETIFLGSRPWPGTFRRLPLRQRYWQMRPLFLELIGNHAOCPYGVLLKTRCPJRAVT 488
 QY 421 PAAVCAREKPOGSAVAPEEDTDPRLVQLRQHSPPQVYGFAVACRLRLVPELMS 548
 Db 489 PAAVCAREKPOGSAVAPEEDTDPRLVQLRQHSPPQVYGFAVACRLRLVPELMS 548
 QY 481 RHEHREFLRTKFKISLGHAKLSLOELTWKMSVRCAMLRSPGVCPAAEHRLREI 540
 Db 549 RHEHREFLRTKFKISLGHAKLSLOELTWKMSVRCAMLRSPGVCPAAEHRLREI 608
 QY 541 LAKFLHMSVYVELLRSPFYVTEFTFOKNRLFYRPSVMSKLOSIGIRQHLKRYQRE 600
 Db 609 LAKFLHMSVYVELLRSPFYVTEFTFOKNRLFYRPSVMSKLOSIGIRQHLKRYQRE 668
 QY 601 LSAEVRQHRBAPALTLRLRFLPKDGLRPIVMNDVYVGARTRRERARLRSRYKA 660
 Db 669 LSAEVRQHRBAPALTLRLRFLPKDGLRPIVMNDVYVGARTRRERARLRSRYKA 728
 QY 661 LFSVLNVERARRRGLGASVLDIHRAMRTFVLRAQDPPPELYPVKQDVTGAYDTI 720
 Db 729 LFSVLNVERARRRGLGASVLDIHRAMRTFVLRAQDPPPELYPVKQDVTGAYDTI 788
 QY 721 PQURLFEVLAITIKPNTYCVRRYAVVQCAAGHAKAKSVSTLTDQPMRQFVAL 780
 Db 789 PQURLFEVLAITIKPNTYCVRRYAVVQCAAGHAKAKSVSTLTDQPMRQFVAL 848
 QY 781 QETSPLRDAVVIQSSSLNEASGLFDVFLRMCHAAVIRKSYVQCGIIPQGSILSTL 840
 Db 849 QETSPLRDAVVIQSSSLNEASGLFDVFLRMCHAAVIRKSYVQCGIIPQGSILSTL 908
 QY 841 LGLCYGDMENKLPAGIRDDGLLRLVDDPLLVTPLTHAKFLTLVRGVEYGVNVL 900
 Db 909 LGLCYGDMENKLPAGIRDDGLLRLVDDPLLVTPLTHAKFLTLVRGVEYGVNVL 968
 QY 901 RKTIVNFPVEDALGTAIVQMPAHGLPFWCGLLDTRILEVQSDYSYARISASLT 960
 Db 969 RKTIVNFPVEDALGTAIVQMPAHGLPFWCGLLDTRILEVQSDYSYARISASLT 1028
 QY 961 NRGFKAGRMRRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020

Db 1029 NRGRKAGNNRRKLFQVLRKCHSLFDLDVNSIQVCTNIIYKLLIQARFPAQVQLP 1088
 QY 1021 FHQGVKNPTEFLEVIDSLCYSLIKAKNAGSLAKAGAGLPSEAVQWLCQAFTL 1080
 Db 1089 FHQGVKNPTEFLEVIDSLCYSLIKAKNAGSLAKAGAGLPSEAVQWLCQAFTL 1148
 QY 1081 KLTFRRTVYVPLGSLRTAQQLSRKLPQTTLTLEAANPALPSDKTLLD 1132
 Db 1149 KLTFRRTVYVPLGSLRTAQQLSRKLPQTTLTLEAANPALPSDKTLLD 1200

RESULT 40
 US-10-325-810-612

Sequence 612, Application US/10325810
 Publication No. US20030204069A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 633

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/325,810

FILING DATE: 20-Dec-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/402,181

FILING DATE: 29-Sep-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ausehus, Scott L.

REGISTRATION NUMBER: 42,271

REFERENCE/DOCKET NUMBER: 015389-002620US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 612:

SEQUENCE CHARACTERISTICS:

LENGTH: 1200 amino acids

TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..1200
 OTHER INFORMATION: /note= "fusion protein composed of His6
 and Anti-Xpress tags", enterokinase
 cleavage site and full length hprt
 protein"
 SEQUENCE DESCRIPTION: SEQ ID NO: 612:
 US-10-325-810-612

Query Match 99.8%; Score 5952; DB 14; Length 1200;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRELISHRYEVLPATFVRRLGPOGMRVQRODPAAPALVAQCLVCPM 60
 Db 69 MPAPRCRAVRELISHRYEVLPATFVRRLGPOGMRVQRODPAAPALVAQCLVCPM 128
 QY 61 DARPPAAPSFRQVSCLELVAVYQRLCERGAKNVLAFGALLDGAAGPEAFTSVR 120
 Db 129 DARPPAAPSFRQVSCLELVAVYQRLCERGAKNVLAFGALLDGAAGPEAFTSVR 188
 QY 121 SYLPNTVDALRGSGAMGLLRVGDVYLHLLARCALFVIVAPSCAYQVGPPIYOLGA 180
 Db 189 SYLPNTVDALRGSGAMGLLRVGDVYLHLLARCALFVIVAPSCAYQVGPPIYOLGA 248
 QY 181 ATQAPPPHPSGPRRLCGERAMNHSVREAGVPLGLPAPGARRRGASRSILPEKPRR 240
 Db 249 ATQAPPPHPSGPRRLCGERAMNHSVREAGVPLGLPAPGARRRGASRSILPEKPRR 308
 QY 241 GAAPPERTPVQGGSMANPGRTRGSDRGFCVVSAPAPAEATSLFEGALSGTRHSHSVG 300
 Db 309 GAAPPERTPVQGGSMANPGRTRGSDRGFCVVSAPAPAEATSLFEGALSGTRHSHSVG 368
 QY 301 RQHHAGPSTSRPPPMWDTCPVYVAETKHFYSSGDEQQLRPSFLSLSPSLTGARRL 360
 Db 369 RQHHAGPSTSRPPPMWDTCPVYVAETKHFYSSGDEQQLRPSFLSLSPSLTGARRL 428
 QY 361 VETITLGRFPWPGTPRRRLPRLPORYWQMRPLFLELNNHAQCPYGVLLKTHCPRAAVT 420
 Db 429 VETITLGRFPWPGTPRRRLPRLPORYWQMRPLFLELNNHAQCPYGVLLKTHCPRAAVT 488
 QY 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVOLLROHSSWQYGFYRACLRVJPGGLMS 480
 Db 489 PAAGVCAREKPGQSVAAPEEDTDPRRLVOLLROHSSWQYGFYRACLRVJPGGLMS 548
 QY 481 RNNRRFPJNTKFFSLGKHAKLSLOELTWKMSVYDCAMLRSDVGCVPAAERLRREI 540
 Db 549 RNNRRFPJNTKFFSLGKHAKLSLOELTWKMSVYDCAMLRSDVGCVPAAERLRREI 608
 QY 541 LAKFLHMLMSYVVVGLASFFYVETTFQKRLFFYRSVWSKQSIIRKHLKRVQRE 600
 Db 609 LAKFLHMLMSYVVVGLASFFYVETTFQKRLFFYRSVWSKQSIIRKHLKRVQRE 668
 QY 601 LSEAEVRQHRERAPALLTSRLRFIPKPDGLRPIVMDVVGARTFRREKRAERLTSRYKA 660
 Db 669 LSEAEVRQHRERAPALLTSRLRFIPKPDGLRPIVMDVVGARTFRREKRAERLTSRYKA 728
 QY 661 LFSVUNTERARPPGLIGASVGLGDDIHRAMRTFVLRYAQPPEPLRYVKVDVGAAYTI 720
 Db 729 LFSVUNTERARPPGLIGASVGLGDDIHRAMRTFVLRYAQPPEPLRYVKVDVGAAYTI 788
 QY 721 PODRLTEVIASIKPQNTYCVRYAVVOKAAHGHRKAFKSHVSTLTLQPYMGQFVAHL 780
 Db 789 PODRLTEVIASIKPQNTYCVRYAVVOKAAHGHRKAFKSHVSTLTLQPYMGQFVAHL 848
 QY 781 QETSLPRLDAVVIQSSSLNEASSGLFDVFLRPMCHHAVRIGKSYVCCGIPQSSILSTL 840
 Db 849 QETSLPRLDAVVIQSSSLNEASSGLFDVFLRPMCHHAVRIGKSYVCCGIPQSSILSTL 908

QY 841 LCSLCYGMENKLFAGIRRDGILLRLVDDPELLVTBPLTHAKTELRTLVGVPEYGVYNL 900
DB 909 LCSLCYGMENKLFAGIRRDGILLRLVDDPELLVTBPLTHAKTELRTLVGVPEYGVYNL 968
QY 901 RKTIVNFPVEDEALGGTAFCMPAHGLFPMCGILLDTRTLEVOQSDYSSYARTSIRASYTF 960
DB 969 RKTIVNFPVEDEALGGTAFCMPAHGLFPMCGILLDTRTLEVOQSDYSSYARTSIRASLTF 1028
QY 961 NRGFKAGRMRRKLFQVLRKCHSLFLDQVNSIQTVCTNIYKILLQAYRFHACVLOLP 1020
DB 1029 NRGFKAGRMRRKLFQVLRKCHSLFLDQVNSIQTVCTNIYKILLQAYRFHACVLOLP 1088
QY 1021 FHOQVKNPTFPLRVISDPTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
DB 1089 FHOQVKNPTFPLRVISDPTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1148
QY 1081 KLTRHRVTYVPLIGSLRTAQOTLSRKLPGTTLTALBAANPALPSDFKTIID 1132
DB 1149 KLTRHRVTYVPLIGSLRTAQOTLSRKLPGTTLTALBAANPALPSDFKTIID 1200

Search completed: December 20, 2004, 16:04:54
Job time : 188 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 20, 2004, 15:50:35 ; Search time 26 Seconds

(without alignments)
4189,130 Million cell updates/sec

Title: US-08-974-584C-118

Perfect score: 5963
Sequence: 1 MPRAAPRCRAVRSILRSHYRE.....TALEMAANPALPSEDFKTIID 1132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 120 summaries

Database :
1: PIR.79:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5952	99.8	1132	2 T03844	telomerase catalyt
2	7177.5	12.0	1123	2 T51517	telomerase reverse
3	588.5	9.9	989	2 T03838	telomerase catalyt
4	388	6.5	1132	2 T31107	telomerase reverse
5	357	6.0	1117	2 T14891	telomerase (EC 2.7
6	355.5	6.0	884	2 S53396	telomerase catalyt
7	175.5	2.9	3530	2 A59266	unconventional myo
8	172.5	2.9	660	1 Q0BE3	BLRF1 protein - hu
9	142.5	2.4	1560	2 T00080	hypothetical prote
10	140.5	2.4	1892	2 T18314	hypothetical prote
11	140	2.3	1460	1 EDBE1F	immediate-early pr
12	139.5	2.3	3511	2 A59295	unconventional myo
13	139.5	2.3	552	2 F75311	ABC transporter, A
14	138.5	2.3	924	2 S27923	Gene Lf3 protein -
15	135	2.3	1356	1 C45219	N-methyl-D-asparta
16	134	2.2	606	2 G75302	otodine 5'-phosp
17	133	2.2	1106	2 JQ0405	hypothetical 119.5
18	132.5	2.2	946	2 JQ0781	inositol 1,4,5-tri
19	131.5	2.2	1184	2 G01763	atrophin-1 - human
20	131	2.2	916	2 T00396	reverse transcript
21	131	2.2	1446	1 A4534	immediate-early pr
22	130.5	2.2	1184	2 A50832	atrophin-1 - human
23	130.5	2.2	2715	2 T13049	eyelid - fruit fly
24	130	2.2	1067	2 T18156	pol protein - silk
25	129.5	2.2	383	2 S32975	gene BCRF2 protein
26	129	2.2	403	2 S52796	prp2 protein - hu
27	129	2.2	403	2 S55543	RNA-directed DNA p
28	128.5	2.2	628	2 S01955	hypothetical prote
29	128	2.1	376	2 C75580	adenine deaminase-

30	128	2.1	1776	2 G86280	protein T5B21.13 (
31	127.5	2.1	1048	2 T31425	C-terminal domain
32	127	2.1	260	2 S22373	proline-rich prote
33	127	2.1	505	2 S72273	actin-depolymerizi
34	127	2.1	580	2 T43481	probable mucin DKF
35	127	2.1	847	1 A53800	mixed-lineage proc
36	127	2.1	862	2 T46289	hypothetical prote
37	127	2.1	1039	2 T35878	hypothetical prote
38	126.5	2.1	603	2 H75272	probable nucleic a
39	126	2.1	330	2 B98119	transposase, uncha
40	125.5	2.1	574	2 T43556	Wiskott-Aldrich sy
41	125.5	2.1	574	2 T38819	viral proteinase -
42	125	2.1	522	2 S52216	tenascin Y precurs
43	125	2.1	1914	2 T42635	immediate-early pr
44	124	2.1	1298	1 EDBE75	N-methyl-D-asparta
45	124	2.1	1323	2 S27224	hypothetical prote
46	123.5	2.1	381	2 S16506	synapsin Ia - rat
47	123.5	2.1	704	2 A30411	68.6K capsid prote
48	123	2.1	646	1 W2BEC8	salivary proline-r
49	122.5	2.1	310	1 P1HUSD	hypothetical prote
50	122.5	2.1	635	2 F75477	hypothetical prote
51	122.5	2.1	915	2 T12526	otogelin - mouse
52	122.5	2.1	2910	2 T42214	MHC class III hist
53	122	2.0	1870	2 S37671	hydroxyproline-ric
54	121.5	2.0	620	2 A30673	guanylate cyclase
55	121.5	2.0	1102	2 UH0717	period protein PBR
56	121.5	2.0	1257	2 T13957	MHC class III hist
57	121	2.0	2142	2 B35098	licheninase (EC 3.
58	120.5	2.0	335	2 T05722	probable proline-r
59	120.5	2.0	891	2 G84693	ataxin-2 - mouse
60	120.5	2.0	1285	2 T14171	probable membrane
61	120	2.0	509	2 T34871	BOLE1 protein - hu
62	120	2.0	1239	1 Q0BE10	DNA-directed RNA p
63	120	2.0	1859	1 A34092	DNA-directed RNA p
64	120	2.0	1862	2 T39959	MHC class III hist
65	120	2.0	1872	2 S36152	hypothetical prote
66	120	2.0	2793	2 B90784	hypothetical prote
67	120	2.0	2806	2 D86644	hypothetical prote
68	119.5	2.0	361	2 T12543	immediate-early pr
69	119.5	2.0	775	1 EDBE11	transcription fact
70	119	2.0	639	2 G02919	FK506 polyketide s
71	119	2.0	7576	2 T17428	hypothetical prote
72	118.5	2.0	628	2 S19150	hypothetical prote
73	118.5	2.0	751	2 D98320	N-chimerin homolog
74	118.5	2.0	903	2 T00705	probable multi-dom
75	118.5	2.0	1334	2 T50568	fatty-acid synthas
76	118.5	2.0	2796	2 UC7743	Ula6 protein - hum
77	118.5	2.0	3164	1 WMBEH6	CW17R protein - mo
78	118	2.0	548	2 S52735	probable non-ribos
79	118	2.0	2352	2 C83229	hypothetical prote
80	117.5	2.0	312	2 A51183	probable serine/th
81	117.5	2.0	576	2 T36729	hypothetical prote
82	117.5	2.0	1222	2 T22490	collagen alpha 1(V
83	117.5	2.0	2944	2 A54849	proline-rich prote
84	117	2.0	300	2 S19560	F02569.2 protein (
85	117	2.0	512	2 B54337	probable integral
86	117	2.0	684	2 T36771	synapsin I - rat
87	117	2.0	1467	2 A25704	larophilin-1, bra
88	117	2.0	1472	2 T18413	Ula3 protein - hu
89	117	2.0	434	1 WMBE73	probable oxidoredu
90	116.5	2.0	1174	2 B85740	hairless protein -
91	116.5	2.0	1174	2 H90878	hypothetical prote
92	116.5	2.0	1182	2 T48378	proline-rich prote
93	115.5	1.9	1322	2 T23149	proline-rich prote
94	115.5	1.9	301	2 S10889	50KD proline rich
95	115	1.9	309	2 T35474	membrane transloca
96	115	1.9	456	2 G47096	probable DNA-bindi
97	115	1.9	753	2 G87178	DNA-binding protei
98	115	1.9	767	2 S41479	protein-tyrosine k
99	115	1.9	1091	2 S33596	DNA-binding protei
100	115	1.9	1091	2 S33596	DNA-binding protei
101	115	1.9	1091	2 S33596	DNA-binding protei
102	115	1.9	2282	2 T42717	DNA-binding protei

103 114.5 1.9 256 2 A60533 tumor-associated a
104 114.5 1.9 496 2 S26402 homeotic protein H
105 114.5 1.9 706 2 E30411 synapsin Ia - bovi
106 114.5 1.9 1069 2 S27922 nuclear antigen EB
107 114.5 1.9 1174 2 E64888 probable pyruvate
108 114.5 1.9 1541 2 T02831 AAA protein L4171.
109 114 1.9 604 2 T35866 hypothetical prote
110 114 1.9 990 2 T14756 hypothetical prote
111 114 1.9 1696 2 T00057 hypothetical prote
112 113.5 1.9 295 2 B48013 proline-rich prote
113 113.5 1.9 649 2 A35816 transcription regu
114 113.5 1.9 1001 2 T50914 hypothetical membr
115 113.5 1.9 1085 2 T03531 cohn protein homol
116 113.5 1.9 1400 2 T31555 hypothetical prote
117 113.5 1.9 2176 2 T13806 coucan gene protei
118 113 1.9 543 1 JC4070 protein kinase (EC
119 113 1.9 1323 1 I78557 N-methyl-D-asparta
120 112.5 1.9 699 2 C43674 US4 protein - huma

ALIGNMENTS

RESULT 1
T03844
telomerase catalytic chain - human
N:Alternate names: telomerase reverse transcriptase
C:Species: Homo sapiens (man)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #ext_change 09-Jul-2004
C:Accession: T03844
R:Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J.
S:Science 277, 955-959, 1997
A:Title: Telomerase catalytic subunit homologs from fission yeast and human.
A:Reference number: Z15111, PMID:97400623, PMID:92552327
A:Accession: T03844
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1132 <NA>
A:Cross-references: UNIPROT:Q14746; EMBL:AF015950; NID:Q2330016; PIDN:AACS1672.1; PID:92
A:Experimental source: kidney
C:Genetics:
A:Gene: TRT
A:Map position: 5p

Query Match 99.8%; Score 5952; DB 2; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 1 MPRAPRCRAVRSILRSHYREVLPATFVRRLGPQGRVQRGDPAFALVAQCUCVPM 60
1 MPRAPRCRAVRSILRSHYREVLPATFVRRLGPQGRVQRGDPAFALVAQCUCVPM 60
QY 1 MPRAPRCRAVRSILRSHYREVLPATFVRRLGPQGRVQRGDPAFALVAQCUCVPM 60
DB 61 DARRPRAAPSFRVSCLELVARVLOLTCERGAKNVLAFFGALDAGSGPPEATTSVR 120
61 DARRPRAAPSFRVSCLELVARVLOLTCERGAKNVLAFFGALDAGSGPPEATTSVR 120
QY 121 SYPLNTVTDALRSGAGWILLRVRGDDVIVHLLARCAFLVVAQCAVQCCPPIYQGA 180
121 SYPLNTVTDALRSGAGWILLRVRGDDVIVHLLARCAFLVVAQCAVQCCPPIYQGA 180
DB 121 SYPLNTVTDALRSGAGWILLRVRGDDVIVHLLARCAFLVVAQCAVQCCPPIYQGA 180
121 SYPLNTVTDALRSGAGWILLRVRGDDVIVHLLARCAFLVVAQCAVQCCPPIYQGA 180
QY 181 ATGAPRPPASGRRRLGCEERAMNSVREAGVPLGIPAPGARRGSGASRSRLPLKRRR 240
181 ATGAPRPPASGRRRLGCEERAMNSVREAGVPLGIPAPGARRGSGASRSRLPLKRRR 240
DB 181 ATGAPRPPASGRRRLGCEERAMNSVREAGVPLGIPAPGARRGSGASRSRLPLKRRR 240
181 ATGAPRPPASGRRRLGCEERAMNSVREAGVPLGIPAPGARRGSGASRSRLPLKRRR 240
QY 241 GAAPBEERTPVGGGWAHFGRTGSDRGFCVVSPPAPAEATSLGALSGTRHSPSVG 300
241 GAAPBEERTPVGGGWAHFGRTGSDRGFCVVSPPAPAEATSLGALSGTRHSPSVG 300
DB 241 GAAPBEERTPVGGGWAHFGRTGSDRGFCVVSPPAPAEATSLGALSGTRHSPSVG 300
241 GAAPBEERTPVGGGWAHFGRTGSDRGFCVVSPPAPAEATSLGALSGTRHSPSVG 300
QY 301 RQNHAPRPTSRPRRWDTPCPRVYAETGHLVSSGDEQLRPSLISLRSLGARLL 360
301 RQNHAPRPTSRPRRWDTPCPRVYAETGHLVSSGDEQLRPSLISLRSLGARLL 360
DB 301 RQNHAPRPTSRPRRWDTPCPRVYAETGHLVSSGDEQLRPSLISLRSLGARLL 360
301 RQNHAPRPTSRPRRWDTPCPRVYAETGHLVSSGDEQLRPSLISLRSLGARLL 360
QY 361 VETIFGSRPMWGTFRRLPLRQRYQWRPLFLELLGNHACPPYGLTKHCPRAAVT 420

DB 361 VETIFGSRPMWGTFRRLPLRQRYQWRPLFLELLGNHACPPYGLTKHCPRAAVT 420
QY 421 PAAGVCAERKPOGSAVAPEEDTDPRLVOLLROHSPMOVGFVACLRRLVPPGMS 480
421 PAAGVCAERKPOGSAVAPEEDTDPRLVOLLROHSPMOVGFVACLRRLVPPGMS 480
DB 421 PAAGVCAERKPOGSAVAPEEDTDPRLVOLLROHSPMOVGFVACLRRLVPPGMS 480
421 PAAGVCAERKPOGSAVAPEEDTDPRLVOLLROHSPMOVGFVACLRRLVPPGMS 480
QY 481 RHNERRLNTKXKFSISGKAKLSLOELTWKMSVRCAMLRSPGVGCVAARHRLREEL 540
481 RHNERRLNTKXKFSISGKAKLSLOELTWKMSVRCAMLRSPGVGCVAARHRLREEL 540
DB 481 RHNERRLNTKXKFSISGKAKLSLOELTWKMSVRCAMLRSPGVGCVAARHRLREEL 540
481 RHNERRLNTKXKFSISGKAKLSLOELTWKMSVRCAMLRSPGVGCVAARHRLREEL 540
QY 541 LAKELHLMGVYVVELLSFFVYETTFQKNRLFFPRSPWSKLQSIGIRHILKRYOLRE 600
541 LAKELHLMGVYVVELLSFFVYETTFQKNRLFFPRSPWSKLQSIGIRHILKRYOLRE 600
DB 541 LAKELHLMGVYVVELLSFFVYETTFQKNRLFFPRSPWSKLQSIGIRHILKRYOLRE 600
541 LAKELHLMGVYVVELLSFFVYETTFQKNRLFFPRSPWSKLQSIGIRHILKRYOLRE 600
QY 601 LSEAEVQHEEAPALITSLRLPIPKPDGRLPVNDVYVGANTFRRERAEHLTERVVA 660
601 LSEAEVQHEEAPALITSLRLPIPKPDGRLPVNDVYVGANTFRRERAEHLTERVVA 660
DB 601 LSEAEVQHEEAPALITSLRLPIPKPDGRLPVNDVYVGANTFRRERAEHLTERVVA 660
601 LSEAEVQHEEAPALITSLRLPIPKPDGRLPVNDVYVGANTFRRERAEHLTERVVA 660
QY 661 LFSVLANERARPPGLGASVLDJHRAARTFVLVRAQDPEPELYFVKVDGTGAYDTI 720
661 LFSVLANERARPPGLGASVLDJHRAARTFVLVRAQDPEPELYFVKVDGTGAYDTI 720
DB 661 LFSVLANERARPPGLGASVLDJHRAARTFVLVRAQDPEPELYFVKVDGTGAYDTI 720
661 LFSVLANERARPPGLGASVLDJHRAARTFVLVRAQDPEPELYFVKVDGTGAYDTI 720
QY 721 PODELFEVIAIIPQNTYCVRRYAVVQAAHGHVKAFFKSHVSTLTDLPYMRQFVAHL 780
721 PODELFEVIAIIPQNTYCVRRYAVVQAAHGHVKAFFKSHVSTLTDLPYMRQFVAHL 780
DB 721 PODELFEVIAIIPQNTYCVRRYAVVQAAHGHVKAFFKSHVSTLTDLPYMRQFVAHL 780
721 PODELFEVIAIIPQNTYCVRRYAVVQAAHGHVKAFFKSHVSTLTDLPYMRQFVAHL 780
QY 781 QETSPLDVAVIOSSSLNASSGLDFVRFRECHHARVIRGSAVQCGGIPGSLSTL 840
781 QETSPLDVAVIOSSSLNASSGLDFVRFRECHHARVIRGSAVQCGGIPGSLSTL 840
DB 781 QETSPLDVAVIOSSSLNASSGLDFVRFRECHHARVIRGSAVQCGGIPGSLSTL 840
781 QETSPLDVAVIOSSSLNASSGLDFVRFRECHHARVIRGSAVQCGGIPGSLSTL 840
QY 841 LCSIQYDMDENKLFAGIRRDGILLRLVDDFLVTPHILTAKFLRLTVRGVEYGCVNL 900
841 LCSIQYDMDENKLFAGIRRDGILLRLVDDFLVTPHILTAKFLRLTVRGVEYGCVNL 900
DB 841 LCSIQYDMDENKLFAGIRRDGILLRLVDDFLVTPHILTAKFLRLTVRGVEYGCVNL 900
841 LCSIQYDMDENKLFAGIRRDGILLRLVDDFLVTPHILTAKFLRLTVRGVEYGCVNL 900
QY 901 RKTYYNFPVDEALGTAFAVQPAHGLFPVCGILLDTLRLVQSDVSSAARISIRSLTF 960
901 RKTYYNFPVDEALGTAFAVQPAHGLFPVCGILLDTLRLVQSDVSSAARISIRSLTF 960
DB 901 RKTYYNFPVDEALGTAFAVQPAHGLFPVCGILLDTLRLVQSDVSSAARISIRSLTF 960
901 RKTYYNFPVDEALGTAFAVQPAHGLFPVCGILLDTLRLVQSDVSSAARISIRSLTF 960
QY 961 NRGFKAGNRKRLFGVLRKCHSLFLDLQVNSLQVCTNINIKILLQARFFHACVQLP 1020
961 NRGFKAGNRKRLFGVLRKCHSLFLDLQVNSLQVCTNINIKILLQARFFHACVQLP 1020
DB 961 NRGFKAGNRKRLFGVLRKCHSLFLDLQVNSLQVCTNINIKILLQARFFHACVQLP 1020
961 NRGFKAGNRKRLFGVLRKCHSLFLDLQVNSLQVCTNINIKILLQARFFHACVQLP 1020
QY 1021 FHOQWKNPFFLRVISTDASISLILKAKNAGMSIGAKGAGPLSEAVQWLCHQAFLL 1080
1021 FHOQWKNPFFLRVISTDASISLILKAKNAGMSIGAKGAGPLSEAVQWLCHQAFLL 1080
DB 1021 FHOQWKNPFFLRVISTDASISLILKAKNAGMSIGAKGAGPLSEAVQWLCHQAFLL 1080
1021 FHOQWKNPFFLRVISTDASISLILKAKNAGMSIGAKGAGPLSEAVQWLCHQAFLL 1080
QY 1081 KLRHRRTVYPLIGSLRTAQTOLSRKLPGLTTLALBAANPALPSPDKTILD 1132
1081 KLRHRRTVYPLIGSLRTAQTOLSRKLPGLTTLALBAANPALPSPDKTILD 1132
DB 1081 KLRHRRTVYPLIGSLRTAQTOLSRKLPGLTTLALBAANPALPSPDKTILD 1132
1081 KLRHRRTVYPLIGSLRTAQTOLSRKLPGLTTLALBAANPALPSPDKTILD 1132

RESULT 2
T51517
telomerase reverse transcriptase - Arabidopsis thaliana
N:Alternate names: protein F5E19_190
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #ext_change 09-Jul-2004
C:Accession: T51517
R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew
submitted to the Protein Sequence Database, August 2000
A:Reference number: Z25394
A:Accession: T51517
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1123 <SAT>
A:Cross-references: UNIPROT:Q9SPU7; EMBL:AL391147
A:Experimental source: cultivar Columbia; BAC clone F5E19
C:Genetics:
A:Map position: 5
A:Introns: 100/3; 125/3; 147/3; 185/1; 300/3; 325/1; 369/2; 414/3; 765/3; 942/2; 1033/2
A>Note: F5E19_190

Query Match 12.0%; Score 717.5; DB 2; Length 1123;
 Best Local Similarity 23.7%; Pred. No. 9e-41;
 Matches 293; Conservative 199; Mismatches 512; Indels 233; Gaps 39;

1 MPKPRKRVKPEILKRLFGNARNLNDALVDLIPRNIGPQCRGCGCCGSSDYPAL 60
 1 MPRKPRKRVKPEILKRLFGNARNLNDALVDLIPRNIGPQCRGCGCCGSSDYPAL 60

39 VQGDPAFPAALVAQCLVCPMDARPPPAAPSPFQVSCLELVAVLQRL---CEGAKX 95
 61 LRSDDPIHYKRLIHRCFV-VLHEQTPELIDPSPTMSQREIVERTIEMQSGCD--CQX 117

96 VLAQFALLDGAAGPEAFPTTSRSYLPNTVTDALRGSGAMGILLRRVGDVVLHLAR 155
 118 VICARYKYOS-----SPILBLT-SSSWFELKRGVHDVWVYLQO 159

156 CALFVLVAPCAVQVCGPPYVQGAAT-----QARPPHASPGRRLGGERAMNSVRE 209
 160 TSIFLPLGKHQGVSGPPLCIKHKRTLSVHNNKRDNDVQPTKQMLSAVDQPKD 219

210 AGVPLGLPAG---ARRGGSASRLPLPKRPRGA-----APEPRTVGGGMA 257
 220 DSATI-TPIVEGDVQHRKKTTRSRITLKRRKQKQKVFQVDCNAPCITP----- 271

258 HPGRTGRPSDRGFCVSPAPPAEATLFGALSGTRASHSPVGRQHNHAGPSTSRPRPW 317
 272 ---STNGKVGSTG-----NDENMLHIGINSGLDFPKQAKQ----- 303

318 DTPCPVPAATKHELYS-SCDKEQLRPSFLLSRLPSLTGARLVETITFGSPMPMGTP 376
 304 ---VKENKMKFGLSETYSVIPNHLIKTLRPPCSKLLMHIIFEEVWVSTPS 356

377 RRLPLRPO---RYWQMRPLFLELGNHACQPCVILKTHCP-----LRAPVPAAG 424
 357 HGKNCNGSSGICLYHSLKSLKILGKTSSHLKMLDRCPCVLLLOEDALSGTTSSQS 416

425 VCAREK---PQGSVAA---PEEEDTPRLVQLRQHSPPQVYGFVACLRVLP 476
 417 --BRQKADKLPHGSSSSQTKPKCPVSEERKL-----YCTNQVVSFIWALCRYIVPS 468

477 LMGSRHRRFLRTKFTISLGGAKLSLOELTMKMSVRCAMLRSPGVCYPAEHL 536
 469 LIGTHOMRLKRIKIANFVSRRRNEKCTVQPLHKVSPFPFARKE--LCCWVNGHEL 526

537 REE-----ILAKFLHMSVYVVELRSFFVETETPQKRLFFPYRPSVSKLSIG 588
 527 QSESIRSTQMLCTKWTSMFLFLEIVKLVHFNFYATESQGRNLITYYRRKSMERLISKE 586

589 IROHLKRVQRLSEAEVVRQREARPAALTSRLRFTPKDGLRPIYNDYVVGARTFERE 648
 587 ISALADQVYLVDDAEASERRK-----LSKRFELPKANGVMVD-----FSSS 630

649 KRAERLTSRKALFESVNYERARRPGLGASVIGLDDIHAMRTFVLRYADQPP-PELY 707
 631 SRQSL-----RDTHAVIKDQIKKEPDVSGSVDFDHDFFYNLCRPIYLHRSQGEPLPY 686

708 FVKAVDTGAYDTTPQDRLEVIASIKPONTYCVRAVAVQAKAHG-----VRRAFKS 761
 687 FVAVADVFAKDSVDQGLLHVIOFLKDE--YILNRCRLVCCGRSMWVKILVSSDKKS 744

762 HVSFTLIDQYMGQFVAHLOETSPRLDAVYIEQSSINEMASGLFDVFLRFMHAVRIR 821
 745 NPSRFTSTVYNA-----LQ-----STVDDKGENRVRKQDLWMTGMMLKNNMLQLD 792

822 GKSYVQCGQIPQGISLSTLCSLCYGDMEKTLFAGI-----RRDGL----- 862
 793 KSFYVQIAGIPQGRHSLSLCCFYGHLERTLILYFLSEASKOVSSKEGSEBELLIPTS 852

863 --LIRLVDDDLVTLPHLTHAKTFLRTLVGRVPEYGVVNIARKYVNVFPVDE----- 912
 853 YKLRFITDDVLFVSTSDQASSFYHRLKHGFKYDNCMNMTKCFINFEDEKERRCSNNK 912

913 --ALGTAFAVQMPAHGLFPWCGILLDTRTLEVOQSDYSSYARTIRASVTEINRGFKAGRN 970

913 FVGDNGVDFVR-----WTGLLINSRTFEQVDYTYTSLGHSISTSVAMQNPVNL 964
 971 RKLFGVRLKCHSLFLDLQVNSLOTVCTNIYKILLQVAFHACVLDLPFHQVWK-NP 1029
 965 ROKLCYFLVPKCHPLFLFNSNINSGEIVRLNITYQIFLLAMKHFHCYVEV---SRFKLHP 1021

1030 TFFLRVSDTASLCYSITKAKNAGMSLGAK-GAAGPLSEAVQVIMCHOAFLIKTRHRT 1088
 1022 CTLFFKFIITVRYMYRLNRVRRINTGSSFRPVLYKYEVEVIMGLDAYIQVLKKNSR 1081

1089 YVPLGSLRTAQTO--LSRKLPGTTLTLEAANDAL 1123
 1082 YMLLITLKSLSKSLSQSLQSSLELRYATDRSNSSL 1118

RESULT 3
 T03838
 telomerase catalytic chain - fission yeast (Schizosaccharomyces pombe)
 N:Alternate names: telomerase reverse transcriptase 1
 C:Species: Schizosaccharomyces pombe
 C:date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T03838; T03839; T40085
 R:Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J.;
 Science 277, 955-959, 1997
 A:Title: Telomerase catalytic subunit homologs from fission yeast and human.
 A:Reference number: Z1511; MUID:97400623; PMID:9252327
 A:Accession: T03838
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-989 <NAK>
 A:Cross-references: UNIPROT:O13339; EMBL:AF015783; NID:g2340167; PIDN:AAC49803.1; PID:g2

A:Experimental source: strain 972h(-)
 A:Accession: T03839
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-524,526-989 <LYN>
 A:Cross-references: EMBL:AF015783; NID:g2340167; PIDN:AAC49802.1; PID:g2340168
 R:Lyne, M.; Raftery, M.A.; Barrett, B.G.; Volckaert, G.
 Submitted to the EMBL Data Library, March 1998
 A:Reference number: Z21904
 A:Accession: T40085
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-524,526-989 <LYN>
 A:Cross-references: EMBL:AF015783; NID:g2340167; PIDN:AAC49802.1; PID:g2340168
 A:Experimental source: strain 972h-, cosmid c29A3
 C:Genetics:
 A:Gene: trt1, SPBC29A3.14c
 A:Map position: 2
 A:Interon: 86/3; 113/3; 153/2; 241/1; 372/1; 395/3; 485/3; 524/3; 582/2; 644/1; 693/3; 76

Query Match 9.9%; Score 588.5; DB 2; Length 989;
 Best Local Similarity 22.2%; Pred. No. 4.9e-32;
 Matches 237; Conservative 202; Mismatches 381; Indels 247; Gaps 42;

5 PCRAVRSLRSHYREVLPLATFVRLPQGRVLRQSDPAFPAALVAQCT----- 55
 7 PKSRILR-FLNQVYYLCTINDY-----QVLRSSPASVSNICERLRSVDQTSFS 57

56 -----VCPMDARPPPAAPSPFQVSCLELVAVLQRL---ACNVLAFFAL-LD 105
 58 IFLHSTVGFDSKDEGV-QFSPPKCSQSELIANVKKMFESFERRRNLMMKGFSMNHE 116

106 GARGPPPAFTTSVASYLPNTVTDALRGSGAMGILLRREVGDVVLHLARCALFVLVAPS 165
 117 DFRAMHNVGVQNDLVSTFPNVLISILE-SKNWQILLLEIGSDAHMYLLSKSIFBALND 175

166 CAYQVCGPPLVQLGAAATGARPPHASPGRRLGGERAMNSVREAGVPLGLPAGARRG 225
 176 NYLQISGIPLFR-----NNVFEEV-----SKRKX 200

Best Local Similarity 20.1%; Pred. No. 3.9e-16;
Matches 192; Conservative 160; Mismatches 369; Indels 234; Gaps 35;

QY 322 PNYAETKHLHYSSGDEQRLPSFLSSLPSTLGARLVETFLGSRPMPGTPRLRLP 381
D 239 PGVF-KSSFNYS-----EIKKGQFVIOEKIQGRQ-----FINSDKIKPHPQITIK 286
QY 382 -LPORF-----WQWRPLFLS-----ILGNHAQCPYGLTKHCPPLRAAVTAAVCAAR 428
D 287 KTLKEXQSNFSCQERDLFLETETKIVQNFHNNINNYLLKFCFL----- 333
QY 429 EKQGVAADEEDTDRRLVQLRQHS-----SPWQVGYFVACL 469
D 334 -----PENQSLKSVKQIVQSENKANOQSCENTFNSLYDTETSLYKQITNFRQIT 384
QY 470 RLIVPPGLMGRSHNERFLNTKKETISLGHAKLISQELTWKMSVDCAMRLRSPGVGV 529
D 385 QNCVFNOLLGKK-NFKVFLKLYEFVQMKRFENOKVDYICMDVDPVWEF-----V 435
QY 530 PAAEHRL-----REELAKFLHMLMSVYVELRSPFYVTEFTFOKRLFFYRPSV 580
D 436 DLAKQKFTQKRYISDRKILGLDILVPIIKVIVPLRYNFYTEKHEGSGQIFYYRKP 495
QY 581 W-----SKQSIGI-RQHAKYQRLSEAEVQRHREARPALTLRLFFIPKPDGLRIYVM 636
D 496 WKLVSKLTVLKEENLEKEEKLIPEDSFQKYPQ-----GKLRIPKKGSRPIM-- 546
QY 637 DYVVGATFRERKAERLTSRYKALFS-----VLYNERARRPGLLGASVGLDIDHRAWT 692
D 547 -----TFLRKQKQXIKILNQLNQLMDSQLVFRNLKMDLGQKIGSVFNKQISKEPQ 599
QY 693 FVLRVRAQDPPELYEVKVDVTGAYDTIPQDLTEVIASITIKQNTYCVRRVAVQKAAH 752
D 600 FIEKWKXKG-RPOLYVYVTLIDIKKCYSDIDQMKLNFENQSDLLQDTYFIKYLDFQRNR 658
QY 753 GHVKAFAKSHVSTLTDQ-----PYV-----ROFVAHIOE----- 782
D 659 PLIQIQOTNNLNSAMEIEBEKINKKPPKMDNINPFYFNLERQIAYSLYDDDDQLQNG 718
QY 783 -----TSLRDVAVIEQSSSLNEASGLFDFELRPMCHAVRIRKASYVQCQIGIPQSSILS 838
D 719 FKEIQSDRPFIYINQKPRCITKDIIHMLKHAISQNVNISFNKVPFRQKGIPOGLNIS 778
QY 839 TLLCSLCYGMENKLFPIGRD-----GLLRVDDFLVTPHILHATFRLTYRGV 891
D 779 GVLCSEFYGLEEBEYTOFLKNAQVNGSINLLMELTDDYLFISDQOMALNTLVQLOCA 838
QY 892 PEVGVVNLKRTVNV--FVVEDEALGTAFCVMPAHGLPWCGLLDTRTLLEVQSDYSY 949
D 839 NNGGFMNDOKITTNFQPOEDYNL--BHFKISVQNECQWIKSISDMNTLEIK--SLQ 892
QY 950 ARPSIRASVTFRNGFAGANRRKLFGLVRLKCHSLFLDI-----QVNSLOTVCNTNY 1002
D 893 KQIQOEINQITINVAISI-KNLKSQLNKRLR--SLFNQIIDIYFNPNINSFEGLCROY 947
QY 1003 ---KILLQAYRPHACVLOL-----PFHQVWK--NPTFFLRVSDTAS-----LCY- 1044
D 948 HHSKATYMKFYPMYTKLFQIDLKSKQYSVQYKENTNENFLDILYVYVEDYCKLCTL 1007
QY 1045 -----SLKAKNAGSLGAKAGAPLPSEAVQWMLCHA 1077
D 1008 QFEDAINSNIKEIFKNLYSWIMMDIIVSYLKKKKQ-----FKGYLNLK----- 1050
QY 1078 FLKLTIRHRTVYPL-LGSLRTAOTOSRLPGTTLTALAAANPALPSDFKITL 1131
D 1051 -LQIKRSRFFTYLKEGCKSLQILISQOKYQNLNKELEAFIDLNLDIDIKTLI 1104

RESULT 6
S53396
telomerase catalytic chain EST2 - Yeast (Saccharomyces cerevisiae)
N:Alternate names: protein L8543.12; protein YLR318w
C:Species: Saccharomyces cerevisiae

C>Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C/Accession: S53396

R/DU: Z.
Submitted to the EMBL Data Library, February 1995
A:Description: The sequence of S. cerevisiae cosmid 8543.

A:Reference number: S53390
A:Accession: S53396

A:Molecule type: DNA
A:Residues: 1-884 <DUZ>

A:Cross-references: UNIPROT:Q06163; EMBL:U20618; NID:q2258165; PTD:g662136; GSPDB:GN00011;
A:Experimental source: strain S288C (AB972)

A:Gene: SGD:EST2; MIPS:YLR318w
A:Cross-references: SGD:S0004310; MIPS:YLR318w

A:Map position: 128

Query Match 6.0%; Score 355.5; DB 2; Length 884;
Best Local Similarity 22.1%; Pred. No. 3.6e-16;
Matches 167; Conservative 127; Mismatches 309; Indels 151; Gaps 28;

QY 329 KHFILSSGDKQQLRPS--FLSSLRPSLTGARLV---ETIFLGRPMPGTPRLRLP 383
D 165 KQFLH-----KUNINSSFFPYSKILPSSSSIKKLTDLREALF-----PTNLVATP 230
QY 384 QRYWQMRPLFLS-ILGNHAQCPYGLTKHCPPLRAAVTAAVCAARKEKQGVAAPEED 442
D 231 QRLKVRINLTQKLLKHKRLNLYSILNSICP-----PLEGTVL----- 269
QY 443 TDRRLVQLRQHSAPWQVGVFVACRLVPPGLMGRSHNERFLRTRTKETISLGKIAK 502
D 270 ---DLSHLSQ-SKEKVLKFIYIYLOKLPQEMFGSKKQKGIKYNLNLISPLNGY 324
QY 503 LSLQELTWKMSVDCAMLRSPGVGVPAAEHRLR--EELAKFLHMLMSVYVELLRSE 560
D 325 LPFDLLKLRKLRKDRWL-----FISDIWFTGHNEENLNQALICFISLWFLQRLIKITGF 380
QY 561 FYVTETTFQKRLFFYRPSVSKQSIGIRQHLKRVQRLSEAEV-RQHREARPALTL 618
D 381 FYCTEIS-STVTIVYFRHDVNRKLTIPRIYVEFYKY---LVENNVCNHSYLSNENH 435
QY 619 SLRFLIPKPDGLRPVNDYVY-----GARTFRERKAERLTSRYKALFSLVLYERARR 672
D 436 SKMRTIPKKS-----NNEFRILAIPCRGADBEETIYKHNKVAIOPTQKILEYLRKR 489
QY 673 PELLGASVGLDIDHRAKRTVLRV--RAQDPPELYEVKVDVTGAYDTIPQDLTEVIA 730
D 490 PLSF-TKIYSPLOADR-KEFKORLLKFNVLPELYFMKFDVKSQYSDISPRKCMRLIK 548
QY 731 SLIKPQNTYCVRRVAVQKAAHGHVKAFAKSHVSTLTDLPQYMRQFVAHLOETSPLRDAV 790
D 549 DAKNENGFYRSQFFN--TNTGYLKF-NVVAASRPKRY-----EL 589
QY 791 VIEQSSSLNEASGLFDFELRPMCHAVRIRKASYVQCQIGIPQSSILSTLCSLCYGM 849
D 580 YIDNRYTALNSQDVINVENMEIEFTALMVEDCKYIRBDEGDFQSSSAPATVDLYDDIL 649
QY 850 ---ENKLFAGIRRDGLLALVDVDFLLVPHLTHATFRLTYRGVPEYGVVNLKRTV-VN 906
D 650 EYSEFKAPSPQDITLLADPFLISTDQOCVINIKKLAMGFGQKYNKAKNRDXILAVS 709
QY 907 FVVEDEALGTAFCVMPAHGLPWCGLLDTRTLLEVQSDYSYARTSIRASVTFRNGFKA 966
D 710 SQSDDDT-----YIOFCAMHI FVEKELEWGHSSSTNNFHIRS-----KS 748
QY 967 GANMRKRLFVYLRKCHSLFLDQVNSLOTVCNTN-----YK-----ILLQCA 1009
D 749 SKGIFRSILAFNTRISYKTIIDTNLNSNTVLMQDHYVKNISBQYKSAFQDLSINTVQN 808
QY 1010 YRFHACVQLPFFHQVWKMPFFFLRVISDTSALC 1043
D 809 MQFH-----SFLQRIIEMTVSGC 826

RESULT 7

A59266
 unconventional myosin-15 - human
 C/Species: Homo sapiens (man)
 C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
 C/Accession: A59266
 R/Liang, Y.; Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probst, F.J.; Barber, T.D.; Man, T.B.; Friedell, R.A.
 Genomics 61, 243-258, 1999
 A/Title: Characterization of the human and mouse unconventional myosin XV genes responsible for non-syndromic deafness
 A/Reference number: A59266; M0ID:20021762; PMID:10552926
 A/Accession: A59266
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-3530 <LIR>
 A/Cross-references: UNIPROT:Q9UKX7; GB:AF144094; NID:66224682; PIDN:AA05903.1; PID:66224682-1867/Domain: myosin motor domain homology <MMO>

Query Match 2.9%; Score 175.5; DB 2; Length 3530;
 Best Local Similarity 20.4%; Pred. No. 0.0048;
 Matches 260; Conservative 145; Mismatches 394; Indels 475; Gaps 67;

107 ARGSPPEAFETTS-----VRSYLP-----NTVTALRGSGAWG 138
 2313 SRGSPKVVGNWSDSDMSTPQPOEHWKVLSDSDGSSHNQDGTNETEAKQGT ATH 2371
 139 LLRRVGDVVLHLLARCALFVLVAP-----SCAYQYCGPPLYQLGAA----- 181
 2372 QESDSLGEPAVPHKGLDCLDFPVLVSGDADLEKFTALAYRMKGGGPGGSSSGTE 2431
 182 -QVAPPP--PHASGRRLGGERAMNHSVRAGV---PLGIPAGARRRGSSAS-RSLP 233
 2432 DTPRRPEPEKPIPGLDASTLALQCAFH--KQAVLLARGMTLQAVALLQOPLSALRLRP 2489
 234 LPRPRRGAPEPEPPTPQSGMAHPRGTRGSDGFCVSPAPAEATSLGALSGTR 293
 2490 AEKPP---APEAQPTSVGTGPAPKPVLLR-----ATPKPLAA----- 2524
 294 HSHPSVGRHHAHPSTSPRRPMDTPEPVYA-----ETKHLPLSGDKEQLRPSFL 347
 2525 -----PLAKAPRLPIKPVAAVLAQOASPET-----TSPSELVAYSTLN 2565
 348 SSLRSLTGARLVERIFLGSRRPMWGPTRRLRLPFRWQWRP-----LLELLGNH 400
 2566 SEHPFPPT--QQTIVRQYQCPFRGGRPEALRKQGVKMRPPEHEALMLKGVTH 2623
 401 ACPQPVG-----VLK--THCPRAAVTPAAGVCAREKPGSVAAPEE-EDTPRRLV 449
 2624 LAAPGTQVSRBAVALVKPVTAP-RPSWAPTSAL-----PSRSLPEPEELTQTLRLI 2677
 450 --QLRQHSSPMQVYGVFR-----ACLR-----RL 472
 2678 NPNFYGYQAPWKT--FLRKEVFPYKDSYSHVQDLDFRQILLDTSEACRISSEDERL 2735
 473 VPPGLMGRHNRERFLNTRKFEISIG-KIAKLSLOELTWKMSVSDCAMLRRSPGVGCPVA 531
 2736 RKAKLPAQNO-----LDTGKPLVTSYKRAVAVSTARDTWEV-----YSRIFPATGSGVT 2785
 532 AEHRLREELIAFLKMLSVYVELLR-----SFYVETTF-QQNR 572
 2786 G-----VQLLA-----VSHVGIKILRMVKGQGAAGQLRVLRAYSFDILFVTMPSQM 2834
 573 LFFYPSVWSKLQSIGIRQHLKRVQLREISEAEVQRHEARPALTSRLRFPKDGRLP 632
 2835 LLENLAS--EKVILFSARAH---QVKTLVDDFIIEELK----- 2867
 633 INMDVVGARTFRRKRAERLTSVKALFSVLTNERA-----RRGGLGAS----- 679
 2868 --DSDVVAVRNLFLEDPFA-----LLAHHKGDIIHLQLEPFRVYSGAGCVAR 2913
 680 --VLGIDDIHR-----AMRTFVLAVRAQDPPELFFVKVDVTGAYD-----TIP-QDRLT 726
 2914 KKVYVLEELRRKRPDGRFGLIHGRVGFSEEL-----VQPAADDFQLPTPERGAA 2969

QY 727 EVASIIKPNQNTVCERY-----AVYQKAHGHVRAKAFSHSTLTDLQPYMRQFVAHLQ 781
 DB 2970 AVAAAVASAAAGVGRBRBGPVVARASADHGEDALALPPY-TMLEPAKVFEDPDRRQ 3028
 QY 782 E-----TSPLRDAVITEGSSSINEASSGLFDFVLRPMCHAVR 819
 DB 3029 DGLRKSKEPRESTRLEDMLCFTKPTLOESLIELSDSSISKMATDMLFVAFMFGDAPLK 3088
 QY 820 IRKSVYQCGGIGQSSILSTLCSLCYSD--MENTLFNGI-----RRDG 861
 DB 3089 GQSDLDVLN-----LTKLC-GHEVNRDECTQVAKQITDNTSSKODSCQRM 3136
 QY 862 LLRLVDDF---LVTPLHTFAKTLFRLVR--GVPEYG---CVNLRKTVANPPVD 911
 DB 3137 RLVIYVAYHSCSEVLAHPHLR---FLQGVSRPPGFQGIKACRONLQKTL----- 3186
 QY 912 EALGGAFFVMPAHGLFPWCGILLDRITLLEVQSDYSYARTSIRASVITNRRGKAGNR 971
 DB 3187 -RRGG-----RLEPSSIEU-RAMLGRSSK 3210
 QY 972 RKLFF---GV---LRKCHSLFIDLQNSLQTVCT-----NLYKILLQAVRFA 1014
 DB 3211 RQLFLPGLERHLKTKCTVLDV---VEEICAMALTRPBAFNEYVIFVYTRNGQHV 3266
 QY 1015 CVL-----QLPFRQVWKPIFF-----LRVSDTASLCY 1044
 DB 3267 CPLSRRAVILDVASEMEQVDDGYMLFRRVLDQPLKFENEDVYTMHNVQVLPDLKGLF 3326
 QY 1045 SILKAKNAGSLAKGAAGPLPSEAVQWLCHOAFILKTRHYVT---YVPLGSLRTAQ- 1100
 DB 3327 SSVPAAR-----PSEQ---LLOQVSKLASIQHAKHFIPL---SVREYGE 3366
 QY 1101 --TQSRKLPGTT 1111
 DB 3367 YIPALYRTTAGST 3380

RESULT 8

Q0353
 BHLFI protein - human herpesvirus 4 (strain B95-8)
 C/Species: human herpesvirus 4, Epstein-Barr virus
 C/Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 09-Jul-2004
 C/Accession: A03742
 R/Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barber, B.G.
 Mol. Biol. Med. 1, 21-45, 1983
 A/Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus.
 A/Reference number: A03742; M0ID:85035713; PMID:6092825
 A/Accession: A03742
 A/Molecule type: DNA
 A/Residues: 1-660 <BAN>
 A/Cross-references: UNIPROT:P03181
 R/Baker, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; He Nature 310, 207-211, 1984
 A/Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
 A/Reference number: A03794; M0ID:84270667; PMID:6087149
 A/Contents: annotation; protein coding region
 C/Comment: The sequence contains four perfect repeats (residues 149-273, 274-398, 399-523; C/Superfamily: human herpesvirus 4 BHLFI protein

Query Match 2.9%; Score 172.5; DB 1; Length 660;
 Best Local Similarity 26.1%; Pred. No. 0.00077;
 Matches 94; Conservative 16; Mismatches 159; Indels 91; Gaps 16;

QY 167 AYQVC--GPPVLYGATQA--RPPHAGPRRLGCEBAMNHSVEAGVPLGPAPGAR 222
 DB 244 AARCPAGPPPTTSGAAAGTARRPPGCRSARNBCPTWR---RSGAQGHPPPGAG 300
 QY 223 RRGASASRLP-LPKPRGAAPEP-ERTPVQGSMAHGRTRGPDGFCV-VSDAR-- 277
 DB 301 QRSQFTGRPAAPGAPTPAAGPGCAAVBSGATPHBRSQGPADPAPAAALPPEBOE 360
 QY 278 -----PAEATSLSEGL-----SGTRHSHAP 297


```

Db      361 PRLPQDLAAQRCPAPPTTSGAAAOQTHRRPPGCRSAKRNPCPTTMRNRSGAQRGP 420
QY      298 SVGRQHAGPPSTSRPPRPW--DTPCPP-----VYATKFLYSSGDKE-----QQR 342
Db      421 PPGAGGRSPSGPTGGRPAAPGAPGPAAPGGAAPVSGATPHPERGSGPADPPAARLP 480
QY      343 PSFLSLRPSLTGARLVETITLGSRPMPG-----TPRLRLPQ-----RYWQM 369
Db      481 PERQEPRLPDLLAAQRCP---AGPPRTSGAAOQTHRRPPGCRSAPNPPCPTTMR 536
QY      390 RPLFLELGNHAOCPPYVLKTHCP--RAAVTPAAVCAREKPGSVAAPEEDTPRR 447
Db      537 RS-----GAQRGHPPAPGAGRPSPGPTGGRPAAPGAPGTPAAPPGGAAPVSGATPHPR 591

```

RESULT 9

```

T00080
hypothetical protein KIA0522 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C:Accession: T00080
R:Ngase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kocani, H.; Nomura, N.; Chata, O.
DNA Ref. 5, 31-39, 1998
A>Title: Prediction of the coding sequences of unidentified human genes. IX. The complet
A:Reference number: Z14086; MUID:98290545; PMID:9628581
A:Accession: T00080
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 11560 <NAG>
A:Cross-references: UNIPROT:O60275; EMBL:AB011094; NID:93043567; PIDN:BA25448.1; PID:93
A:Experimental source: Brain; clone HG1393
A:Genetics:
A>Note: KIA0522

```

```

Query Match      2.4%; Score 142.5; DB 2; Length 1560;
Best Local Similarity 29.5%; Pred. No. 0.28;
Matches 65; Conservative 15; Mismatches 89; Indels 51; Gaps 12;

```

```

QY      173 PPIYOLGATQAPPPHSGPRRLGGERAMNHSVEAGVP-----LGTPAGARRRG 226
Db      1365 PPIYOLGATQAPPPHSGPRRLGGERAMNHSVEAGVP-----LGTPAGARRRG 226
QY      227 SARRSLPLPRP--RKGAPPEPRTPVGQGSMAHPGSTRGSDRGFCVSPAPAEATSL 285
Db      1416 GHDQFAPHGHPHOPRPLPLYSPPAPQHPAH---KQGPKRFIFGHPQMPMAAGNAG 1472
QY      286 EGAL--SGTRSHPSVGRHAGPPSTSR---PPRPMDTPCPVYAETKHF----- 331
Db      1473 PGRPRPGGSGSHR-----HHQSPLSPHSRIHPHSPPLPPSPPTTPSPPLPPTSPHGP 1527
QY      332 LVSSGDKQIRPSFLLSSLRPSLTGARLVETITLGSRPW 371
Db      1528 LHASGPPAQTPP--VQTPRPSQA-----GSAPW 1554

```

RESULT 10

```

T18314
hypothetical protein L7610.4 - Leishmania major
C:Species: Leishmania major
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18314
R:Oliver, K.; Murphy, L.; Quail, M.; Lawson, D.; Harris, D.; Rajandream, M.; Ivens, A.;
submitted to the EMBL Data Library, May 1999
A:Reference number: Z18876
A:Accession: T18314
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1892 <OLI>
A:Cross-references: UNIPROT:O97007; EMBL:AL034356; NID:e1371878; PID:e1371559; PIDN:CAA2
C:Genetics:
A>Note: L7610.4

```

```

Query Match      2.4%; Score 140.5; DB 2; Length 1892;
Best Local Similarity 23.4%; Pred. No. 0.5;
Matches 111; Conservative 47; Mismatches 195; Indels 121; Gaps 25;

```

```

QY      44 PAARFALVAOCIVCPWMDARPPAPSPFROVSCIKELVARVILQRLCEGAKNVLAFGPAL 103
Db      366 PSLHLPQQQPIVILVP---QPRPAPQOERLPRLYSSSTRAGGSSRAVQNNIYAGGAA 422
QY      104 LDGAGCPPEAFATVRS-----VLENTVDALRGSGAGLLLRVGDVIVHLARCAL 158
Db      423 EDTSSGASEVSTSRSTRQVFRAPVYASDIPGS--PYGAM-----PT 465
QY      159 FVLVAPSCAYOCPPYVLQATGAPRPPHSG---PPRLGQ-----ERAWN 204
Db      466 YAVVMPQ--RSILPAPFKGASAGAGLPPSPAPPEAAQQPHNSRCPPSSSRPPQESRD 523
QY      205 HSRERAGVPLGLPAGAR-----RRGSAASRLP---LPKRP--RGAAPPEPRT 249
Db      524 HAAREQ--PLQPPQKRPALPQRHQPORAETAKSQPPRRRLPADPYSSELPEQGR-- 580
QY      250 PVGQGSMAHPGRTGSDNR--GFCVSPAPRA-----EATSLGALSGTRSHR--SVGRQ 302
Db      561 --EGAWDGNASTQSGHGRGSHVVRPSQQQLSLSHEDLSLAWLSATVAAPISTKTD 637
QY      303 HHAGPSTSRPPRPMDTPCPVYAETKFLYSSGDKEQLRPSFLLSLRPSLTGARRL-V 361
Db      638 PYAGHTADGSRPLHVMPPIIQRP--YAATEEE-----GAPRSV 678
QY      362 ETIFGSRPMMPGPRRLPRLPQRYWQMPFLFLGNHAOCPPG--VLKTHCPRLA-- 418
Db      679 RKVTAPQESDAPSGRSHR-----PHEHTLHSRGADAGAAAKTRQLSLAK 728
QY      419 ---VTPAGVCAEKEPQ-----GSVAPEEEDTPRRLVQ---LLRQHSSP 458
Db      729 EAVTAMTAVGQSSKKRQLOHEPDGS---PNGDDVD--ELLEADDLIMQSRP 777

```

RESULT 11

```

EBB31P
Immediate-early protein IE180 - suid herpesvirus 1 (strain Indiana-Funkhauser)
C:Species: suid herpesvirus 1
C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C:Accession: S04713
R:Cheung, A.K.
Nucleic Acids Res. 17, 4637-4646, 1989
A>Title: DNA nucleotide sequence analysis of the immediate-early gene of pseudorabies vi
A:Reference number: S04713; MUID:89315207; PMID:2546124
A:Accession: S04713
A:Molecule type: DNA
A:Residues: 1-1460 <CHB>
A:Cross-references: UNIPROT:P11675
C:Superfamily: herpesvirus immediate-early protein IE175
C:Keywords: DNA binding; early protein; transcription regulation

```

```

Query Match      2.3%; Score 140; DB 1; Length 1460;
Best Local Similarity 24.3%; Pred. No. 0.38;
Matches 114; Conservative 35; Mismatches 163; Indels 158; Gaps 27;

```

```

QY      46 AFRALVAOCLVCPWMDARPPAPSPFROVSCIKELVARVILQRLCEGAKNVLAFGPALD 105
Db      704 ACRGVLRLPLPC-PLRIPAPARAPALQACLEBTVALL-----ALRD 746
QY      106 GARG-GPPE-----AFTTSVRSYLPNTVTDALRGSGAGLLLRVGDVIVHLIAR 155
Db      747 AIPGAPRERQQAADSVLVARTVAPLVRSVDCARAREAAW-----TYA 791
QY      156 CALFVLVAPSCAYOCPPYVLQATGAPRPPHSGPRRLGGERAMNHSVEAGVP-----S 206
Db      792 AALF---APA---NVAGRL---AQAARGPAREAP---GLPPLMPBQGLVAPAPA 837
QY      207 VREAGVPGLPAPG---ARRRGSAASRLPLRPPRGAAPPEERTPVGQGSMAHPGRT 262
Db      838 PAAAGAPSGLPGSPSSPASTKSGSTKSSGSGTSGLSSG-----GYARLPRR 887

```

QY 263 RPSDRGCVFVSP---ARF-AEFAITSLG-ALSGTSHSPSVGRQHNAPESTSR-- 313
 DB 888 PPSARAAQEEAFRAGARPGGDEDEGLSGSALGDGHRD--DEDRPRPKRKSLSG 945
 QY 314 --PRPMDTPCPVVAETKHFIVSSGDKQLRPSFILSLRPSLTGARLVETIFLGSRPV 371
 DB 946 LGPAP--DAPALVSSSS--SSSEDDRRLR-----RP-----LGRPE 980
 QY 372 MGTPTRLRLPQRYQWRPLFLELGNHACQPVVLKTHCP-----L 415
 DB 981 HPAAPDGGFRVAVAG-----ETHPRFSAALAAAYCPREAVALVDQEVPELW 1028
 QY 416 RAAVT--PA--AGVACAREKQGSVAAPBEDTDPRLVOLLROHSPQV 461
 DB 1029 RPAITPDPALAHIAAR--RGAAP-----LRRAAMRQLADPADV 1069

RESULT 12

AS59295
 Unconventional myosin-15 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
 C/Accession: AS59295
 R/Liang, Y.; Wang, A.; Beljantseva, I.A.; Anderson, D.W.; Probst, F.J.; Barber, T.D.; Mian, T.B.; Fridell, R.A.
 Genomics 61, 243-258, 1999
 A/Title: Characterization of the human and mouse unconventional myosin XV genes
 A/Reference number: AS59266; MUID:2002162; PMID:10552926
 A/Accession: AS59295
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-351 <L1A>
 A/Cross-references: UNIPROT:Q9QZ4; GB:AF144095; NID:g6224684; PID:AAF05904.1; PID:g6224684
 C/Genetics:
 A/Genes: MGI:Myo15
 A/Cross-references: MGI:1261811
 A/Map position: 11:33.9
 F/1209-1871/Domain: myosin motor domain homology <MMO>
 Query Match
 Best Local Similarity 17.6%; Score 140; DB 2; Length 351;
 Matches 189; Conservative 115; Mismatches 387; Indels 380; Gaps 44;

QY 3 RAPRCRAVSLLRSHYEVLPATVRRLLGPGQWRLLVGRDPAFRAVLVQCLVCP-- 59
 DB 677 RPPRLASPYGSLRQH-----PPPW-----AAPAHVPFPQA 707
 QY 60 --WDAPPRA-----PSPRQVSCXELVARVLQRLCRGANVLAFGFA 102
 DB 708 NMWGFAPDPTGEVAPDLAPVPRPFR-----ASRSSRRAVGF 751
 QY 103 LLDGARGPPEAFTTSVRSYLPTVTD--ALRGSGAMGLLRVGDDVLLHARCALFV 160
 DB 752 -----SPSLIGSRRLPRLSPQSLRLSLPGQ----- 778
 QY 161 LVAPSAVQVCPPLVQLGAATQARPPLASGPRRLGCEPMNSVREAGVPG-- 215
 DB 779 -----YHSPLEPLSFLQLRRGPQPPPPPPRQSLREAF--SLRPSGRLLPPSP 830
 QY 216 -----LPAPGARRRGSASRLPLPKR-----PRKGAPEBERT--FVGGGS 255
 DB 831 VLSGPPRPPLPKHGRHRSILNPSRLPRTWRRLSEPTAVAVPWVRAVPPPSGP 890
 QY 256 WAHPTGTRGSDRGFCVSPAPAEATSLGALGTRSHSVGRQHNAPESTSRPR 315
 DB 891 W--GASTGALD-----QOENQREADESETPVPLAPSWDMPTQRPSS 935
 QY 316 PMDTPC-----PVAETKHFIVSS--DKQLRPSFILS 348
 DB 936 PMBEIGSLRGSRPPVPEPNLEHTSCEPQSEDRAVSNLTGIFLQGHDPGCGULTX 995
 QY 349 SLRPSLTGARLVETIFLGSRPWMGTPRRL--PLRQRYQWRPLFLELGNH----- 400

DB 996 SADPSL---EKPEVTVLTD--PQPAPEPALPTPKNKVVSEKVLRLASAVPLVTCQ 1051
 QY 401 --AQCP-----YVLLKTHCPPLAAVTPAAGVACAREPQGS----- 434
 DB 1052 ARATQWHRWKVSTPAPLAPTRAQGLKAGSQRAEPGRFAVVPQVGVSSFRPK 1111
 QY 435 ---VAPEBEDTDPFR-----LVOLLRQHSPPMVGFFVRAC 468
 DB 1112 GPAPVQPEHPDPPQGPAPQACSLRWCPLMPPTDAHCLWRIRITYSQSLRHGGDC 1171
 QY 469 LRRL--VPPGLWGSNHNERRPLRNTKFTISLQKAKLSQLLTKWMSVRCAMLRPSG 525
 DB 1172 HKSIMKTRPQSV---QNKQHSIRNLPSMRSEOHEDVEDEMTLEDLQETTVLAN-- 1225
 QY 526 VGVPAAEHRLREILAKFL-----HWMISVYVVELLSF-----FYVT 564
 DB 1226 ---LKTREPNLLYTYIGSLVSNVYRKFATIGPQVOQYGRALGEMPHLFAA 1279
 QY 565 EITFOR-----NRLFYRPSVWS-----KL-----SGIRQLKRVQLRELS 603
 DB 1280 NLAFAMWLDAKQNCVIGESGSGKTEATKLRLCLAMQRPVMOQIKLEATPLIE 1339
 QY 604 A-----EYQHRARARALLTSRLFTPKPDGLRPIVMQYVGARTFRERKAER----- 653
 DB 1340 AFGNAKTVRNDSSR--FKGFVEIFLEGVIGCATTSQYLEKSRIVFOAKERNYHIF 1396
 QY 654 -----LTSRKALFSLVNYE-----RARRGLGASVGLDDIHRARVFLRVRAQD 701
 DB 1397 YELLAGLPALQRAFSLQZAEETYYVINGGNCIEACKS--DADDFR----- 1441
 QY 702 PPELVFKVDVTVGADTIPQRLTVLSTIKPQNTYCVRYAVVQKAHGVKAFKS 761
 DB 1442 ---LAAAEVLG--FTSDDQSIFFRLASIHLAGVYKEKETDAQEVA----- 1485
 QY 762 HVSITLDLPYMQFAHLOETSP--LRDAVYIEGSSSINEASGLFVFLRFMGHAYR 819
 DB 1486 SVASABEIQ-----VAELLQVSPBGLQALIFKVTETIRE-----KIFTLVYESAVD 1534
 QY 820 TRKSYVQCGIPQSGILSTLCLSGYGMENKLFPGI--RRDGLLRBYD 868
 DB 1535 AR-----DAIAKVYALFLGWLIRVNAVLPKODTLIALID 1572

RESULT 13

F75311
 ABC transporter, ATP-binding protein - Deinococcus radiodurans (strain R1)
 C/Species: Deinococcus radiodurans
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: F75311
 R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Smith, H.O.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; May Science 286, 1571-1577, 1999
 A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1
 A/Reference number: A75250; MUID:20036896; PMID:10567266
 A/Accession: F75311
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-552 <WHI>
 A/Cross-references: UNIPROT:QGRSH9; GB:AE002048; GB:AE000513; NID:g6459929; PID:AAF1168
 A/Experimental source: strain R1
 C/Genetics:
 A/Genes: DR2145
 A/Map position: 1

Query Match
 Best Local Similarity 22.3%; Score 139.5; DB 2; Length 552;
 Matches 134; Conservative 38; Mismatches 196; Indels 233; Gaps 27;
 QY 132 RSGAMGLLRVGGDVLLHARCALFVLVAF-----SCAYOVCGP 173
 DB 24 RGS---RLQFRVSGKSTRIRFTSTBSLFLCLARLGLTASSTGFSIHSSDVATTAAPR 80

QY 174 P----LYQLGATQAPPPPHASGPRRLG-----C 199
 Db 81 PGTNRHRRRGAG--AARPFADGPARRGAAAGERRRRONHAAAARACASERHPDV 138
 QY 200 ERAMNHGVREAGVPLGLPAPGARRRGSASRSLLPRLPRRGAPAEPEERTPVQGSNAHP 235
 Db 139 ARRGSGAFRRAGA--AIPERGAGRRGVLSRLGTDPRARRAAGRGGRTPAAVGSDA-- 194
 QY 260 GRTGSPDRGFCVVSPPAPAEATSLGALSGTRHSHPSVGROHNAQPPSTSRPPRPMDT 319
 Db 195 -RTTRPVGRG-----DYTRRGALAGALSHPLA-----RAAPPGDAGP----- 232
 QY 320 PCPPVVAETHNFIYSSGDKQLRPSFLSSRLPSLTARSLVETIFLGSPPMPCPTPRL 379
 Db 233 -----RPRARA-----PAAARL 246
 QY 380 PRLPQRYWQMRPLLEL--LGNH-----AACPYGLLKTCTCPRAAVTPA 422
 Db 247 HRMFERSGPRPRRRAPGPGCGHVGADPPAPGSPDALAGVSGRTERRAALPI 306
 QY 423 ----AVCAREKQGSVAAPDEEDTD-----PRLVOLLROHSSPMQV---YGF 464
 Db 307 RSPRYSGASTGPLCGTAAVVELTDAEVFNHGRALGPLMTWAAGH--WLTGENGS 363
 QY 465 VRACLRRLVP-----PGLMGRHNERFLRNTKFKTISLGHAKLSLQELTWKMSVRDC-AM 519
 Db 364 GKSLTALILAGELHPLAGGS--VARPL-----ARDVQGS 396
 QY 520 LRNSPGVGCVPAAEHRLKEELAKFLHMLSVYVELLSFFVYTE---TFQKRLP 574
 Db 397 RRRRTG---LYSAVGVIRORSVSGREMLGR-----DIVASAFGTGEGTCDVTAEQ--- 445
 QY 575 FYRPSVSKXQSIGIR-----CHLKRYQLRELSAEVRQREARPALLTSLRLP 623
 Db 446 ----NDAVGTALERLELGBELLSDVQALSGQLRLLILAAVAHR-PRLLLDLGLDF 498
 QY 624 I 624
 Db 499 V 499
 RESULT 14
 S27923
 gene LF3 protein - human herpesvirus 4
 C/Species: human herpesvirus 4, Epstein-Barr virus
 C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C/Accession: S27923
 R/Paraker, B.D.; Bankier, A.; Satchwell, S.; Barrell, B.; Barrell, P.J.
 Submitted to the EMBL Data Library, August 1990
 A/Description: Sequence and transcription of Raji Epstein-Barr virus DNA spanning the B9
 A/Reference number: S27923
 A/Accession: S27923
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1924 <PAR>
 A/References: UNIPROT:Q99307; EMBL:M35547; NID:G330420; PID:AAA5896.1; PID:G3304
 C/Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;

Query Match 2.3%; Score 138.5; DB 2; Length 924;
 Best Local Similarity 27.0%; Pred. No. 0.26;

Matches 80; Conservative 25; Mismatches 136; Indels 55; Gaps 16;

QY 179 GAATQARP-----PHASGPRRLGGERAMNHGVREAGV-----PLGLPAPGARRRGSA 228
 Db 26 GAADPADPVGHPAPAPGPEPRTRIQPA---TPRSSGAADPADPVGHDA--APRAPGE 80
 QY 229 SRAELP;PKRRRGAAPPERTPVQGSNAHPGRTGRPSDRGFCVVSPPAPAEATSLGSA 288
 Db 81 PRTRLQATRRSGADP--ADPVG---HFAAPRAPGPEPRTRLPATPRSSGAADPAD 134
 QY 289 LSGTRSHSPSVGRQHNAQP-----PSTSR-----PPRPMDTFCPPVVAETHFIYSSGD 337

Db 135 PVG----HPAABRAPGPEPRTRLPATPRSSGAADPADPVGHDAAP-----RABGP 181
 QY 338 KEQLRPSFLSSRLSGTARSLVETIFLGSPPMPCG--TPR-RL-PRLPQRYWQMRPL 394
 Db 182 EPRTR-----LQPTARRSGAADPADPVGHDAAPRAPGPEPRTRLPATPRSSGAADP--A 235
 QY 395 ELLGNHAQCPYVLLKTHCPPLAAVTPAAGVCAAREKQGSVAAPDEEDTDPRRLVQ 450
 Db 236 DVG--HPAABRAPGPEPRTRLPATPRSSGAADPADPVGHDAAPRAPGPEPRTRIQ 290

RESULT 15
 C45219
 N-methyl-D-aspartate receptor chain NMDAR2D-1 - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C/Accession: C45219
 R/ishi, T.; Moriyoshi, K.; Sugihara, H.; Sakurada, K.; Kadotani, H.; Yokoi, M.; Akazawa, J.
 J. Biol. Chem. 268, 2836-2843, 1993
 A/Title: Molecular characterization of the family of the N-methyl-D-aspartate receptor
 A/Reference number: A45219; MUID:93155102; PMID:8428958
 A/Accession: C45219
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-1356 <ISH>
 A/Experimental source: brain
 A/Note: sequence extracted from NCBI backbone (NCBI:124264)
 C/Superfamily: N-methyl-D-aspartate receptor 2D; glutamate receptor homology
 F/51-879/Domains: glutamate receptor homology <GRH>

Query Match 2.3%; Score 135; DB 1; Length 1356;
 Best Local Similarity 27.2%; Pred. No. 0.76;

Matches 88; Conservative 16; Mismatches 102; Indels 118; Gaps 22;

QY 59 PWDARPPPA-----PSFRQVSCLEIVARVQLRCERGAKNVLAFGALDQ----- 106
 Db 1084 PRRAAPPCAYLDLEPS-----PDSSEDSLSLGASIGLEPMWFA 1124
 QY 107 -----ARGPPREFTTSVSYLNTVTDALRG--SGAKGLLRVGDVTVHLARCA 157
 Db 1125 DFPYVARELGPPEGRYVSV-----DLTGWRASWDYLLPRGSP--AMHCRHCA 1172
 QY 158 LFLVLPVAP-----SCAYQVC-----GPLYQLGATQAPPPPHASGP-----RRRLCERAMN 204
 Db 1173 SLELLPPRRHLSGSHDGLDGGWMAFP-----PPPAAGPPRRRARCGGPRHP 1221
 QY 205 HSYREA-GVPLGLPAPGARR--GG-----SASRSI-PLPKPRRGAAPEPERT-PVG 252
 Db 1222 HRPRASHRAPAAPHHRRRAAGGWDFPPAPPTSRLSDLSNP---CP-PRTGDTG 1276
 QY 253 QGSMAHPRTGSPDRGFCVVS-----ARPAEATSLGALSGTRHSHPSVGROHNA 305
 Db 1277 AGTAHDAALR-----ISPMSRYDAAPAPTPRAPPSVA---GHGPRGRAKMT 1324
 QY 306 GPPSTSR---PPR--PMDTPCP 323
 Db 1325 GPSWVGXDRNPGCRTPPGAASCAP 1348

RESULT 16
 G75302
 orotidine 5'-phosphate decarboxylase - Deinococcus radiodurans (strain R1)
 C/Species: Deinococcus radiodurans
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C/Accession: G75302
 R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 S.; Smith, H.O.; Venter, J.C.; Frazer, C.M.; McDonald, L.; Uitterback, T.; Zalewski, C.;
 Science 286, 1571-1577, 1999
 A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A/Reference number: A75250; MUID:20036896; PMID:10567266
 A/Accession: G75302
 A/Status: preliminary

```

A:Molecule type: DNA
A:Residues: 1-606 <WH>
A:Cross-references: GB:AE002053; GB:AE000513; NID:G645999; PIDN:AAF1749.1; PID:G646000
A:Experimental source: Strain R1
C:Genetics:
A:Gene: DR2200
A:Map position: 1

```

Query Match	2.2%;	Score 134;	DB 2;	Length 606;
Best Local Similarity	22.4%;	Pred. No. 0.29;		
Matches 100;	Conservative 45;	Mismatches 137;	Indels 164;	Gaps 21;

Qy	132	RSGGAGGLILRRGGDDVILHLLARCALFLVAVPSCAVYCGPFLYUUGAALQARPPHAS	157
Db	21	RSEBRGVALLOQGERRRVHLTARHPALQV----	57
Qy	192	GPRRRIGCEAMNHSVREAGVFLGLPAPARRRGGSASRLPLPRRRRCARPP----	246
Db	58	-PERRFG-----VGVPVSGGQRRG-----VLLPEBOQ----POPFOGVF	91
Qy	247	-ERTPVQGGSWAHPGRTRGSDRGFCVSPAPARAEATSLGALSGTRKSHSPVSGROHNA	305
Db	92	RQRT-----GLVRAKQO--VAVVEPRPPAAGV-GVYVGAQ-VHPPVUGQALVA	136
Qy	306	GPESTSPRPPMWDTPCPPVYAETKHFVYSSGKEXLRPSFLISSLRPSLTCARLVETIF	365
Db	137	A-----PR-----RAQORRLPPAPVAARLVV--GPORRQOT--	167
Qy	366	LGSRPMMGCPRRRLPRLLPQRYQMQRFLPELLGNHAGOCYGLLKTCHCPRYLAATPAGV	425
Db	168	AGEQOLVPG--LPQCPHRV-----QHARQEDVALNRHYRPEEARP--GV	209
Qy	426	CAR-----EKPQGSVAPAREEDTDPRLVOLLROHSSPMQVYGFVACLR	471
Db	210	AARVAGEGRALPVARADQPELPLLDVGGLTKXADDGRLREPLREQOTRTBIGVADIALR	269
Qy	472	LVPBGWLKSGSHNERRLPLNTKKFISIGKAKXLSLOELTWKHSVRCDAWLRRSPGVG----	527
Db	270	YRPLAAAHBHQ-----RHRBELARHNRPAEVA-----GPGVADHDR	306
Qy	528	-----CVPAEHLRLREBELAKLFIH	547
Db	307	KGNARQCTGPAQHPPFPVOLRLFIH	332

```

RESULT 17
J00405
hydropathic 119.5K protein (uvra region) - Micrococcus luteus
M.alternate names: ORF 1 protein
C.Species: Micrococcus luteus, Micrococcus lysodeikticus
C.Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 04-Feb-2000
C.Accession: J00405
R.Shiota, S., Nakayama, H.
Mol. Gen. Genet. 217, 332-340, 1989
A.Title: Micrococcus luteus homolog of the Escherichia coli uvra gene: identification of
A.Reference number: S04781; MUID:89364717; PMID:2549377
A.Accession: J00405
A.Molecule type: DNA
A.Residues: 1-1106 <SH1>
A.Cross-references: EMBL:X15867
A.Note: this reading frame extends between two stop codons and does not begin with a start
A.Note: the gene encoding this protein overlaps uvra gene
C.Superfamily: collagen alpha 1(I) chain, fibrillar collagen carboxyl-terminal homology

```

Query Match	2.2%;	Score 133;	DB 2;	Length 1106;
Best Local Similarity	23.9%;	Pred. No. 0.78;		
Matches 129;	Conservative 33;	Mismatches 198;	Indels 180;	Gaps 25

QY 183 RPPHAGGPRRLICE-----EAMNHSVREAGVPLGLPA--PEARRGSGAS-----KSLP 233
 Db 516 RGPQPGGEPBARCRPVNRRGHRPALARGHGVLLGAAALGDPAAALRGCAAGDPGPAPV 578
 QY 234 LPKPRRAGAPDEPRRTVGGSGMAHNGRTGSDRDFCVSPARPAEATSLGALSCTR 291

Db	576	AGRRPR---	VPQR-----	RAAGNHPLRRRG-----	PAHPRGHTBRLR---	AGRR	613
Qy	294	HSNBSVGRONHAGRPSTSRPRRPWDTCSPVYATKHFVYSSGDKEOLRBSFLLSSLRPS	353				
Db	614	PLRP----	RAVNHRAAPAGRPRRHNDPRAPAGRPQHPRRRBARRGND--	FRGGLDRGHPS	668		
Qy	354	LTGARLVEITFL--	GSRPMWPGTRRLRLPRQYUWMQRLFFLELLGNHAGCPGVLLKT	411			
Db	669	RGVRRRGALGLPGSGQGEHVAHNRLLPLRP	-----PL-----	-----	702		
Qy	412	HCPRLAAVTAPAGVCA-----	REKPGQSAVA-----	AREED-----	TD	444	
Db	703	HREGAASRPEEGARADGPRRRPGEORGRGLDCEPARGPHGHDGVRLRQVHADRDPLQG	762				
Qy	445	PRRLVQLLRONHSSPWQYGFVACLRRLVPRGLWSSHNERRFLRNTKFTSLGKNAVL	504				
Db	763	PGCAQGRQARARAPRVGTRRA-----	PGQGGPRGDEH-----	RAHATLQ	804		
Qy	505	LQELTWKMSVDCAMLRSP--	GVGCVPAANHLRBEILAKFLHMLMSVYVVELLSFF	561			
Db	805	FRHLHGVR--	RDPOALGDPRGEGRP--	LPGAPVLL-----	837		
Qy	562	VYETTTQOKRLLFFYRPSVMSKLQSIGIRQLKXVOLRELSAEVROHREARPALTSRL	621				
Db	838	-----	QD-----	QGRLRGVTCGRRAEDRDLPAQRL	864		
Qy	622	RFI--PKEDG--	LRPIVMDYVGARTFRREKAER-----	LTSRVALLPSVLNYEBARRBGL	675		
Db	865	RAVAGVRRGPRQPDADGHLOGQSHNRGGRPRADGSGRGLQRYVPHNLAVPHARRRRRGL	924				

```

RESULT 18
JC7810
inositol 1,4,5-trisphosphate 3-kinase B - human
C/Species: Homo sapiens (man)
C/Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #ext_change 03-Jun-2002
C/Accession: JC7810
R/dewaste, V./ Roymans, D./ Moreau, C./ Erneux, C.
Biochem. Biophys. Res. Commun. 291, 400-405, 2002
A/Title: Cloning and expression of a full-length cDNA encoding human inositol 1,4,5-trisphosphate 3-kinase B
A/Reference number: JC7810; PMID:11846419; MUID:21835501
A/Contents: Frontal cortex
A/Accession: JC7810
A/Molecule type: mRNA
A/Residues: 1-946 <DEW>
A/Cross-references: GB:Y18024
A/Comment: This enzyme, an isoenzyme of inositol 1,4,5-trisphosphate (InsP3) 3-kinase, catalyzes the phosphorylation of inositol 1,4,5-trisphosphate to 1,4,5-bisphosphate and inorganic phosphate. This enzyme is particularly sensitive to Ca2+ in the presence of calcium homeostasis. This enzyme is particularly sensitive to Ca2+ in the presence of
Query Match 2.2%; Score 132.5; DB 2; Length 946;
Best Local Similarity 20.1%; Pred. No. 0.68;
Matches 130; Conservative 7%; Mismatches 249; Indels 195; Gaps 27;

```

```

QY      178  IGAATQAPRPBHAGCPR-----RLGCEPAMNHSVREAGVLLGIPAPARRRG----- 225
Dd      350  LGSETS--PAERGGPRDGEPPGMG-----KYLCPGMGSGEPDEVGXREBETT 397
QY      226  ----GSASRLPLPKPRRGALAPEPR-----TPYGGSSAMHPGTRPSPDRGFCVSP 276
Dd      398  VSVQSAESDLSMSRLPRALASVGPPEARSGAPVGGGRWOLSDPVSGS----- 447
QY      277  RPAEATSLGALSSTRHSHSPVROCHHAGCPSTSRPRP--WDT-----PCPEVYAE 328
Dd      448  -----PTLGLLGGSPACPGTGVNVEAGTFSGRMLEPLPCMDAKDLKEPCCP----- 495
QY      329  KHFLYSSGDKQLRPSFLLSLRPSLTGARRLVETIFLGSRPWWGTPRRRLRPLRQRYW 388
Dd      496  -----GDRGVQPG-----NSRWQGMTEKAGLAWTRGTIVQ-----SEGTWE 533
QY      389  MR-----PLFELTGNHAAOCYGVILTKTCPLRAVTPA--AGVCAREKPOGSAVA 437
Dd      534  SQORDSDALPSP--ELLRPOQDKRF-----LRACSPSNIPAVIITDMQOEDGA 581

```


Db 804 -----LAPCLFYGLQVYGIAMKSHLNKIRIIOAKTIRISGAPWYKRT 846

RESULT 21

445344
immediate-early protein - suid herpesvirus 1 (strain Kaplan)

C/Species: suid herpesvirus 1
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C/Accession: A45344

R/Vicsek, C.; Kozmik, Z.; Paces, V.; Schirm, S.; Schwyzer, M.

Virology 179, 365-377, 1990

A/Title: Pseudorabies virus immediate-early gene overlaps with an oppositely oriented

A/Reference number: A45344; PMID:91021039; PMID:2171211

A/Accession: A45344

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-1446 <VLC>

A/Cross-references: UNIPROT:P33479; GB:M34651; NID:G334070; PIDN:AAA47470.1; PID:G334071

C/Superfamily: herpesvirus immediate-early protein IRI75

C/Keywords: DNA binding; early protein; transcription regulation

Query Match 2.2%; Score 131; DB 1; Length 1446;

Best Local Similarity 21.4%; Pred. No. 1.6;

Matches 105; Conservative 37; Mismatches 156; Indels 192; Gaps 25;

46 APRVAOGLVCPMDARPPAPSPROVCLKELVARVLCRGAKNVLAFGALD 105

693 ACRGVLERLPC-PLRLPAPAPALGACLEVTALL-----ALRD 735

106 GARG-GPPPAFTTSVRSYLPNTVDALRGSGAMGLLRVGDVLLHLCARFVLVAP 164

736 ATRGAPAPR-----ROADSVA--LVAR-----TVAP 761

165 SCAYVCGEPFLVGLG-----AATQARPPHAGSPRRRLGGERAMNH- 205

762 LVRYSDGAPARAPAAVTAALFAPANVAARLAPALAPGAPAP-----GLPPLWPEQ 817

206 -----SVREAGVPLGLPAPG--ARRGSGASRLPLPK-----RPRGA 242

818 PGLVAPAPAPAAAGAPSGLPSSGSPSPASTKSSSTKSLGSSGVAASPAAGP 877

243 APEPERTVGGGSMHAPGTRGSDRGFCVSPAP--AEKRTSLG-ALSGTRHSPSV 299

878 DPAPER-----RKKRRAPGAR--RPGGEEDEEGSGALGDDGHD- 919

300 GRGHHGPPSTSRP--PRPMDTCPVYATKTFLYSGDKQLRPSFLSLRPSLT 355

920 -DEEDGPRKRRSLGLGAP--DAPALLSSSS--SSSEDDLR-----RP--- 961

356 GARLVETIFLGRPMWPGTPRRLLPRLPQRYQMRPLFLLEIGHAQCPRYGLLKTGCP 415

962 -----LGPMEHPAPDCGFRVPAG-----ETHTPPSEALAAACP- 998

416 RAAVTPAAGVCAKEKQGVAAPEE-----DTDPRLVQLRGHSPMVGFFV 465

999 -----PEVARALVDQVPELWRPALTDPALAHIAARRGAPLRRRA-- 1041

466 RACLRRLVPP 475

1042 -AMMRQIADP 1050

RESULT 22

550832

atrophin-1 - human

C/Species: Homo sapiens (man)

C/Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 07-May-1999

C/Accession: S50832

R/Nagatuchi, S.; Yanagisawa, H.; Ohsaki, E.; Shitayama, T.; Tadokoro, K.; Inoue, T.; Yan

Nature Genet. 8, 177-181, 1994

A/Title: Structure and expression of the gene responsible for the triplet repeat disorde

A/Reference number: S50832; PMID:95144175; PMID:7842016

A/Accession: S50832

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1184 <NAG>

A/Cross-references: EMBL:D31840

C/Genetics:

A/Genes: GDB:DRPLA; B37

A/Cross-references: GDB:270336; OMIM:125370

A/Map position: 12p13.31-12p13.3112P-12P

Query Match 2.2%; Score 130.5; DB 2; Length 1184;

Best Local Similarity 22.6%; Pred. No. 1.3;

Matches 88; Conservative 23; Mismatches 154; Indels 125; Gaps 16;

162 VAPSCAYVCGEPFLVGLGATQARPPH-----ASGRRLRGGERAMNHVRA 210

189 VTPGVYAPMEPTSRMPPQAPGAPPPHPPQLYFGTGVLGSP----- 231

211 GVPLGLPAPARR--GGSASRLPLPKRP-----RGAAP-EPERTVGGGSMHAPG 260

232 --FMGRGGAASVGGPNQKHPPPTTIVSVSSGAGAPPTKPTTPVGGN----- 284

261 RTGPRSDRGFCVSPAPRAEATSLGALSGTRHSPVGRQNHG----- 306

285 LPAPPPANPPHTPMLPAPPALR--PLNNASAPPGAGAPLPHLSPYAMGQXG 341

307 -----PSTSRPPRPMDTCPVYATKTFLYSGDKQLRPSFLSLRPSLT 354

342 LPGPXKGPFLASPHSLPPASSAPAPM-----RFPSSSSSSAAAS--SSSSSS 393

355 TGARLVETIFLGRPMWPGTPRRLL-----PLP-QRYQMRPLFLLEIGHNAQ 402

394 SSASPPFASQALPSYHSPFPPTSLSVSNQPKYTPSLPSQAVWSQGP-----PPP 445

403 CPYGLVLTGHTCPLRAAVTPAAGVCAKEKQGVAAPEEEDTPRRRLVQLRGH--SSPW 459

446 PYYGLLANSNAHPGFPSTGASTAHPPVSTHHHHNQOQQOQQOQQHNGSGF- 504

460 QVYGFVAPACLRLLVPPGLW-----GSRN 483

505 -----PPGAFPHPLGSSSH 521

RESULT 23

T113049

eyelid - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T113049

R/Teisman, J.E.; Luk, A.; Rubin, G.M.; Heberlein, U.

submitted to the EMBL Data Library, March 1998

A/Reference number: Z17592

A/Accession: T113049

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-2715 <TRE>

A/Cross-references: UNIPROT:Q8IN94; EMBL:AF053091; NID:G2981220; PID:G2981221; PIDN:AA006

C/Genetics:

A/Genes: eld

A/Cross-references: FlyBase:FBgn003013

C/Function:

A/Description: could act as a transcription factor antagonistic to the Wg pathway

C/Keywords: DNA binding

Query Match 2.2%; Score 130.5; DB 2; Length 2715;

Best Local Similarity 22.5%; Pred. No. 4;

Matches 80; Conservative 29; Mismatches 140; Indels 107; Gaps 18;

173 PPLYUGAATQATQAPPPHAGP--RRRLGGERA--WNHSVREAGVPL-----GLPAPG 220

1293 PPOOQOQOQOQOQPPVGGGPPAPPOHBPQVPSPOQHVPAPACAPYPPGSSGYPTPV 1352

221 ARRGGSASRLPLPRPRGA-----APEPERTVGGGSMHAPGSTRGSDRG 269

Db 676 INPCFLTKLSPVTAIELE-----GVLD-----QSQAYLGI 710
 QY 953 STRASTENNGFKA 966
 Db 711 TLDRKLTGPHLKA 724

RESULT 28

hypothetical protein, 69k - turnip yellow mosaic virus
 C/Species: turnip yellow mosaic virus, TYMV
 C/Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
 C/Accession: S01955
 R/Morch, M.D.; Boyer, J.C.; Haenni, A.L.
 Nucleic Acids Res. 16, 6157-6173, 1988
 A/Title: Overlapping open reading frames revealed by complete nucleotide sequencing of t
 A/Reference number: S01955; MUID:86289359; PMID:3399388
 A/Accession: S01955
 A/Status: preliminary
 A/Molecule type: genomic RNA
 A/Residues: 1-628 <MOR>
 A/Cross-references: UNIPROT:P10357; EMBL:X07441; NID:G62222; PIDN:CA0321.1; PID:G62223
 A/Note: the authors translated the codon ACG for residue 459 as U
 C/Superfamily: Hydroxypoline-rich g-Lycoprotein

Query Match 2.2%; Score 128.5; DB 2; Length 628;
 Best Local Similarity 27.6%; Pred. No. 0.73;
 Matches 89; Conservative 21; Mismatches 130; Indels 83; Gaps 18;

QY 172 GPVLQIGATQAPPPHAS-GPRRLGGERAMNHSVREGVGLG-----PAPGARRG 225
 Db 157 GPVLTEKPTPTSVQPRSATRG-----SFRPLLRKVHVHDDPHSSLLRR 204
 QY 226 GSASRSY-----PL-----PKRP-----RGAPAEPEPTVGGGSAHPG 260
 Db 205 GSASRQOPTVRKPLAPNQHSPRCPPASDDPGILGPPPLAFHSTRD-----PP 256
 QY 261 R--TRGPD-----RGFCVSPAPPAEATSLGALSGTRHSHPSVGGQHHAGPSTSRPP 314
 Db 257 RPTPGPSNTHDLRLPLSLVLRTPSR-----RGILPFRHRHRTSTG---HIPPTTSRPT 307
 QY 315 RPNMTPCPVYAEKHEFLVSSGXDELRLPSFL-----LSSLRPSLTGARLVERITFGSRP 370
 Db 308 GP-----PSRLQRPVHLVYSSPHTPNFRPSIRKDALLLQCGPLGHERGQGANLRTSE 362
 QY 371 WMGTPRRRLPLPQRYWQMRPLLELLG--NHAQCPYGVLLKTHCPLRA-AVTPAAGVC 426
 Db 363 RSPPTKRLRLPRSSPNRLPKPLPEATLAPSYRHR--PYPLPMPALPISATYSRGI 421
 QY 427 AREKPGSVAPAE-EDTPRRL 448
 Db 422 HHSLPKG-ALPKGADPPRRRL 442

RESULT 29

adenine deaminase-related protein - Deinococcus radiodurans (strain R1)
 C/Species: Deinococcus radiodurans
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: C75580
 R/White, O.; Eisen, J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A/Reference number: A75250; MUID:20036896; PMID:10567266
 A/Accession: C75580
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-576 <WHI>
 A/Cross-references: UNIPROT:Q9R9P2; GB:A0001863; GB:A0001825; NID:G6460670; PIDN:AAFI237
 A/Experimental source: strain R1

C/Genetics:
 A/Gene: DRA0268
 A/Map position: 2

Query Match 2.1%; Score 128; DB 2; Length 376;
 Best Local Similarity 25.1%; Pred. No. 0.35; Mismatches 123; Indels 150; Gaps 20;
 Matches 99; Conservative 23;

QY 3 RAPCRVRSLLRSYREVLPLATFVRLLGFGQWELVQCGDPAFPAALVAQCLVCVMDA 62
 Db 93 RADRAGRAGSAGARYRI-----LGPAR-----PRGDR-----EWS 125
 QY 63 RPPAPSFROYSCIKELVAVLQPLCRKAXNYLAGFALLDARG-----GPEPAF 115
 Db 126 RLRLAARLATL-----RGAGN-----LRGRKSAARRDAPPAW 161
 QY 116 TTSVRSYLPNTVTDALRSGAMGLLRVGDVLVHLARCALFVLVAPSCAYVCGPPL 175
 Db 162 RRRPRAI-----GRG-----HLRSAL-----AAPVSRDR 191
 QY 176 YQGAATGAPPPHAGGRRLGGER-----AMNSVREGVPLGLPAP 219
 Db 192 HRACAGGRRRP---AGRRRLPRARRVVELDVQRPARRHGHQSHARRAS---GGPAR 245
 QY 220 GARR---RGASASLPLPKRPRRGAPEPRTVGGGSAHP---GSTR---GPSDRGFC 271
 Db 246 RQRGPARGGSGGARARRRRHRRPGRRGPRVAVAPLRGSDRPRASGGRRCFGHGG-- 303
 QY 272 VVSPARPAEATSLGALSGTRHSHPSVGGQHHAGPSTSRPPWDTCPVYAEKHF 331
 Db 304 -----GALAGL---HLALSRHH-----PEFSRPEBDSGAQADARPARADG 341
 QY 332 LYSGGDKQLRPS-----FLSSLRPSL--TGAR 358
 Db 342 VALAGPRVRRPFSAPASFLALHTLAPPVHRTGAQ 376

RESULT 30

G66280
 protein T5E21.13 [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C/Accession: G66280
 R/Chellogis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 aneun, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A/Authors: Hunter, J.B.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A/Reference number: A66141; MUID:21016719; PMID:11130712
 A/Accession: G66280
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-1776 <STO>
 A/Cross-references: UNIPROT:Q9MA20; GB:A0005172; NID:G7527720; PIDN:AAFI3169.1; GSPDB:GNK
 A/Genes: T5E21.13
 A/Map position: 1

Query Match 2.1%; Score 128; DB 2; Length 1776;
 Best Local Similarity 21.8%; Pred. No. 0.33;
 Matches 131; Conservative 63; Mismatches 204; Indels 204; Gaps 33;

QY 252 GQGSNAHPGRRTRGPDSDRGCVVSPAPPAEATSLGALSGTRHSHPSVGRQHH-----G 306
 Db 664 GDGVYGDPSFPGPA-----AFPPPRP-----GVPTVAPLPPLPPQALNLNLRP 706
 QY 307 PSTSRP---PRPWDRP-CPVYAEKHEFLVSSGXDELRLPSFLSSLRPSLTGARLVEIT 363

Db 707 PPSVYFGAARPLGVPMQPMYQQ--HQLSMGPHG--HPSMMMSR--PPQMGVNRV--- 758
 QY 364 IFLGSPKMPGTPRRRLPLPQRYWQMRPLFELGNHQAQPYVLLKTHCPRAAVTPAA 423
 Db 759 -----PPPPGQFSIMQVPPQYQQLPLSMGM-----QPPMAKMP-- 796
 QY 424 GVCAREKPGGSVAAPSEEDTDP--LV---QLRQSSPMQYGFVACTRLV 473
 Db 797 -----PPPPGEAPPLPEEPPEPKRQKLDLSALVPEDQFLACHPG-----AIIIRSK 843
 QY 474 PPGWMSRNERFLNNTKFTS--LG-----KHAISQELTWKNSV 514
 Db 844 P-----NENDQVMEITVQSLSENVSLKEXIAGEMQIPANKQKRNPTVAFERTW--- 893
 QY 515 RDCAMLRBPVGCVAAPAAHRLREI---LAKFLMWSVYV-----VEL 556
 Db 894 -----MKEIETTGPREMPFNLLIQRCGLIDVFTWPKLVVYDALLVFCGIIIEG 949
 QY 557 L-----RSFFVETETFOKNLFY-----RPSWKSLOSIGR----- 590
 Db 950 ILSLQYQWRLNGRFFRLITSREINRMWFYFLKQTRLMKFSMQLPLEAPPTDGK 1009
 QY 591 -----QHL--KRYQAREISEAVRQHRARPALTLRLRFT---PKPDGLRPIYKMD- 637
 Db 1010 LGPLPPSQTLDQVEBEREL-QAEQNNNSLAPPAVAATHRTIGIHPEDD-IRITVEKTA 1067
 QY 638 YVVGARTFEREKRAEHLTGRVALFSLVNERARRPGLIGASVLDGDIHRAMPTFVLRV 697
 Db 1068 QPFSKNGLEFEKRI-----IYSNEKNAFNLKSS---DYHAFYKXKLTLEY 1111
 QY 698 RQAD-----PPPELYFVKVDVTGAYDITP---QDRUTEVIASITKQNTYC 740
 Db 1112 RQNKMGAGOTDSDGTTPQDLDGAADSEAGDTPQLQAFRIPSKPLAEPEEK-YT 1170
 QY 741 VR 742
 Db 1171 VR 1172

RESULT 31

T31425
 C-terminal domain-binding protein ra4, splice form 2 - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T31425
 R:Yuryev, A.; Paturajan, M.; Litingtung, Y.; Joshi, R.V.; Gentile, C.; Gebara, M.; Cord
 Proc. Natl. Acad. Sci. U.S.A. 93, 6975-6980, 1996
 A>Title: The C-terminal domain of the largest subunit of RNA polymerase II interacts with
 A:Reference number: 221024; MUID:96293459; PMID:8692929
 A/Accession: T31425
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1048 <YUR>
 A:Cross-references: UNIPROT:Q63627; EMBL:U49058; NID:g1438535; PID:g1438537; PIDN:AAC526
 A:Experimental source: hippocampus

Query Match 2.1%; Score 127.5; DB 2; Length 1048;
 Best Local Similarity 22.4%; Pred. No. 17; Indels 171; Gaps 25;

Matches 109; Conservative 38; Mismatches 169; Indels 171; Gaps 25;
 QY 8 RAVSRILSRSHYR---EVLPLATFVRRLGPGQWRLVQSGDPAFAFRAL--VAQCLVCPWDA 62
 Db 472 RALQKLSRNGYKVNQKSIKIA-----WAL-NKGIKADFKQYMWELGVYIYIPD- 519
 QY 63 RPPPAAPSRQVSCIKELVARVLQRLCERGAKNVLAFFALLDG----- 106
 Db 520 -----KVVAEELSFCEG-----MLDSDTLNPDKWGIKKKEN 553
 QY 107 --ARGPPEAFTTSVSYLVNTVDALRGSGAMGLLRVGDVDVLVHLALCALFVIVAP 164
 Db 554 EVAQNGGAASHTEVSPKPKV-----PPVPLALPVPALITVPPP 594
 QY 165 SCAYVVCPPYLQDLAATQAPPPPHASGPRRLGGERAMNSVSEAGVPLGLPAPGARRR 224

Db 595 QVPPHOGPPV--VGA---LQPP--AFTP-----FLGIDPPPF-- 625
 QY 225 GGSASRLPLPKRPRGADEPERTVGGQSWAHGRTGSPDRGFCVVSAPPAEATS 284
 Db 626 -GPVPPPPPPPPPPGPGFNMHLDPG--FLPPG-PPPIPLPVISIPPHPTPISIN 680
 QY 285 LEGALSGTRSHSPVGRQNHAGPSTSRPPMDTCCPVYAEKHFILYSSGKGLRPS 344
 Db 681 LVSGARQNASADSAMQYSGAGPPAA-----PISLTPPV--TQVSLITQG---VADG 730
 QY 345 FLISLRPSLTGARRLVETIFLGSRPM-----PGTP-----RLPLRQRYWQMRPLF 394
 Db 731 PVIGLOAPS-----TGLIGRPLGLPLQRPQMPPHLQRFPMMPR--PVPFNM 779
 QY 395 ELIGNAQCPYVULKTHCPRLAAYTPAAGVCAKEKPGSVAP----- 440
 Db 780 -----HRGPPPG-----PGFAMPPPHGMKGPFPFHGPFVRPGMPLGDPGPGGS 827
 QY 441 EDTPPRR 447
 Db 828 EDRDGRQ 834

RESULT 32

S22373
 Prolin-rich protein - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C/Accession: S22373
 R:Dayfield, R.; Bannister, A.J.; Pierce, E.J.; McDonald, C.J.
 Eur. J. Biochem. 204, 591-597, 1992
 A>Title: cDNA clones for mouse parotid proline-rich proteins. mRNA regulation by isopren
 A:Reference number: S22373; MUID:92174915; PMID:1339347
 A/Accession: S22373
 A:Molecule type: mRNA
 A:Residues: 1-260 <LAY>
 A:Cross-references: UNIPROT:Q64306; EMBL:X63004; NID:g53798; PIDN:CAA44733.1; PID:g53799
 C:Superfamily: proline-rich protein

Query Match 2.1%; Score 127; DB 2; Length 260;
 Best Local Similarity 27.1%; Pred. No. 0.27; Indels 60; Gaps 12;

Matches 56; Conservative 18; Mismatches 73; Indels 60; Gaps 12;
 QY 172 GPLVLQGAATQARP-----PHASGPRRLGGERAMNSV-----R 208
 Db 81 GPP--PQGSQQRPPQPGNQGGPPQGGPQ---GPPRFGNQVPPQEGSQQRPPQGNQ 135
 QY 209 EAGVPLGLPAPGAR---RQGSASRLPLPKRPRGADEPERTVGGQSWAHGRTG 264
 Db 136 QGPPPGGPRPRGNGQGGPPQGGPQG-----PSRFGNQGGPPQGGP--QDRPFGNGQG 188
 QY 265 PSDRGFCVVSAPPAEATSLGALSGTRHSHPSVGRQHAGP--STRPPRPMDTPC 321
 Db 189 PPGGGPQGGPQGGPQGNQGGPPQGGPQGP---PRGNGQ--GPPQGGPQGRPPQGNHG 242
 QY 322 PPVYATKHFIVSSGDXQLRPSFILS 348
 Db 243 PPGY-----GNNEQ--PSYLWS 257

RESULT 33

S72273
 actin-depolymerizing protein N-WASP, brain - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 23-Apr-1998 #sequence_revision 01-May-1998 #text_change 09-Jul-2004
 C/Accession: S72273
 R:Miki, H.; Miura, K.; Takenawa, T.
 EMBO J. 15, 5326-5335, 1996
 A>Title: N-WASP, a novel actin-depolymerizing protein, regulates the cortical cytoskeleton
 A:Reference number: S72273; MUID:97050838; PMID:8895577
 A/Accession: S72273
 A>Status: nucleic acid sequence not shown

A: Molecule type: mRNA
 A: Residues: 1-505 <MIK>
 A: Cross-references: UNIPROT:Q95107; EMBL:D67066; NID:g1644231; PIDN:BA11082.1; PID:dl01
 A: Experimental source: brain

Query Match 2.1%; Score 127; DB 2; Length 505;
 Best Local Similarity 24.7%; Pred. No. 0.69; Indels 112; Gaps 14;
 Matches 74; Conservative 17; Mismatches 97

173 PPVYQGAATQAPPPAPASGPRRRRLGGERAMHSVBAAGVPLGLPAPGARRRG----- 226
 279 PPPPSRGPPPPPPPPHSSGP-----PPPPARGGAPPPPS 315
 Db
 227 ---SASLSLPLKPRRRGAPPEPRRTVGGGSMANRGRTGSDRGFCVSPAPAEAT 283
 316 RAPPAAPPPPPSRPGVAPPP-----PPRMVPP-----LPALPS----- 352
 Db
 284 SLEGALSGTRHSHSPVGRQHAGPPSTRPRPMDTPCPVVAETKHFLYSSGDKQLRP 343
 353 ---SAPSGPPPPPPPLSVSGSVAPPPPPPPPPGPPPP-----GLPSGDHQVPTP 402
 Db
 344 ---SFLSSLRPSLTARLVETIFLGSPPMPPGTPRRLLPLPQKRWQKPLFLELGN 399
 403 AGSKYALLDQIR--EQAQ--LKKEVQNSRP-----VSCSGR 434
 Db
 400 HA---QCPYGVTLK--THCP--LRAAVTPAAGVCA-----REKQGSVAAPSEEDPD 444
 435 DALDDQIRQGIQLKSVTDAPESTPPAPAPTSIGVGLMEVQKRSKRIHSDDEDDDD 494

RESULT 34
 T43481
 probable mucin DKFZp434C196.1 - human (fragment)
 N: Alternate names: protein DKFZp434B0635.1
 C: Species: Homo sapiens (man)
 C: Date: 21-Jan-2000 #sequence revision 21-Jan-2000 #text_change 09-Jul-2004
 C: Accession: T43481; T34549; T17264
 R: Koehler, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, December 1999
 A: Reference number: Z22514
 A: Accession: T43481
 A: Molecule type: mRNA
 A: Residues: 1-580 <AAA>
 A: Cross-references: UNIPROT:Q9UF83; EMBL:AL133561; NID:g6599133; PIDN:CAB63715.1; PID:g6
 A: Experimental source: adult testis; clone DKFZp434C196
 R: Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, October 1999
 A: Reference number: Z21540
 A: Accession: T34549
 A: Molecule type: mRNA
 A: Residues: 262-580 <POU>
 A: Cross-references: EMBL:AL12069; NID:g6102864; PIDN:CAB59245.2; PID:g7018420
 A: Experimental source: adult testis; clone DKFZp434B0635
 R: Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, September 1999
 A: Reference number: Z18723
 A: Accession: T17264
 A: Molecule type: mRNA
 A: Residues: 262-580 <POU>
 A: Cross-references: EMBL:AL117481; NID:g5911959; PIDN:CAB5954.1; PID:g5911959
 A: Experimental source: adult testis; clone DKFZp434B061
 C: Genetics
 A: Note: DKFZp434C196.1; DKFZp434B0635.1; DKFZp434B061.1

Query Match 2.1%; Score 127; DB 2; Length 580;
 Best Local Similarity 26.6%; Pred. No. 0.83;
 Matches 74; Conservative 18; Mismatches 110; Indels 76; Gaps 13;

141 LRRGDDVVLHLLARCALFVLVAPSCAYQVCPYLQGAATQARPPPHAS-----GP 133
 52 LTKHESTALLTLTPASL--WRTPTRASLWRTTP-----RASPTPKPPRASPTPSASP 104
 194 RRRIGCERAMHSVBAAGVPLGLPAPGARRGGSASRLPLPKPRRGAAPPEP--RTPVG 252

Db
 105 TRRL-----PRASPM-----GSPHASPRTPTPPASPTGPTASTPTG 142
 Db
 253 QGSWAHPGRT-----RQPSDRGFCVSPAPAEATLSGAL-----SGTRHSHSPV 299
 143 TPSSASPTGTPPPRASPTGTPPRAMATRSSPTASLRTPTSSRASLTRWPPRASPTTPRES 202
 Db
 300 GQGHAGPSS-----TSRPPRPMDPCPPVVAETKHFLYSSGDKQLRPFLSLSLR 351
 203 PRMSHRASPTTPPPRASPTTRKPPRASPTTRTP-----RESLTSRASPTR 248
 Db
 352 --PSLTGARLVETIFLGSRP--WMPGT--PRRLPLPQR 365
 249 MPPRASPTRRPPRASPTGSPPRASPMTPPRASPTTRPR 286

RESULT 35
 A53800
 mixed-lineage protein kinase (EC 2.7.1.-) 3 - human
 N: Alternate names: protein kinase PTK1; protein kinase SPRK
 C: Species: Homo sapiens (man)
 C: Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C: Accession: A53800; I58395
 R: Gallo, K.A.; Marx, M.R.; Scadden, D.T.; Wang, Z.; Gu, Q.; Godowski, P.J.
 J. Biol. Chem. 269, 15092-15100, 1994
 A: Title: Identification and characterization of SPRK, a novel src-homology 3 domain-conte
 A: Reference number: A53800; MUID:94253068; PMID:8195146
 A: Accession: A53800
 A: Status: preliminary
 A: Molecule type: mRNA
 A: Residues: 1-847 <GA>
 A: Cross-references: UNIPROT:Q16584; GB:U07747; NID:g464027; PIDN:AA19647.1; PID:g464028
 R: King, Y.L.; Leung, I.W.; Heng, H.H.; Tsui, L.C.; Lassar, N.J.
 Oncogene 9, 1745-1750, 1994
 A: Title: MLK-3: identification of a widely-expressed protein kinase bearing an SH3 domain
 A: Reference number: I58395; MUID:94239754; PMID:8183572
 A: Accession: I58395
 A: Molecule type: mRNA
 A: Status: preliminary; translated from GB/EMBL/DBJ
 A: Residues: 1-847 <RES>
 A: Cross-references: GB:I32976; NID:g488295; PIDN:AAA59659.1; PID:g488296
 C: Genetics
 A: Gene: GDB:MLK3; PTK1; SPRK
 A: Cross-references: GDB:134755; OMTN:600050
 A: Map position: 11413.1-11413.3
 C: Superfamily: mixed-lineage protein kinase 3; protein kinase homology; SH3 homology
 C: Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific protein ki
 F: 48-100/Domain: SH3 homology <SH3>
 F: 115-383/Domain: protein kinase homology <KIN>
 F: 123-131/Region: protein kinase ATP-binding motif
 F: 403-424/Region: leucine zipper motif
 F: 438-459/Region: leucine zipper motif
 F: 468-482/Region: basic

Query Match 2.1%; Score 127; DB 1; Length 847;
 Best Local Similarity 23.1%; Pred. No. 1.4; Indels 178; Gaps 34;
 Matches 122; Conservative 49; Mismatches 179

44 PAAPALVAGCLVCFWMDARPPAPSPFOV--SCIKELVARYLQL-----CERGAN 95
 348 PEPFAQLMADC-----W-AQDPHRPDDASIIQQLALEAQLTRMPRDSFHSQGWKR 401
 Db
 96 VLAFFALIDGARG-----GPEAFTTSVRSYLNTYTDALRGS-----GAW 137
 402 EIQ--GLPDELRAXEKELISREBELTRAR--QRQAQQLRRREHLLAQELEVFERE 456
 Db
 138 -GLLRRV-----GDDVVLHLLARCALFVLVAPSC-----A 167
 457 LTLILQGVDRPHVRRRGTFKRSKLARODGESISMPLDKRITVQASGLDRRRNV 516
 Db
 168 YQVCGP--PLYQLGAATQAR--PPHASG--PR-----LLGERAMHSVBAAG 211
 517 FEV--GGGDSPTPRFRALQLEPAEFGQAWGROSFRLEDSNGERRAC--WAWGDS----- 569

QY 212 VPLGLPAPGARRRGSGASR-----SLPL-----PKPRRGAPAPERT 249
 Db 570 -----SRPBGACQGRRRSRNDEATWLDSDSPLOSPTPALNPNRPRLBEPBPK 625
 QY 250 PVQGSMAHPDRTGSDRGFCVSP---ARPAEATSLGALSGTRHSPVSGQHAG 306
 Db 626 PV-----PAERGSSSGTPEKLTORALLRGTALLAGLGRDLPQPGCGRERG 672
 QY 307 PSTSSPPRPMDTRPCP---PYAETKHFLLSSGDKQEGRLSPFLSSL-----RSLTGAR 359
 Db 673 ESETT-PPPTTPAPCTBEPSPFLICSLKTPDSP-TPAPLLDLGIVGQSRSAKSPR 730
 QY 360 LVE-----TFLGSRPMPGCTPRRLPRLPQRYWQMRPLELLGNHACPYVLKTH-CP 414
 Db 731 EEPFRGTV---SP-PCGTSRGAFCGP-----GTPRSPGLISRPSP 771
 QY 415 LRANVPAGVCAREKPGQSVAPAEEDDPRLVQLRGHSPQVY 462
 Db 772 LRSRIDPMSFVSAGPRP-SPLSPQPA---PRR-----APWTLF 806

RESULT 36

T46289
 hypothetical protein DKFZp434A1010.1 - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #ext_change 09-Jul-2004
 C/Accession: T46289
 R/Duesterhoef, A.; Lamber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, January 2000
 A/Reference number: Z23035
 A/Accession: T46289
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-862 <AAA>
 A/Cross-references: UNIPROT:Q9NT23; EMBL:AL137579
 A/Experimental source: adult testis; clone DKFZp434A1010
 C/Genetics:
 A/Note: DKFZp434A1010.1

Query Match 2.1%; Score 127; DB 2; Length 862;
 Best Local Similarity 21.8%; Pred. No. 1.4;
 Matches 102; Conservative 28; Mismatches 147; Indels 190; Gaps 23;

QY 43 DPAAPFALVAQCLVCPMDARPP-----PAASTFQV 74
 Db 316 DPTTR-----CSSPFGDPAFPASBPAPASAPFPRTPOAISPRGTPSPASPAIDI 370
 QY 75 SCUKELVARVQLRCERGAQNVLAFGFALLDGARGPPEAFTTSV-----RSYLPYTVTDA 130
 Db 371 S--EPLAVSVPAVLE-----LLGAGAPASATPTPALSPGRSLRPHLLPL 415
 QY 131 LSGSGMGILLRRVGDVIVHLARCALFVAVSCAIVCG----- 172
 Db 416 LKGAEE-----PLTDCCQDEMCKLKGAGQPLGPMWESPLP 451
 QY 173 -PPLYOL--GAATARPAPHASGPRRLG--CERAMHNSVREA-----GVPLGLPARGA 221
 Db 452 PPPLSLRRGGA-----PPPPKPNPARIMALAAHAAQVABQSGQEGCGTPPASQSPFH 507
 QY 222 RRRGSASASLPLPKRP--RRGAAPPEPTPYGQSWAHPG----- 260
 Db 508 R-----SLSTVEGEPPLCTSGSGPP-----NSLHAPGAWVGPFPYLRQOSDGL 554
 QY 261 ----RTRGSDRGFCVSPAPAEATSLGALSGTRHSPVSGQHAGPSTSRP-- 314
 Db 555 LRSQPMGSRKGL-----RGPAQVSAQURA--GGGAGDAEPAALAAQSCVSPQVPTPGF 607
 QY 315 -RPWDTPC-PPVYATKHFLLSSGDKQELRSPFLLSLRPSLTGARRLVETIFLGSRRWM 372
 Db 608 FSPAPRECIPLPLGVKPGIYPLGP-----PSFGSSAP-----VVR 645
 QY 373 P--GTPRRRLRPLQRYWQMRPLELLGNHACCPYVLKTHCPURA 417

Db 646 SSLGPAPALDRNGENLYE-----IGASEGSPYSLTMSWSPFRS 684

RESULT 37

T35878
 hypothetical protein SC9B10.09 - Streptomyces coelicolor
 C/Species: Streptomyces coelicolor
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #ext_change 09-Jul-2004
 C/Accession: T35878
 R/Oliver, K.; Harris, D.; Parkhill, J.; Barrett, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, November 1997
 A/Reference number: Z21592
 A/Accession: T35878
 A/Status: preliminary; translated from GB/EMBL/DDJ
 A/Molecule type: DNA
 A/Residues: 1-1039 <OLI>
 A/Cross-references: UNIPROT:O50516; EMBL:AL009204; PIDN:CAAL5799.1; GSPDB:GN00070; SCODE
 A/Experimental source: strain A3(2)
 C/Genetics:
 A/Gene: SCODEB:SC9B10.09

Query Match 2.1%; Score 127; DB 2; Length 1039;
 Best Local Similarity 26.1%; Pred. No. 1.9; Indels 80; Gaps 16;
 Matches 89; Conservative 26; Mismatches 146;

QY 4 APRCAVRSLLRSHREVLEPLATFVARLPGQGRVLYQGDPAFRAVLAQCLVCPMDAR 63
 Db 462 APQCHAVRAR-----LPHATVSALLRQAG---VIRVD--TITDLVAGLLLA---RO 506
 QY 64 PPPAPSFQVSCUKELVARVQLRCERGAQNVLAFGFALLDGARGPPEAFTTSVRS-- 121
 Db 507 PLPAPPRVALIGNSESL-----GLTYDACISGLRPOPLDTTASAD 552
 QY 122 ----YLPNTYDAL-----RSGAWGLLRVGDVIVHLARCALFVAVPSCA 167
 Db 553 FHAAALRALADTCDVAVVTAIPTLGEA-----AGDAALAEALRSAAAAPPTPVLY 605
 QY 168 YQVCGPEPLYLGATQARPAPHASGPRRLG--CERAMHNSVREAGVPLGLPA--PGAR 222
 Db 606 VHV-----ELGIALBALSAASTAPQTAQGTAAQAEGRASRAASAAIPADPDVAV 659
 QY 223 RRGASASRLPLPKRRRGAPPEPTPYGQSWAHPGTRGSDRGFCVSPAPAEBA 282
 Db 660 RRG-----TSGASASGAPASGATP-GTAPHAP--GPAQD--LPSGASGSPGP 703
 QY 283 TSLEGALSGTRHSPVSGQHAGPSTSRPPAPMDTPCP 323
 Db 704 SCPSGSPGSPGSPGSPS-GPSGSPGSPGSPGSPRPSAPGRP 743

RESULT 38

H75272
 probable nucleic acid-binding protein, HRDC family - Deinococcus radiodurans (strain R1)
 C/Species: Deinococcus radiodurans
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #ext_change 09-Jul-2004
 C/Accession: H75272
 R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M., Shen, M.; Vamathevan, J.U.; Lam, P.; McDonald, L.; Uitterlinden, T.; Zalewski, C.; Ma
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A/Reference number: A75250; MUID:20036896; PMID:10567266
 A/Accession: H75272
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-603 <HNT>
 A/Cross-references: UNIPROT:Q9RP4; GB:AE002074; GB:AE000513; NID:G6460357; PIDN:AAFI1987
 A/Experimental source: strain R1
 C/Genetics:
 A/Gene: DR2444
 A/Map position: 1

Query Match 2.1%; Score 126.5; DB 2; Length 603;
 Best Local Similarity 25.0%; Pred. No. 0.95;
 Matches 131; Conservative 39; Mismatches 184; Indels 171; Gaps 32;

QY 37 RLNVQ---RGDPAFRALVAQCLVQVWMDARPPPAAPSPQVSC-LKELVARYLQRLCER 91
 DB 12 RLVLGHAERGDPPGRLLAALAALEDTEWGLLAGBALAQALALGPGLRVDRGL-DV 70
 QY 92 GAKNVLAFGALDD-----GARG---GPPPAFTTSVRSYLVNTYTDALRSAGGAGLL 140
 DB 71 GRALLAAGALVADLHGLDLAGARAVWLEBPRAAVERARAGRVATDATALAGGGM--- 127
 QY 141 LRRVGDVVLVHLARCAFLVAPSCAYQCGPLVQLGAA-TQARPPH-----189
 DB 128 -PRGADYVYVRNAVITLGHADAPLAA-----LFGSGTAPTPPAAPPSDLVALALND 179
 QY 190 -ASGPRR-----RLGGERAMNHSVRAGVPLGLPAPGA---RRRG-8A 228
 DB 180 VALPLRLAFARATATQTLTRLGA-----SVRQAGFTALLLPDSADTPAQIGVLA 213
 QY 229 SRSLP-----LPRRRGAAPPEPRTVGGSNMHPGRTGSPDRGF 270
 DB 234 ARHVFDGLLTPGLEDEBOVLGLRDQP---ARRQQRASGGGESAQC-REGQORDER 287
 QY 271 CVVSPAPAEATSLLEGALSGTRSHSPSVGRQHNAGPPSTSRPPRMDTPCPVVAETKH 330
 DB 288 -QRVEDRPRDNA---EGRAPADREDRPERRSEQVSRPERSRDRPREDR---FRDDR 339
 QY 331 FLVSSGKEQLRPSFLSSLRPSLTGARLVETIFLGSRPMWGTPTPRRLPRL---PQRY 386
 DB 340 ---REGRRDRFRBS-EGPDRPTKTER-----RQDAAPAELEERFTFEAPQA 384
 QY 387 ---WQMRPLFLELLGNHAQCPYGLKTHC-----PL-----415
 DB 385 PASEEDLPWEPELVF---SDHA--PQNVPL-THVSSGSDAPPLPTPLTLEADA 437
 QY 416 ---RAAVTPAAGVCARE-----KQGSVAAPDEEDTPR 446
 DB 438 GDAAGQTPAELFEVHAAPVSSAQTFEPQ--VEAPEPAEPQ 480

RESULT 39
 E98119
 Transposase, uncharacterized, truncation [Imported] - Streptococcus pneumoniae (strain R
 C:Species: Streptococcus pneumoniae
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C:Accession: E98119
 R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; E
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.U.; Lu, U.; Matsushima, P.; Mcahren, S.; M
 y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain Re.
 A:Reference number: A97872; MUID:21429245; PMID:11544234
 A:Accession: E98119
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-330 <KUR>
 A:Cross-references: UNIPROT:Q8DN10; GB:AE007317; PIDN:AL00786.1; PID:GL5459687; GSPDB:G
 C:Genetics:
 A:Gene: transposase H

Query Match 2.1%; Score 126; DB 2; Length 330;
 Best Local Similarity 21.8%; Pred. No. 0.45;
 Matches 46; Conservative 29; Mismatches 62; Indels 74; Gaps 4;

QY 707 YFVAVDTGAVDTIPQDRLTEVIAIKPONTYCVRRYAVYQKAHGVAKAFKSHVSTL 766
 DB 39 WIVDIDLEKFPDIPQDRIMSLVNIITEDGT-----70
 QY 767 TDLQPNKQVVAHLQETSPLRDAAVVIQSSSLNASSGLFDVPLRMCHAVNIRKSYI 826
 DB 71 -----ESLRKYLHSGVILINGQRYK 90

QY 827 QCGIPQGSISTLLCSLCYGDMEKLFAGIRBDL-LRLVDDPLVTPH:THAKTFLR 885
 DB 91 TLVGTPOGNSLPLLSN-----MUNELEKEKRLRFVYAADCVITVSEAAKRMV 146
 QY 886 TLVRGVPY-YGCVVNLKRTVVNFPVEDEALG 915
 DB 147 SVSRFIEKRLGLKVMMTKTKITRRELKYL 177

RESULT 40
 T43556
 Wiskott-Aldrich syndrome protein homolog - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T43556
 R:Zankel, T.C.; Ow, D.W.
 submitted to the EMBL Data Library, December 1997
 A:Description: A Wiskott-Aldrich Syndrome protein homolog in Schizosaccharomyces pombe,
 A:Reference number: 222575
 A:Accession: T43556
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-574 <ZAN>
 A:Cross-references: UNIPROT:O36027; EMBL:AF038575; PIDN:AAB92587.1
 A:Experimental source: strain JS21
 C:Genetics:
 A:Gene: wsp1
 A:Map position: I
 A:Introns: 72/3; 519/3; 564/1

Query Match 2.1%; Score 125.5; DB 2; Length 574;
 Best Local Similarity 25.7%; Pred. No. 1;
 Matches 72; Conservative 16; Mismatches 107; Indels 85; Gaps 12;

QY 173 PLYQLGATQA---RPPHAGSPRRRLGGERAMNHSVRAGVPLGLPAGARRGSA 228
 DB 294 PSSRSVSAALAAANKRRPPPPPPRRNRGKPPICNGSSNSLPP---PPPPR---SNA 347
 QY 229 SRSLLPFRPRGAAPPEPRTFVGGSWAHPGRTGSPDRGFCVVSPAPAEATSLGGA 288
 DB 348 AGSILPFPQGSAPPPPPR-----SAPSTGRQPPPLSSSRANSPAPP-----392
 QY 289 LSGTRHSHPSV-GROHAGPP---STSRPPRMDTPCPVVAETKHFLLYSSGDKQLR 342
 DB 393 ---PAIPGRAPALPPLGNASRTSTPPVPPLP-----SA 427
 QY 343 PSFLLSLRPSLTGARLVETIFLGSRPMWGTPTPRRLPQRYWQMPLELLGNHAQ 402
 DB 428 PPSLPPSAPPPLP-----MGA-PAPPLPSSAIIAP-----PL-----459
 QY 403 CPYGLLTKHCPRLAAVTPAAGVCAREKPGQSVAAPEED 442
 DB 460 -PAGMPAAPPLPPAPAPPAPAPAPAPVASIALPQOD 498

Search completed: December 20, 2004, 16:01:06
 Job time : 40 secs

This Page Blank (uspto)